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Community News



Rhine River, Cologne, Germany

SOL 2008

Dear Colleagues,

It is our pleasure to announce that the 5th Solanaceae Genome Conference (SOL2008) will take place from October 12 to 16, 2008 in Cologne, Germany. Please mark these dates in your calendar for 2008. The conference is organized by the Max-Planck-Institute for Plant Breeding Research (MPIZ). Cologne is a beautiful and lively city located at the river Rhine in the mid West of Germany, with lots of things to do and to see, with two international airports nearby (Köln-Bonn and Düsseldorf) and fast train connections (e.g. ICE train between Frankfurt Airport and Köln). We cordially invite you to visit us next year. We'll do our best that you can experience an excellent conference with an attractive and stimulating scientific and social program.

The local organizing committee plans for a scientific program of ca. two full days of plenary sessions, a poster session and 5-6 satellite workshops. In case you would like to forward ideas and suggestions for session topics or other issues related to conference organization, please contact us by sending an email to gebhardt@mpiz-koeln.mpg.de. Details on conference site, registration, accommodation, etcetera will be announced next year.

The local organizing committee, represented by

Christiane Gebhardt (Max-Planck Institute for Plant Breeding Research)



A New Co-Chair Team for SOL

Dear Friends,

Sandy Knapp pointed out that we have to be more aggressive about the sequencing of the euchromatic portion of the tomato genome. Sandy proposed that we appoint a new Co-Chair team composed of people that specialize in genomics.

We are glad to announce that we now have a Co-Chair team composed of five people who are equipped to get the sequencing job done: Akhilesh Tyagi, Dani Zamir, Giovanni Giuliano, Jim Giovannoni and Satoshi Tabata.

I take this opportunity to thank Sandy for her leadership, enthusiasm and commitment to the SOL project.

Best Wishes
Dani Zamir



Group photo in Wuhan Botanical Garden at the end of the general discussion.

UK-China Discussion Meeting on Solanaceae Genomics and Biodiversity

by Sandy Knapp (NHM, London) & Ying Wang (Wuhan Botanical Garden)

From September 15 to October 2, 2007, a discussion meeting on how to build a consensus for research linking *Solanaceae* biodiversity and genomics was held in Wuhan Botanical Garden and Xishuangbanna Tropical Botanical Garden in China, with a subsequent trip to Lushan Botanical Garden and vicinity. The event was organized by Ying Wang and Sandy Knapp and funded by the Royal Society (UK) and the Chinese Academy of Sciences (China). Three days of talks and discussions were held in Wuhan, and participants subsequently travelled to Xishuangbanna in southern Yunnan province to continue discussions and to see the wide variety

of native Chinese *Solanaceae* in the field. Knapp remained in China to visit Lushan in Jiangxi province and to collect some key SOL species. Twenty talks were given over the three days in Wuhan, and the symposium was attended by many students and others interested in the *Solanaceae*. Several key themes emerged from the meeting, among them a common interest in genomics (including sequencing) and breeding of eggplant (*Solanum melongena*) coupled with in-depth studies of its huge diversity and ancient history of cultivation in China, the need for wide understanding of both the taxonomy and genomics of the many Chinese medicinal *Solanaceae*, and the continued imperative to complete and make publicly available the sequence from all chromosomes being sequenced (3, 4 and 11) for tomato and potato. The meeting was successful in its aims to stimulate joint thinking about future research in the *Solanaceae* and to promote synergy and cooperation in Chinese-UK science. New projects are already in the formative stages to come under the SOL umbrella!



The Hani minority village near the border of Laos where we found several interesting varieties of *Solanum melongena*.



Introducing EPSO, the European Plant Science Organization

Provided by Isabelle Caugant

EPSO is an independent academic organization representing fifty-seven institutional members bringing together more than 140 research institutes, departments and universities from twenty-five European countries.

The association was founded in 2000 to represent the needs and interests of the European plant science community. Since then, it has focused its work on two areas: science policy and support to plant scientists.

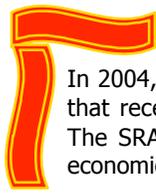
EPSO's mission is to improve the impact and visibility of plant science in Europe. Its top priorities are to facilitate the understanding of plant science, to boost funding for basic research and to coordinate research activities on the national and European levels – and beyond.

EPSO has two European industrial organizations and individual companies as observers. It is a member of the Initiative for Science in Europe (ISE) and of the European Life Sciences Forum (ESLF), and has links to specialized organizations in the area of plant and life sciences in Europe and worldwide.

Science policy

EPSO provides recommendations on European science policy to the European Commission, members of the European Parliament and national politicians. EPSO was a key driver to ensure that funding is available for plant research in the Sixth and Seventh Framework Programme for Research (FP6 and FP7) and to foster the establishment of the ERA-NET on Plant Genomics, an EU-supported network which supports international research efforts in the field.





In 2004, EPSO and EuropaBio started one of the first Commission-backed European technology platforms, 'Plants for the Future', that recently launched, with great success, its final Strategic Research Agenda (SRA) at the European Parliament in Brussels. The SRA presents how a previously published vision paper for the next twenty years can be realized to address key socio-economic challenges facing Europe. Work towards the implementation of the SRA is currently underway.

EPSO regularly publishes position papers to make the voice of plant scientists heard and to outline the opportunities they offer to address current societal challenges. Released in September 2007, EPSO's position paper on bioenergy and renewable materials presents insights into plant research activities that can contribute to tackling global warming.

Supporting scientists

EPSO has built a strong reputation among scientists in Europe and has become the preferred European contact for scientists and companies worldwide interested in plant-related issues.

EPSO organizes a biannual conference that is one of the top plant science events. This major gathering brings together plant scientists from Europe and other continents to present and discuss cutting-edge science. Together with scientists in other disciplines, they build an interface to new areas. The next conference will take place in France, from 22 to 26 June 2008, and registration is now open. Please, read the announcement section on page 8 of this newsletter for more information.

Like its conferences, EPSO workshops have established a reputation for being visionary and high-quality think tanks in emerging areas of plant science. These workshops bring together disparate disciplines so as to overcome barriers and facilitate collaboration. After two days of thorough discussion, workshop participants compile a white paper defining prioritized objectives that are then communicated to the European Commission and national policy-makers. The next workshop, on biofuels, will take place in May/June 2008 in Umeå, Sweden.

EPSO News, the organization's bimonthly e-newsletter, presents the latest developments in plant research and provides EPSO members with information on the various international, European and national funding programs. The online newsletter is only accessible to EPSO members.

EPSO's institutional membership is open to universities and research institutions conducting research in the field of plant science worldwide, while its personal membership is targeted at individuals interested in plant science, regardless of their nationality, profession, seniority or age.

EPSO is looking forward to welcoming you as a member.

For more information: www.epsoweb.org

Membership information available at: www.epsoweb.org/about/membership.htm

Contact at: epsoweb@epsoweb.org

TOMATO IMPROVEMENT IN GHANA

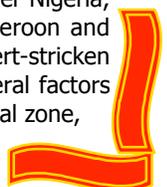
Eric Danquah¹ and Theresa Fulton²

¹University of Ghana, Legon and ²Institute for Genomic Diversity, Cornell University

Tomato (*Solanum lycopersicum*) originated from the area lying between Mexico and the West coast of South America. After its introduction into Spain in the 16th century, it was widely spread throughout Africa. Tomato is adapted to an extremely wide range of climatic conditions as such it is found throughout tropical Africa. The highest yields are recorded in Nigeria, Ghana, Cameroon, Sudan and Benin. In Ghana, tomato is the most important crop in recently established dry season gardens in Northern and Upper Regions and in Southern Volta Region. It is also a fairly important cash crop in the outskirts of urban areas in the forest zone. Tomato production has greatly increased in recent years, along with (to a lesser extent) potatoes, peppers and in some cases even eggplant. Tomatoes are the most important vegetables in Ghana and a primary cash crop, and annual production has doubled over the last thirty years, up to 176,264 tons in 2006. In larger Nigeria, tomato production is up to one million tons per year, and potatoes are not far behind at 776,000 tons. In Cameroon and Senegal, tomato production has quadrupled in the last thirty years, while even in battle-scary Ivory Coast and desert-stricken Mali, production, though small, has increased (FAO Statistics Division, 2007). The yield of tomato depends on several factors including the cultivar planted, spacing, method of growing (whether pruned, staked, etc.), date of planting, vegetational zone,



Library at the University of Ghana





soil fertility, etc. In general, the average yield is very low ranging from 7.5 - 15.0 t/ha. However, with improved production practices including the use of improved varieties, yields of 32.5 - 46.0 t/ha have been recorded in the forest zone of Ghana (Norman, 1992). Despite the increasing yields and the acreage cultivated in tomato, the full genetic resources available to breeders remain to be exploited.

In Ghana, tomatoes are mainly for in-country or regional consumption, particularly in the form of stews and a very spicy sauce used as a condiment (see recipe on page 9 of this newsletter), but raw consumption in salads is gaining popularity. Agriculture is extremely important to Ghana's economy, accounting for 42% of the country's GDP and employing more than half of its work force. Land area used for tomato production grew to 37,000 ha in 2000, mostly in the hands of small-scale farmers. However, larger amounts of tomato paste are now being imported, threatening the market share of the small farmers. Ghana has some ecological advantages over other African countries in that it contains the largest fresh-water lake in West Africa and some regions of the country receive more than 200 cm of rain per annum. Furthermore, Ghana has the most developed finance sector, good quality universities, a stable democratic government, and a good airport with convenient flights to Europe and elsewhere. So there is a clear need and an opportunity for increased tomato production.

There are two types of tomato fruit cultivated in Ghana, the fresh market type (eaten freshly as a vegetable) and the processing types that are converted into paste for use in preparing various delicacies. The two types differ in the fruit characteristics required for efficiency in their utility. Desirable characteristics for processing cultivars include a determinate growth habit, an intense red color, high total soluble solids, high sugar content, low acidity, high pulp content with fewer seeds (i.e. a high pulp to seed ratio), and high yields. In Ghana, most of the local land varieties suitable for processing have a low level of total soluble solids, a poor pulp to seed ratio with too many seeds, air pockets and a thin flesh. This renders the fruit of these varieties unsuitable for processing. Failure to set under high night temperatures is another major problem of tomato cultivation in Tropical Africa where night temperatures could be as high as 36°C. The fresh market types need to have round (not scallopy), larger fruit sizes to attract premium prices, firmer to prevent post-harvest losses during packaging and transport to the market, and also have the preferred taste. They must possess the jointless gene which allows the calyx to detach once harvested to prevent the piercing of fruits when packed layers upon layers. In Ghana, most local fresh market types are small, scallopy and are not of the required firmness (Personal Communications with Prof. E.T. Blay, 2007). Both tomato types in Ghana have common problems of susceptibility to drought, a wide range of bacterial, fungal and viral disease as well as infestations of root knot nematodes and pests resulting in low yields and undesirable coloration of the fruit.

Plant breeders tend to develop varieties that combine maximum resistance to parasites with interesting agronomic characteristics (adaptation to growing conditions) and better fruit quality (shape, grade, color, firmness, keeping quality and soluble dry matter content). Top priorities of West African tomato breeders include increasing yield and fruit size, improving fruit shape, introducing drought tolerance into superior local varieties, and developing virus resistant cultivars. Insect resistant varieties are needed to reduce the large amount of pesticides currently being used. Post-harvest issues such as spoilage and storage must also be addressed, as well as the lack of processors and efficiency in the seed supply systems.

To achieve these objectives, there is the need for collaborations that would allow for the training of more plant breeders, sharing of knowledge, genetic resources, and the use of advanced molecular diagnostic tools. These molecular tools would be used for phenotyping, genotyping, marker assisted introgression, marker assisted backcrossing, and a more targeted approach to solving the problems identified. Cornell University has developed mapping populations, Near Isogenic Lines, and QTL identification strategies that have resulted in genomic studies yielding valuable information on the evolution of many genes and their location in the tomato genome. Among the many QTLs identified are for fruit shape and size, brix, firmness, puffiness, color, etc. A new graduate student program, the West African Centre for Crop Improvement (WACCI), initiated by the Alliance for a Green Revolution in Africa (AGRA) will train new African plant breeders. This program will create more linkages and collaborations that will allow West African breeders to develop superior varieties, such as a processing variety that would outperform other processing varieties with the focus on improving soluble solids, while maintaining or improving yield, viscosity, firmness, puffiness, color, and fruit size.

References

Norman, J. C. 1992. Tropical Vegetable Crops. Arthur, H. Stockwell Ltd. Devon.

FAO Statistics Division <http://faostat.fao.org>

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Tomato Sequencing Updates



Chromosomes 1, 10 (US)

Contact: Joyce Van Eck (jv27@cornell.edu)

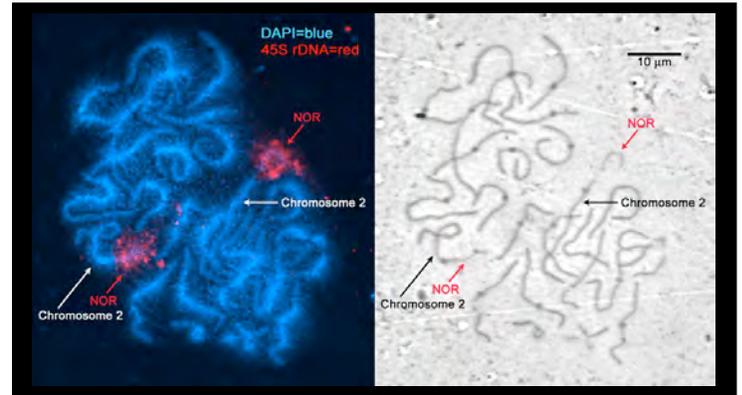
End sequencing of fosmid clones is in progress. We have end-sequenced 1,152 fosmid clones and 50,000 clones are being end-sequenced by the EU-SOL project through a subcontract of research funds needed for the sequencing, which will be performed by the Sanger Center. An additional 50,000 fosmid clones will be end-sequenced by our sequencing project collaborators in Italy.

To date, the Stack lab at Colorado State University has localized a total of 116 BAC clones on tomato pachytene synaptonemal complex spreads using fluorescence *in situ* hybridization (FISH). This number includes twenty-four BACs (listed below) that have been localized since the last newsletter. FISH has also been used to position two other landmarks on pachytene SC spreads: 1) the location of 5S rDNA at 9.8% ± 1.9% of the arm length from the centromere on the short arm of chr 1 and 2) the proximal border of the NOR (45S rDNA) at 28.9% ± 3.6% of the arm length from the centromere on the short arm of chr 2.

Chromosome Arm

Chromosome Arm	BAC ID
2Q	LE_HBa0060G11
3P	LE_HBa0020P05
3P	LE_HBa0031M05
3P	LE_HBa0137K15
3P	LE_HBa0203C09
3P	LE_HBa0257N18
3P	LE_HBa0030A11
3Q	LE_HBa0299H10
4Q	LE_HBa0077O05
6P	LE_HBa0095C08
6Q	LE_HBa0184G14
7P	LE_HBa0095C18
7P	LE_HBa0111F22
7P	LE_HBa0007H24
7Q	LE_HBa0188B22
7Q	LE_HBa0178O02
9P	LE_HBa0026P14
9P	LE_HBa0300E15
9P	LE_HBa0255E01
9Q	LE_HBa0099F14
9Q	LE_HBa0107P11
9Q	LE_HBa0248I10
11P	LE_HBa0214E16
11P	LE_HBa0015A13

This figure illustrates labeling of the NOR by *in situ* hybridization with digoxigenin-tagged 45S rDNA followed by immunolabeling with an anti-digoxigenin antibody coupled to TRITC.



Chromosome 2 (Korea)

Contact: Sanghyeob Lee (sol6793@kribb.re.kr)

Update pending.

Chromosome 3 (China)

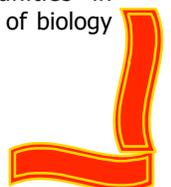
Contact: Chuanyou Li (cyli@genetics.ac.cn)

In order to further promote the sequencing efforts of tomato chr 3, a workshop was held on September 8, 2007 in Beijing. Participants included Prof. Yongbiao Xue and six PIs involved in this project.

The workshop was chaired by Professor Yongbiao Xue, director of the Institute of Genetics & Developmental Biology, Chinese Academy of Sciences. Dr. Chuanyou Li gave an overview of the progress of the project in the past two years. Dr. Mingsheng Chen, together with Drs. Ying Wang and Changbao Li summarized the work on the construction of a physical map of chr 3. Dr. Zhukuan Cheng presented his FISH studies with forty-seven BAC clones. Dr. Hongqing Ling presented his work on repeat sequence analysis.

Through discussions, the workshop raised the following directions for the next step of the chr 3 sequencing effort:

- 1) In order to build a strong SOL-community in China, invite more scientists, especially bioinformatics experts to participate in the chr 3 sequencing effort; continue to seek funding support through versatile channels.
- 2) Based on the current progress of the physical map, identify 200 BAC clones for sequencing, the identity of these BAC clones on chr 3 will be confirmed with FISH.
- 3) Continue to identify cutting-edge opportunities in *Solanaceae* research to better meet the needs of biology and agriculture in China.





Chromosome 4 (UK)

Contact: Karen McLaren (kb1@sanger.ac.uk) or Helen Beasley (hr1@sanger.ac.uk)

11,192,079 bp of sequence have been generated at the Wellcome Trust Sanger Institute for chr 4 as of October 19th, 2007. Of this figure, 10,503,263 bp are unique. The sequence has been produced from 101 BACS originating from the LE_HBa and SL_MboI libraries. We intend to finish all BACS that will contribute to chr 4 to HTGS phase 3 and currently sixty-nine BACS that correspond to 7,947,176 bp of sequence have been deposited in the public databases at EMBL/GenBank/DDBJ as phase 3. All other chr 4 BACS with EMBL/GenBank/DDBJ accessions are currently active in our sequencing pipeline at HTGS phases 0 to 2.

Eight BACS on chr 4 contigs with conflicting map and/or sequence information were sent for FISH analysis. The FISH analysis, which was performed by the Hans de Jong laboratory in Wageningen, confirmed six of the eight BACS did not localize to chr4. Although they were found to be heterochromatic, the BACS were not localized to any specific chromosome. This affected a total of five chr4 contigs and six BACS which were finished to HTGS phase 3. These BACS will be genetically mapped by SGN in order to place them on other chromosomes, and have been removed from the chr4 minimal tilepath. We will continue to use the FISH analysis as a resource for mapping confirmation.

Work is ongoing with the WTSI AGP viewer (presented by G.Bishop at SOL 2007 Korea) to extend mapped contigs and select gap closures continues. The first round of clones selected from the AGP viewer have entered our sequence pipeline and should yield sequence by the end of October to allow a further round of BAC selection.

The progress of chr 4 can be viewed through the development of the TPF and AGP files that we upload monthly to SGN. The TPF indicates the expected relative positions of the BACS along the chromosome and the AGP provides assembly information.

Chromosome 5 (India)

Contact: Akhilesh Tyagi (akhilesh@genomeindia.org)

At the Indian Initiative on Tomato Genome Sequencing, we have been able to confirm forty-nine BACS on chr 5. Sequencing is in progress on all of these BACS, out of which twelve BACS are in phase III, twenty-five BACS are in phase II and seven BACS are in phase I. The sequences for all the phase III as well as phase II BAC clones have been submitted to GenBank. The remaining five BACS are in the early phase of sequencing. In an effort to obtain new landing positions on different tomato chromosomes, we have started to screen the 200 BACS assigned to India for mapping, by designing CAPS markers. Since BAC extension is posing a great problem with the current available resources, we are looking forward to more results from Giovanni Giuliano and the fosmid end sequences. Efforts are also ongoing at our end to search for extension BACS by performing overgo hybridizations on the filters available for the three tomato libraries.

Chromosome 6 (The Netherlands)

Contact: Sander Peters (sander.peters@wur.nl)

Currently, we have sequenced 14.6 Mb for chr 6 including BAC overlaps. Of this, we have 2.4 Mb of non-redundant sequence for the top arm, and 9.7 Mb for the long arm. In the last period, we have focused mainly on completing the top arm of chr 6 as much as possible. A total of twenty-seven BACS have been physically mapped on the top arm, of which ten are seed BACS. Currently, we have identified seed BAC LE_Hba_016K14 to be the most distal BAC, and FISH analysis shows this BAC lands just below the short arm telomere at 0 cM. We have found some copies of a TTTGAAA repeat in the insert sequence of 016K14, but whether this belongs to the (sub) telomeric repeat is not certain yet. We would like to show an increased copy number of this repeat towards the north end of chr 6.

However, we have not yet found candidate BACS to extend further north. Although the coverage for the top arm is quite considerable, considering the estimated euchromatin size of 2.7 Mb, we have to bridge four gaps. Despite attempts, we have not been able to identify candidate extension BACS to get across these gaps, and we think this is most likely due to lack of coverage within the BAC libraries. In this respect, the sequencing of additional fosmid ends would help to increase coverage and increase the chance of finding new candidate extensions.

Chromosome 7 (France)

Contact: Farid Regad (regad@ensat.fr)

Update pending.

Chromosome 8 (Japan)

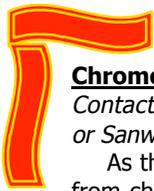
Contact: Erika Asamizu: (asamizu@kazusa.or.jp)

We finished eighty-four BACS to Phase 3 that produced a non-redundant length of 8,469,989 bp. We are continuing the accumulation of Selected BAC Mixture (SBM) shotgun data, which reached to 1 million files generating 700 Mb of total length. We genotyped 696 EST SSR markers using the EXPEN 2000 F2 population and so far mapped 418 of them on all tomato chromosomes. We obtained forty additional seed points for sequencing chr 8.

Chromosome 9 (Spain)

Contact: Antonio Granell (agranell@ibmcp.upv.es)

As of today, fifty-one BAC clones have been completed. Fifteen BACS are in HTGS 3, twenty BACS are in stage HTGS 2, and sixteen BACS are in HTGS 1. Nine additional BACS are currently in the sequencing pipeline. The identity of four more BACS containing markers for chr 9 has been confirmed by PCR and ILs mapping, and they are waiting to be sequenced to see how much they overlap with close BACS that are currently being finished. Nine other BACS are in the FISH pipeline to confirm they correspond to chr 9 as they contain markers in chr 9 but no polymorphism was found in that region between *Solanum lycopersicum* and *S. pennellii*; the verification of nine additional BACS is in progress. The 3D DNA pools of BAC library from the Kazusa DNA Research Institute (Dr. Tabata/ Dr. Erika Asamizu) are being used to find positive BAC clones associated to Tomato- EXPEN 2000 markers, and eleven additional markers from Dr. Tabata / Dr. Erika Asamizu's lab have been selected for PCR screening using the 3D DNA pools.



Chromosome 11 (China)

Contact: Zhonghua Zhang (zhangzhonghua.caas@gmail.com) or Sanwen Huang (huangsanwen@caas.net.cn)

As the first step to sequence tomato chr 11, ten BAC clones from chr11 have been sent for sequencing. Three BAC clones have been assembled into one contig and will be completed as Phase III soon. One and six BAC clones are at Phase I and Phase II, respectively. Furthermore, these BAC sequences have been submitted to GenBank/EMBL/DDBJ and SGN. Next we will extend these BAC clones and also select more seed BACs.

To complete tomato chr 11 as soon as possible, we also planned to select seed BAC clones for tomato chr 11 by using potato BAC sequences from chr 11. All tomato BAC end sequences are aligned to potato BAC sequences. If the positions of BAC ends on potato BAC are consistent with the tomato physical map, one BAC will be selected as a candidate seed BAC. Currently, we have selected four seed BAC clones using potato BAC sequences, two of them contain markers which are mapped on chr 11, another two will be verified by IL mapping soon.

Chromosome 12 (Italy)

Contact: Mara Ercolano (ercolano@unina.it)

Fifteen BAC clone sequences have been released to the NCBI repository database in HTGS phase 3. Two additional

BAC sequences are ready to be submitted in HTGS phase 2 and an additional fifty-two BACs are in different sequencing stages. Tilepath selection continues across the contigs using a strategy that combines the use of bioinformatics PABS tool and molecular validation based on IL mapping. Fluorescent hybridization on combed DNA using BAC clones as probes was also set up. We wish to use this technique to estimate: 1) the length of the BAC insert prior the sequencing, 2) the length of gap between two BACs, and 3) relative order of BAC clones on chr 12. Moreover, Italy will contribute to the international sequencing effort providing the end sequences of approximately 50,000 fosmid clones. In order to provide a preliminary annotation of the BAC sequences, the Italian groups set up two annotation pipelines. To accomplish this task, ESTs from the different plant source collection at CAB (*Solanaceae* and *Rubiaceae* species), and the corresponding TCs, created by assembling ESTs in a cluster are both used. This platform also includes alignments of all the RNA sequences from Arabidopsis to the tomato genomic sequences, in order to identify genes that are conserved between the two species. At the University of Padua, an informatics platform for the tomato genome annotation was able to integrate different data (EST, comparison with Arabidopsis and *Oryza* genome) was also set up.



What's New on SGN?

Locus of the Week

SGN now showcases a locus every week on the SGN homepage. If you have information to contribute towards the locus of the week, please consider becoming a locus editor. To become a locus editor, click on the link "Contribute annotations to this locus", which is below the locus of the week. You can edit and add new information for this locus, such as the locus description, Gene Ontology annotations, allele information, associated accessions (with images), associated sequences and publications. Of course, if you wish to become the editor of any other locus, please contact SGN at sgn-feedback@sgn.cornell.edu.

Locus of the week

Monoterpene synthase 1 (MTS1)

Tomato monoterpene synthase

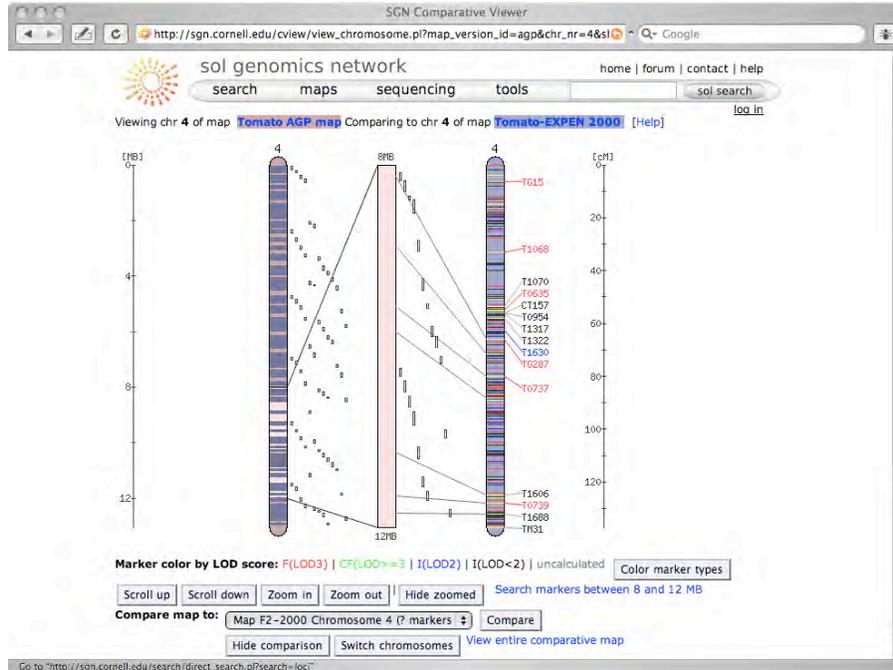
[Contribute annotations to this locus](#)





Accessioned Golden Path Map and Comparison to the Genetic Map (F2-2000)

The Accessioned Golden Path map represents the order of the finished tomato BAC clones on its respective chromosome. The AGP map can be compared to the F2-2000 genetic map so that you can easily identify BACs that lie between two markers of interest. Click on the maps menu and select the Tomato AGP map. Click on a chromosome of interest and then choose the F2-2000 in the "Compare map to:" drop down menu. This draws an image similar to the one below. It allows you to identify the BACs that are located between particular markers.



Announcements

Conferences



Fourth EPPO Conference Near Toulon (Côte d'Azur), France, 22-26 June 2008

It is now time to register for the 2008 EPPO conference that will take place in Presqu'île de Giens in the south of France (Côte d'Azur), from June 22 - 26, 2008. Early registration is open until February 29, 2008.

Over the years, EPPO's biannual conferences have built a strong reputation as one of the top plant science events. After Switzerland (2002), Italy (2004), Hungary (2006), France will be the place to be for the fourth EPPO Conference. This time the theme is 'Plants for Life'. Scientists from Europe and continents will present and discuss cutting-edge science. Together with non-plant scientists, they will build multidisciplinary interfaces.

The conference is organized by Karin Metzloff, EPPO's executive director, and the local conference organizer is Hélène Lucas, head of the Genetics and Plant Breeding Division of France's Institut National de la Recherche Agronomique (INRA).

Abstract submission is open until April 25, 2008 for oral presentations and until May 11, 2008 for poster presentations.

Conference webpage: www.epsoweb.org/catalog/conf2008.htm

Registration: www.epsoweb.org/catalog/conf2008/register.htm

Program: www.epsoweb.org/catalog/conf2008/4CF_Program_web.pdf



Publications

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Solanaceae Recipes

Shitor

(Traditional Ghanaian hot sauce, served as a condiment, with everything!)

Contributed by Theresa Fulton

Shake the pepper shaker over your food in Ghana and you will be surprised to see RED pepper instead of black. Yes, Ghanaians like it hot! Along with most meals comes a spicy pepper and tomato sauce used as a condiment much in the way that ketchup is used in the US or salsa is used in Latin America.

1 cup of olive or other oil
1 onion, chopped
4 tbsp tomato paste
30 - 40 g hot red pepper flakes
2 oz chopped shrimp (optional, or more to taste) or 1 tsp dried shrimp powder
salt to taste
dash of ginger powder

All ingredient amounts are flexible, make to taste.

Heat a small amount of the oil and sauté the onions until golden. Stir in the other ingredients, stirring constantly and adding more oil as needed. Heat while stirring until well mixed (approximately 20 minutes), being careful to add oil to avoid burning the sauce. More tomato paste or a little chicken broth or water can be added if it is too spicy. Let cool before serving.





Tomato Bruschetta (Bruschetta al pomodoro)

Provided by Andrea Mazzucato and Maurizio E. Picarella

This is a very popular appetizer or side dish with tomato in Italy, traditionally prepared in summer. The name *bruschetta* comes from the Roman vernacular *brusco*, meaning toasting as referred to bread. In its simplest original version, bruschetta is made with a slice of toasted bread spread with a bit of garlic, salt and olive oil. In this form, bruschetta is still considered the best way to taste the aroma of olive oil and as such adopted by professional tasters. The version with tomato comes immediately after for popularity.

Ingredients:

1 loaf country-style bread cut into slices
8 ripe middle-sized tomatoes
2 cloves garlic
1 pinch salt
1 pinch ground black pepper
2 - 3 tbsp extra-virgin olive oil

(makes 12 servings)

Preparation:

Chop tomatoes in small pieces (leave or discard seeds as preferred). In a bowl, combine the tomatoes, salt, pepper, and extra-virgin olive oil. Allow the mixture to sit for about 15 minutes for flavors to blend. In the meantime, grill or toast the slices of bread on both sides and spread garlic on. Top the still warm toasted bread slices with the tomato mixture and serve immediately.

This is basic tomato bruschetta. To have it more interesting in flavor and taste, fresh basil or thyme leaves are finely cut into small pieces and swiftly added to the tomato mixture. A number of other ingredients may be added for variations on the theme. These include: red pepper, anchovy, onions, balsamic vinegar, etc.

More fancy in preparing bruschetta comes whether using fruit colors other than red, as we have recently done with tomato color mutants. The result is presented in the photo below. Good appetite!



Bruschetta made with tomato color mutants.

