

Sol Newsletter



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Community News

Plant Breeding and Genomics Focus of New National Web Resource

As global food needs increase, so does the need for crops that can be efficiently and safely produced. Traditional plant breeding methods have served well in the past and breakthrough technologies are now available to aid this process. These breakthroughs include key information on the genetics, or "genomes" of crops. A group of researchers and educators from America's land-grant universities, government agencies and industry, have banded together to create the first-ever internet resource aimed at quickly putting basic research on crop genomes into practice through plant breeding programs across the U.S. to more efficiently improve crops. The resource is a new online community housed at eXtension (pronounced E-extension), www.extension.org, at the www.extension.org/plant_breeding_genomics.

eXtension Resource Areas

The researchers and educators working on this project are what the new national U.S. Cooperative Extension System project calls an eXtension Web Community. This group, the Plant Breeding and Genomics (PB&G) community of practice, is one of many within eXtension. Other communities in eXtension include geospatial technology; corn and soybean production; cotton production; horticulture; pest management; science, engineering and technology for youth; organic agriculture; bee health and more. There are currently 37 published resource areas. Each community continues adding new information on a regular basis. New communities are also being added every month.

Putting Research into Practice

Development of crop varieties through plant breeding has traditionally focused on selection of the best plant lines based on traits (phenotypes). In the past decade, research has yielded extensive databases of gene sequences and of the complete genetic makeup (genomes) of entire plants. As sequencing technology improves, available information to aide in crop improvement is expanding rapidly. This basic research information is utilized when linking important agricultural traits to genetic sequence variations and incorporating this knowledge into crop improvement strategies.

David Francis, associate professor at The Ohio State University noted, "The eXtension portal provides an entry point into the research knowledge of the Land-Grant University System. We've developed a resource to help train the next generation of plant breeders, help current professionals keep abreast of new developments, as well as inform growers and processors about the technological advances that bring them new varieties."

In 2009 the international community was still working to complete the first draft of the tomato genome sequence, in 2010 two draft sequences became public. The research community expects as many as 100 Solanaceae genomes to be available within the next year or two. This complements whole genome sequences already known in key crops such as potato, rice, poplar, soybean, maize, cotton and cucumber to mention a few. David Francis explained, "This information explosion means that practitioners need resources for continuing education to keep up with new developments."

Dave Douches, a Michigan State University potato breeder, and leader of the Solanaceae Coordinated Agricultural Project (SolCAP) highlighted the need for this eXtension outreach effort, "SolCAP developed over 5.7 GB of sequence data for three potato varieties, we mined this data for genetic differences and developed a tool that allows breeders and their support crews to quickly survey breeding populations for 8,300 genetic differences. The outreach material will help the breeding community make better use of genetic information and will increase the likelihood that plant breeding will benefit from genotype-based selection processes."

Allen Van Deynze, director of research for the Seed Biotechnology Center at the University of California, Davis emphasized the importance of accessibility to information, "The goal of the Plant Breeding and Genomics resource on eXtension is to act as a portal to the vast number of public databases in crops and genetic and genomic resources."

Resource for Agricultural Producers

Another important function of the eXtension site will be to provide up to date production information on new varieties available to agricultural producers. Members of the barley Coordinated Agricultural Project (Barley CAP) provided a template for this goal by including information on barley production practices and other basic barley information needed by barley producers and growers.

Gary Muehlbauer, professor at the University of Minnesota and lead PI of the Barley Coordinated Agricultural Project (CAP), emphasizes that "providing helpful information on barley improvement efforts is a central goal of eXtension and CAPs". He states that the barley grower site on eXtension "highlights information available for growers regarding planting and production of existing varieties, as well as those improved through the genomics and breeding efforts of Barley CAP research".

An example of information provided for producers and plant breeders alike is the Barley CAP-produced podcast on the threat of a new rust virus. Barley, like all crops, is attacked by disease-causing organisms. One potential threat, which can dramatically reduce yield and quality, is the fungus, Ug99, first detected in Uganda in 1999. "Although Ug99 is not yet confirmed in the U.S., this highly virulent strain is spreading in Africa and to the Middle East and will ultimately come to the U.S." Brian Steffenson, plant pathologist at the University of Minnesota, points out. He states "what concerns barley researchers and growers is that most U.S. varieties are susceptible to the fungus".

Barley CAP researchers, partnering with the USDA-ARS Ug99 Cereal Rust Initiative, screened over 2000 U.S. breeding lines in Africa, identified Ug99 resistance in several advanced barley lines and were able to find molecular markers associated with the resistance. Leading this study, Steffenson shares that, "the genomics efforts of Barley CAP made it possible to identify the genes responsible for resistance and develop the tools that will dramatically accelerate breeders' efforts to develop stem rust-resistant barley varieties for growers".

Contributors

Experienced researchers and extension personnel in the United States contributed to the new site. The effort is led by SolCAP, a USDA National Institute of Food and Agriculture (NIFA)-funded program focused on potato and tomato. SolCAP recruited a community of experts from a wider range of Coordinated Agricultural Projects (CAP). The Barley CAP, another ongoing CAP project, played a pivotal role in organizing a template for other groups to develop information pages geared toward growers' needs. Other educational information in the CAP eXtension materials included those developed by Wheat CAP and Rosaceae CAP (RosBREED). The PBG community currently has 195 members who represent 30 universities and federal agencies, 11 educational institutions outside of the USA, and 5 industry groups. Over forty individuals representing 15 universities and agencies have directly written, edited, and reviewed the content, which includes articles, videos, and tutorials. Content continues to be written and updated, with new information to be published monthly.

Terry Meisenbach, a Communications and Marketing expert with eXtension explained, "eXtension is a direct response to concerns about information quality on the Internet. Users can access eXtension with the same confidence they access their own state extension networks."

eXtension is an educational partnership of more than 70 land grant universities helping Americans improve their lives with access to timely, objective, research-based information and educational opportunities. eXtension's interactive Web site is customized with links to local Cooperative Extension sites. Land-grant universities were founded on the ideals that higher education should be accessible to all, that universities should teach liberal and practical subjects and share knowledge with people throughout their states. *eXtension* is an educational resource designed to help people acquire skills and knowledge to help them grow and empower them to improve their quality of life. eXtension takes the best university-based research and turns it into practical information people can use to solve today's problems and develop skills to build a better future.

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Resources

New Plant Breeding and Genomics Web Resource Available!

A group of researchers and educators from U.S. land-grant universities, government agencies and industry have created the first internet resource aimed at quickly putting basic research on crop genomes on the web to support plant breeding programs. The resource is new at eXtension (pronounced E-extension), <http://www.extension.org> and can be found at <http://www.extension.org/plant-breeding-genomics>.

This resource is for students and professionals involved with plant breeding, and for agricultural producers who utilize the new varieties resulting from traditional and emerging plant breeding methods. This is a growing collection of educational information,

collaboratively authored and reviewed by our community of researchers, educators, and eXtension personnel who have experience and expertise in plant breeding and genomics topics and crop production topics.

The Goals of the Plant Breeding and Genomics Resource

Help put genomics research and tools into practice through plant breeding by:

- Presenting unbiased science-based information in a variety of media formats
- Sharing the most current, relevant, and accurate information available on techniques, procedures, and bioinformatics software
- Being a reliable resource that is responsive to the changing needs of the plant breeding industry and agricultural producers
- Fostering collaboration among members of the plant breeding and genomics community

Plant Breeding and Genomics Tools You Can Use

Feature Articles: Our feature articles keep you up to date in this rapidly emerging field and cover everything from the basics of population development and molecular markers to the latest plant breeding and genomics research and technologies and crop production information.

Tutorials: Our tutorials, in the form of webinars, interactive animations, and self-paced lessons, walk you through the details of how to make use of plant breeding and genomics research and resources in your breeding program.

Aggregation: Partnering with other educational efforts, our experts have organized links to other excellent genomics, plant breeding and agricultural production resources.

Ask an Expert: eXtension's Ask an Expert tool allows you to submit specific questions to the community's plant breeding and genomics experts.

As eXtension and its plant breeding and genomics community grow, our content will grow. Look for additional opportunities to connect with other plant breeders and service providers.

Contact Us

Please join us! If you have experience and expertise in plant breeding and genomics or crop production and would like to be a part of our community, create an account with eXtension and indicate your interest in joining our plant breeding and genomics community at <https://people.extension.org>.

KaPPA-View4 SOL: a pathway tool for gene co-expression and metabolite co-accumulation analysis of Solanaceae plants

By Nozomu Sakurai and Daisuke Shibata (Kazusa DNA Research Institute)

To accelerate the functional genomics in tomato and Solanaceae species, we set up a web-based metabolic pathway tool, KaPPA-View4 SOL (<http://kpv.kazusa.or.jp/kpv4-sol>). It is unique that the KaPPA-View system has a function to overlay relationships of gene co-expression and/or metabolite co-accumulation on the metabolic pathway maps, helping researchers to hypothesize novel regulatory mechanisms of metabolism [1]. We utilize the SGN unigenes of Solanaceae and related species to assign them on the metabolic pathway maps of Kyoto Encyclopedia of Genes and Genomes (KEGG). The viewer has a gene co-expression dataset of tomato from the tomato database MiBASE (<http://www.pgb.kazusa.or.jp/mibase/>) [2], and also accepts user's correlation datasets. Furthermore, users can view the microarray data deposited in MiBASE, which already utilizes the Application Programming Interface (API) for the KaPPA-View4 system. Please visit MiBASE to perform the viewing of the 50 microarray datasets (currently, the data are viewed on the classic, but not KEGG maps of the KaPPA-View4) [3]. The microarray datasets in SGN will be viewed through the KaPPA-View, when the API is adapted to SGN. The system complements the SolCyc function in the unique manners mentioned above. We welcome your suggestions to the KaPPA-View4 SOL.

[1] Sakurai N et al (2011) Nucleic Acids Research 39: D677-684

[2] Yano K et al (2006) Plant Biotechnology 23: 195-198

[3] Click the "view" links of the "KaPPA" column in the list of microarray datasets at http://www.pgb.kazusa.or.jp/mibase/geo_exp.php?clone=LesAffx.65757.1.S1_at

Highlight Article

***Solanum tuberosum* (+) *S. pinnatisectum* somatic hybrids: a new source of horizontal resistance to potato late blight in India**

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Late blight caused by the oomycete *Phytophthora infestans* is the most important disease of potato in India. It may cause losses up to 85% in the hills and up to 60-70% in the plains of India. Conditions for late blight remain conducive throughout the crop season in hills and frequently in plains. In India, all the present-day potato cultivars have a very narrow genetic base (Gopal and Oyama, 2005). Indian potato varieties mainly have the major *R* genes providing vertical resistance to late blight. This resistance has broken down with the appearance of complex races. For example, cv. Kufri Jyoti once resistant to late blight is now highly susceptible. Therefore, race non-specific resistance or horizontal resistance to late blight is now being favored for variety development programs in India.

The horizontal resistance for late blight has been found in several wild potato species. Hence, gene introgression from wild sources into cultivated potato is inevitable to develop late blight resistant potato genotypes. But many sources of useful genes cannot be included through a conventional breeding program primarily because of sexual incompatibilities due to a difference in ploidy and endosperm balance number (EBN) (Spooner and Salas, 2006; Gopal, 2006).

S. pinnatisectum, a diploid ($2n = 2x = 24$, 1 EBN) Mexican wild tuber-bearing species has resistance to late blight (*Phytophthora infestans* (Mont.) de Bary) as well as to soft rot (*Erwinia carotovora* ssp. *carotovora* (Jones) Bergéy et al. and tolerance to heat and drought (Hawkes, 1994). We used this wild species for somatic hybridization with an androgenic dihaploid C-13 ($2n = 2x = 24$) of *S. tuberosum* L. cv. Kufri Chipsona 2. Protoplast isolation and fusion were carried out following a protocol described by Binding et al. (1978). The somatic hybrids were confirmed using random amplified polymorphic DNA (RAPD), and simple sequence repeat (SSR) (Ghislain et al., 2009) markers. Ploidy status of the hybrids was confirmed by flow cytometry (Arumuganathan and Earle, 1991).

Twelve confirmed tetraploid somatic hybrid plants were screened for late blight resistance in the field under epiphytotic conditions of Shimla hill (mid-Himalayas) of India. Late blight reaction was scored thrice during the crop season. Based on the AUDPC (area under disease progressive curve) the somatic hybrids were found to be highly resistant to late blight as compared to the susceptible control Kufri Jyoti (Fig. 1). Important morphological characteristics of the parents and somatic hybrids are shown in Fig. 2. These somatic hybrids are pollen fertile and thus can be used in a potato breeding program for developing improved late blight resistant cultivars. To our knowledge, this is the first report of production of interspecific potato somatic hybrids for late blight resistance in India.



Fig. 1 Late blight resistant somatic hybrids (right) and susceptible control Kufri Jyoti (left).

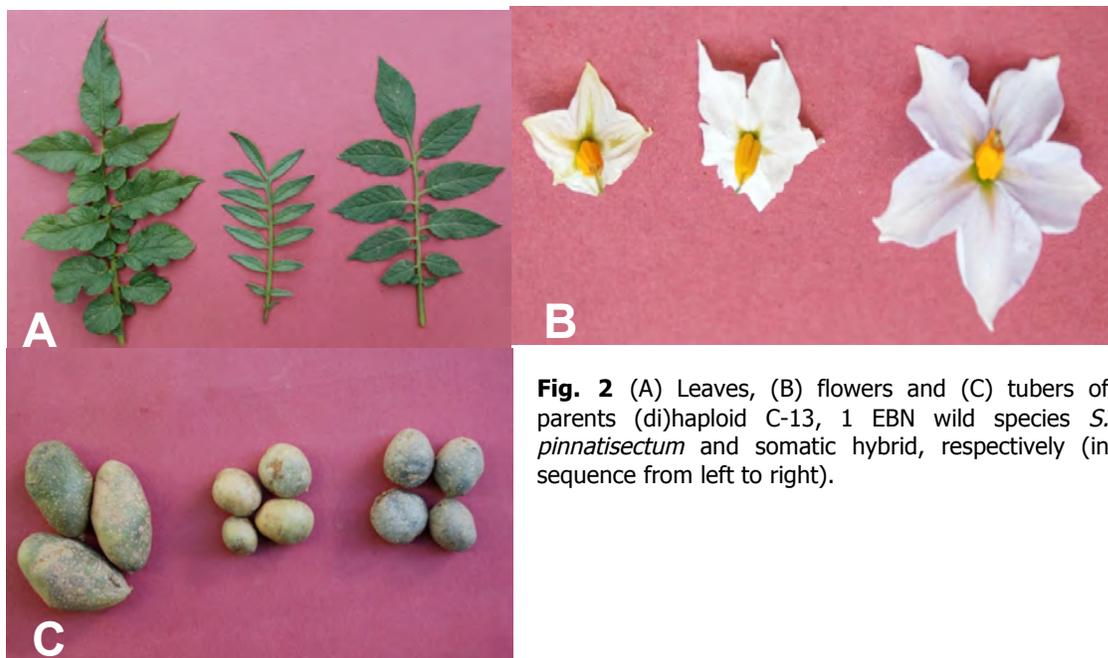


Fig. 2 (A) Leaves, (B) flowers and (C) tubers of parents (di)haploid C-13, 1 EBN wild species *S. pinnatisectum* and somatic hybrid, respectively (in sequence from left to right).

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Genome Updates

Coffee

Contact: Marco Aurelio Cristancho (Marco.Cristancho@cafedecolombia.com), Cenicafe-FNC, Colombia

The main cultivated coffee species *Coffea arabica* is a tetraploid and as such the assembly of its genome is more challenging than for diploid species. For this reason, its two progenitor species, *C. canephora* and *C. eugenioides* are being sequenced first by two independent consortia.

The progress of the *C. canephora* genome sequencing was presented during the Coffee Genomics workshop that took place at PAG 2011.

Research centers from France, Brazil, USA, India, Italy, Australia and Canada are combining their scientific resources and expertise to sequence, assemble, and annotate the entire genome of *C. canephora*. The *C. canephora* genome consists of 11 chromosomes, is about 710 Mb in size, and is being sequenced de novo with deep coverage using 454 paired-end and single reads, and 50x coverage with Illumina GAIIX data to obtain a reference genome for Coffee. The overall sequencing strategy as well as progress of the project was discussed in the workshop. Data of the first draft of the assembly should be available at the end of 2011.

The genome of the species *C. eugenioides* will be sequenced by a project led by CENICAFE and Cornell, on behalf of the International Coffee Genomics Network (ICGN), and partially financed by the InterAmerican Development Bank (FONTAGRO). The de novo sequence of the *C. eugenioides* genome will be started in 2011 by using a combination of 454 and Illumina technologies. Once completed, the high coverage reference sequences for the diploid species *C. canephora* and *C. eugenioides* should serve as a solid framework for future sequencing and assembly of the genome of the allotetraploid species *C. arabica*.

In reference to coffee transcriptomics data, the Brazilian Coffee Genome Consortium published a set of EST sequences in GenBank in November 2010. The EST set included 65,161 sequences from the species *C. arabica*, 12,834 sequences from the species *C. canephora* and 17 sequences from the species *C. eugenioides*. As of February 2001, there is a total of 108,725 *C. arabica* EST sequences and 56,231 *C. canephora* sequences published in dbEST.

Petunia

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The Petunia Genome Sequencing Project is on the road!

Garden petunias have been cultivated for around 150 years and especially over the last 50 years the system has developed into what we consider to be a fully fledged research model system (for an overview, see Gerats and Vandebussche, see TiPS 10: 251, 2005). Two developments, not considered in this note, concern the elucidation of the transcriptome (in progress) and the creation of a large 'insertome' library, which will harbor over 100,000 transposon-flanking sequence tags (in progress; see also Vandebussche et al, TPJ 54:1105, 2008); both will foster from the project, that we briefly describe below.

It is accepted already for a long time that the origin of the classical cultivars is to be found in interspecific crosses between the white-flowered *Petunia axillaris* and the purple flowering *P. inflata*. It's for these founding fathers and mothers that we could sign an agreement to perform a sequence analysis of the entire genome for both species. The project is carried out in cooperation with the Beijing Genomics Institute-Hong Kong, and the so called PetuniaPlatform <http://www.petuniaplatform.net> in which most of the groups that use Petunia as a research system are united.

Projections are that by mid 2011 sequencing and raw assembly will be ready for both species and these data will be made public upon publication of the first major paper. Members of the Platform that contributed financially to the project get early access (you can still become a Contributing Member!). All analyses will ultimately be made public via SOL/SGN.

Adding the genome sequences to the already available assets further completes our system and now that sequencing no longer is the major stumbling block, more emphasis can be put upon other characteristics: established record, transformation efficiency, transcriptome, insertome and even further down: easy cultivation, good seed set, and last but not least an open-minded platform with regular meetings, full of exchanges on every level. We're looking forward to sharing the sequence with all of you!

Tobacco

Construction of tobacco physical map using Whole Genome Profiling

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Tobacco (*Nicotiana tabacum*) is an important agricultural crop and a model plant organism harboring ~4.5 Gb of genomic DNA. It belongs to the Solanaceae family, which also includes important crops such as *Solanum lycopersicum* (tomato) and *Solanum tuberosum* (potato). To date, 425,088 BACs clones from three libraries made with *HindIII*, *BamHI* and *EcoRI* enzymes from the allotetraploid genome of *Nicotiana tabacum* cv. Hicks Broadleaf have passed quality testing with the objective to build a physical map. They represent a 10.4X coverage and have an average size of 100 kb. To construct high quality sequence-based physical maps of tobacco, we have used the new cost-effective Whole Genome Profiling (WGP) method developed by KeyGene.

Using the Illumina Genome Analyzer II, WGP maps were assembled by sequence-based fingerprinting of BAC libraries. BACs were ordered into contigs at two different stringency levels and three different tag lengths using an adapted version of the Finger Printed Contigs (FPC) software capable of processing sequence-based BAC fingerprint (WGP) data instead of fragment mobility information as used in the original FPC software. To date, the resulting tobacco physical maps have between 9,750 and 12,720 contigs containing between 293,000 and 330,000 BACs, representing from 69 to 78% of BACs tested. The N_{50} contig sizes are larger than 530 Kb and the calculated genome coverage is >4,500 Mb. The tobacco WGP maps will serve as an essential scaffold to anchor and order DNA sequences to yield a draft sequence of the tobacco genome.

Keygene N.V. holds patents and patent applications covering its Whole Genome Profiling technology.

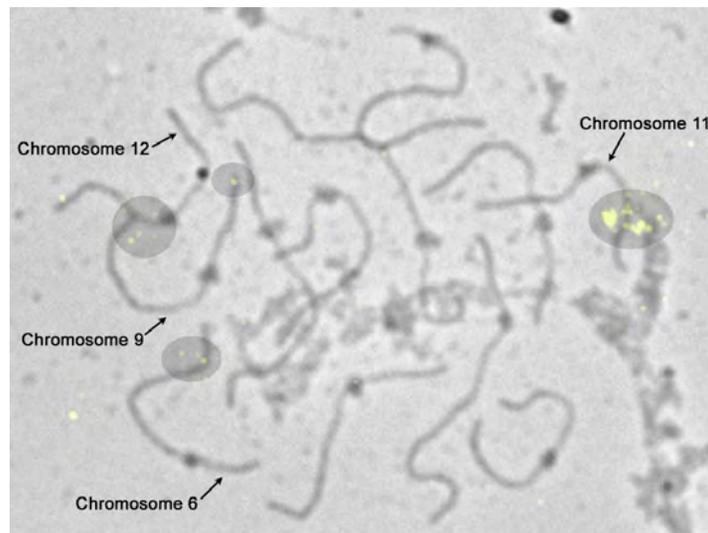
Tomato

Contact: Joyce Van Eck (jv27@cornell.edu), The Boyce Thompson Institute, Ithaca, NY

The latest developments on the international tomato genome project since the last Sol Newsletter in October 2010 involve efforts related to assembly and annotation. Assembly version 2.31 was released in November 2010 and version 2.4 was released in January 2011. These versions are accessible from the SOL Genomics Network (<http://solgenomics.net/>).

A total of 323 BACs have now been localized by the Stack lab at Colorado State University using FISH on pachytene synaptonemal complex spreads. This total includes 23 BACs added since the last SOL newsletter. These new BACs (all from the HindIII library unless otherwise noted), listed by chromosome arm, are: 1P - 027P13, 081I16, SL_MboI0081L19; 1Q - 061J17, 100N21, 164D24, SL_EcoRI0127B04, 305L18, 006D05; 3Q - 077H15; 4P - 008K08; 4Q - 203K18; 5P - 255N21; 5Q - 164O03, 006D05; 6P - SL_MboI0081L19; 6Q - 081D06, SL_MboI0030C09; 10P - 036L10, SL_EcoRI0040D01, SL_MboI0020C04; 10Q - 044H12, 045L17, 114B06; 11Q - 187P23, 305L18. Three BACs in this group each hybridized at two loci: 05L18 (1Q and 11Q), 006D05 (1Q and 5Q) and SL_MboI0081L19 (1P and 6P). The underlined BACs are currently listed as unmapped on the SOL Genomics Network website. The 323 localized BACs are distributed at 331 loci among the chromosomes as follows: 1 – 89; 2 – 22; 3 – 22; 4 – 22; 5 – 18; 6 – 14; 7 – 32; 8 – 9; 9 – 23; 10 – 42, 11 – 19, 12 – 19. The total number of loci reflects the fact that there are now eight BACs that have each been localized to two positions.

The Stack lab has also been using mitochondrial DNA (provided by Fernando Carrari of the Instituto de Biotecnologia in Buenos Aires, Argentina) as a probe in FISH experiments aimed at locating insertion sites of mitochondrial DNA within the tomato genome. Four such sites (shown in the photo below) were located using FISH, including a very large locus on 11Q and smaller loci on 6Q, 9P, and 12Q. Other insertion loci are probably present but have not been consistently demonstrated with our FISH technique.



SGN News (<http://solgenomics.net/>)

In the last few months, SGN has added several new datasets and made improvements to the website and tools. Here we present a short overview of the most recent additions.

Maps and markers

Three new maps have been added to SGN and are available in the comparative map viewer (<http://solgenomics.net/cview/>):

- *Solanum phureja* diploid map, with 2,530 markers, submitted by Dan Bolser

- Maps of two *Nicotiana* species, submitted by Feinan Wu
- Maps of two F2 tomato populations, and an integrated map generated from the two, submitted by David Francis

In addition, we will release the Kazusa F2-2000 map shortly, on which the genome assembly is based, submitted by Shusei Sato. We are also excited about a potato consensus map that shows several dozen QTLs for plant resistance and maturity, submitted by Véronique Lefebvre. Both maps will be available shortly.

SNP markers

The SolCAP project (<http://solcap.msu.edu/>) generated more than 8,000 verified SNP markers for tomato and potato. All SNP markers are currently loaded into SGN, and will be available for searching in the coming month. The SNP markers are mapped on the tomato and the potato genomes respectively.

Genotypes and phenotypes

SGN has loaded the first data set from SolCAP 2009 experiments. More than 160,000 phenotypes for 480 tomato accessions are available. These data will go live in the coming month, and we will add SolCAP phenotyping results from experiments in four different locations and two years. Genotyping of 480 potato accessions and 480 tomato accessions will be added as well, as SolCAP results from the Illumina Infinium assay with the SolCAP SNP markers are released.

Solanaceae Phenotype Ontology

We have added about 100 new terms for potato traits, including tuber quality and morphology. The traits are based on the Potato Cooperator guide. This controlled vocabulary is designated to serve the Solanaceae community, and specifically breeders.

http://solgenomics.net/search/direct_search.pl?search=trait

Please contact SGN (sgn-feedback@solgenomics.net) if you would like to map your phenotypic descriptors to an ontology format. The Solanaceae Phenotype ontology provides standardization in terminology, and enables cross-species and cross-database queries.

LycOTILL mutant collection

The LycOTILL tomato mutants database has more than 14,000 tomato accessions of EMS mutants <http://www.agrobios.it/tilling>. All accessions were phenotyped using the Solanaceae Phenotype ontology, and will be available for browsing on SGN with links back to the LycOTILL database. If you have a population of Solanaceae plants with genotype and/or genotype information, SGN would love to work with you on adding your resource to the SGN website. We provide accreditation, crosslinks to the donor database, and a submitter account for on-line editing of your data.

Tomato Genome

A new tomato genome build, 2.4, has been released. The build differs from 2.3 by correcting a number of gap sizes to conform to a Genbank submission format. The annotation version 2.3 has also been released, consisting of remapped coordinates for the new build, and includes a number of manually corrected gene models. All Tomato genome data is available for browsing and downloading at SGN http://solgenomics.net/genomes/Solanum_lycopersicum/genome_data.pl.

If you have any questions about the tomato genome data, please contact SGN at sgn-feedback@solgenomics.net.

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Construction of a potato consensus map and QTL meta-analysis offer new insights into the genetic architecture of late blight resistance and plant maturity traits

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Background

Integrating QTL results from independent experiments performed on related species helps to survey the genetic diversity of loci/alleles underlying complex traits, and to highlight potential targets for breeding or QTL cloning. Potato (*Solanum tuberosum* L.) late blight resistance has been thoroughly studied, generating mapping data for many Rpi-genes (R-genes to *Phytophthora infestans*) and QTLs (quantitative trait loci). Moreover, late blight resistance was often associated with plant maturity. To get insight into the genomic organization of late blight resistance loci as compared to maturity QTLs, a QTL meta-analysis was performed for both traits.

Results

Nineteen QTL publications for late blight resistance were considered, seven of them reported maturity QTLs. Twenty-one QTL maps and eight reference maps were compiled to construct a 2,141-marker consensus map on which QTLs were projected and clustered into meta-QTLs. The whole-genome QTL meta-analysis reduced by six-fold late blight resistance QTLs (by clustering 144 QTLs into 24 meta-QTLs), by ca. five-fold maturity QTLs (by clustering 42 QTLs into eight meta-QTLs), and by ca. two-fold QTL confidence interval mean. Late blight resistance meta-QTLs were observed on every chromosome and maturity meta-QTLs on only six chromosomes.

Conclusions

Meta-analysis helped to refine the genomic regions of interest frequently described, and provided the closest flanking markers. Meta-QTLs of late blight resistance and maturity juxtaposed along chromosomes IV, V and VIII, and overlapped on chromosomes VI and XI. The distribution of late blight resistance meta-QTLs is significantly independent from those of Rpi-genes, resistance gene analogs and defence-related loci. The anchorage of meta-QTLs to the potato genome sequence, recently publicly released, will especially improve the candidate gene selection to determine the genes underlying meta-QTLs. All mapping data are available from the Sol Genomics Network (SGN) database.

Conferences

**BGI Europe
Seminar Series
Next Generation Sequencing Application**
March – May 2011
bgi-europe@genomics.cn
<http://www.genomics.cn/en/index.php>

XVIIth EUCARPIA Meeting of the Tomato Working Group
April 11 – 14, 2011
Hotel Beatriz Palace & Spa
Fuengirola (Málaga), Spain
<http://www.eucarpiatomato2011.org>

**International Conference on the Second Progress of
1000 Plant and Animal Reference Genomes Project**
July 10 – 12, 2011
Shenzhen, China
<http://ldl.genomics.cn/event/conference.jsp?conId=48>

The Potato Association of America
August 14 – 18, 2011
Wilmington, North Carolina
<http://paa2011.org>

Tomato Breeders Roundtable
October 9 – 11, 2011
Holiday Inn
Ithaca, New York
<http://tgc.ifas.ufl.edu/>

SOL & ICuGI 2011
8th Solanaceae and 2nd Cucurbitaceae Joint Conference
October 16 – 20, 2011
Tsukuba, Japan
<http://www.sol2011.jp/>

The Sixth International Conference on Genomics
November 7 – 11, 2011
Shenzhen, China
www.genomeconference.org.cn

Solanaceae Recipes

Stuffed Peppers
<http://www.cookingchanneltv.com>

Ingredients

2 potatoes, boiled and then mashed
1 cup spinach, chopped
1 cup cooked brown rice
2 tablespoons grated ginger
1 tablespoon garam masala
Pinch red chile flakes
1 teaspoon pomegranate powder
1 teaspoon salt
3 peppers, red, yellow or green



Directions

Preheat the oven to 425 degrees F.

Place the mashed potatoes, spinach, rice, ginger, garam masala, pomegranate powder, and salt in a bowl and mix well.

Cut off the tops of the peppers, remove the stems and then scrape out the seeds with a spoon. Fill each pepper with 1/3 of the potato filling and mound it around the rim. Place them in a baking dish and bake for 40 to 45 minutes, or until the peppers are a little wrinkly and soft and the filling is golden.