SOL NEWSLETTER

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COMMUNITY NEWS

Solanaceae Genetic Resources in Europe

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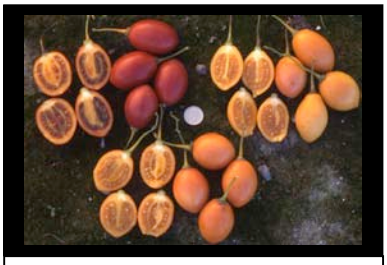


Tree tomato

The European Cooperative Programme for Plant Genetic Resources (ECPGR), coordinated by the International Plant Genetic Resources Institute (IPGRI), facilitates the cooperation between European countries from North to South and from the U.K. to Azerbaijan. In 2000, a survey about the genetic resources of Solanaceous crops (eggplant, pepper, tomato, husk tomato and tree tomato) and their wild relatives, identified a first group of genebanks, universities, institutes and NGOs holding *Solanaceae* germplasm in Europe, and yielded an estimate of the total number of accessions of eggplant (about 6,000), pepper (over 20,000) and tomato (over 30,000). It also gave an overview of the various regeneration and conservation protocols used throughout the region. This survey showed that most of the *Solanaceae* collections in Europe are quite safe, although a few need to be better secured. The first report of the Solanaceae Working Group is available at (http://www.ipgri.cgiar.org/networks/ecpgr/meetings/allmeetingWG.asp?groupID=34).

Depending on the countries, the genetic resources are centralized in one place (e.g. Nordic countries, Germany, Russia, Turkey) or scattered among different institutions (e.g. Czech Republic, Italy, Portugal). Collections of some institutions cover the whole range of Solanaceous crops (which is generally the case at the national genebanks), while others are focused exclusively (e.g. pepper in Hungary, Vegetable Research Institute of Budapest) or preferably on one crop (e.g. tomato in Czech Republic). The number of accessions per collection is highly variable, ranging from some units to several thousands.

The wealth of *Solanaceae* genetic resources (GR) held in Europe justified the initiation of the ECPGR Solanaceae Working Group (WG) aimed at promoting the collaboration between countries for establishing reference protocols for regeneration, conservation and plant descriptions, creating central European databases for each crop, identifying duplicates, helping organize the safety duplication of the collections in long term conditions, and more generally, harmonizing the management of *Solanaceae* GR in Europe. The ECPGR Solanaceae WG (http://www.ecpgr.cgiar.org/Workgroups/solanaceae/solanaceae.htm) is a group of officially designated national representatives (presently 28 members), and its activities are based on self funding and good will, except for the meetings and a few targeted actions that are financially supported by ECPGR. Unfortunately, this type of arrangement cannot lead to rapid achievement of goals as would a group with funding, however, it is possible to make significant steps forward thanks to a committed collaboration.

The Solanaceae WG benefited from the momentum created by the project on eggplant genetic resources (EGGNET), which was financed (2000-2005) by the European Union. Thanks to two joint meetings between EGGNET partners and ECPGR Solanaceae WG members held in 2001 and 2004, several decisions were implemented as outlined here:

Central crop databases: The eggplant database [http://www.bgard.science.ru.nl/WWW-IPGRI/eggplant.htm) is managed by the Botanical and Experimental Garden of Radboud University, Nijmegen (NL)]. First created for EGGNET, this database includes passport data (based on the FAO/IPGRI Multicrop passport descriptor list), as well as primary and some of the secondary characterization data obtained by EGGNET partners. It also includes photographs of some accessions and is connected to a literature database. The process of including the passport data of the ECPGR countries is ongoing. The European eggplant database includes genetic resources of the common eggplant (*Solanum melongena)*, the African eggplants (*S. aethiopicum* and *S. macrocarpon)*, the pepino (*S. muricatum*), the lulo or naranjilla (*S. quitoense*) and cocona (*S. sessiliflorum*), various other edible secondary *Solanum* species (e.g. *S. scabrum*), and wild relatives of all these cultivated species.

Solanum aethiopicum

The pepper database (http://www.bgard.science.ru.nl/WWW-IPGRI-Capsicum/Pepperdb.htm) has the structure of the eggplant database, and is managed by the Aegean Agricultural Research Institute, Izmir, Turkey. In a short time, the passport data of twelve countries will be included.

The tomato database, the largest of the WG, is not available yet on the Internet. The managing institution is the Vavilov Institute of St. Petersburg, Russian Federation. For the time being, data from fifteen countries have been gathered and the work is ongoing.

Husk tomato

The husk tomato (http://www.comav.upv.es/Physalis.html) and the tree tomato databases (http://www.comav.upv.es/Cyphomandra.html) have been completed by the Centro de Conservación y Mejora de la Agrodiversidad Valenciana (COMAV), Valencia, Spain. The European collections for these last two crops are limited in the number of accessions, respectively including 284 and 83 accessions, but of great interest for possible increase in use of these crops in Europe.

Minimum protocols for a safe regeneration and conservation: On-line available guidelines have been prepared, listing the basic methodology for good quality regeneration and conservation.

Minimum descriptors list: The objective of the WG is to define a set of ten morphological descriptors for each crop to be used by each germplasm holder, in addition to his/her own descriptors. These minimum descriptors, aimed at being included into the central crop databases have been so far defined for eggplant, pepper and tomato. The help of experts on *Physalis* sp. and *Cyphomandra* sp. is needed for establishing minimum descriptor lists of those two species as well (please contact: daunay@avignon.inra.fr).

Next steps

Uploading the tomato database on the Internet and completion of the eggplant and pepper databases are the group's first priority. Once the databases are completed, the degree of duplication within and among collections will be analyzed to help germplasm curators define their Most Appropriate Accessions (MAA) and hence to rank their priorities for conservation. The second priority of the group is to rationalize the safety-duplication of the collections.

Access to *Solanaceae* European GR

Accessibility of the *Solanaceae* accessions held in European collections is dependent on the international legislation on genetic resources. Being a member of the category "*Solanum* sp.", eggplant is the only *Solanaceae* (with potato) to be included in the list of crops covered under the multilateral system defined by the International Treaty (IT) for Plant Genetic Resources for Food and Agriculture, provided they are under the management and control of the Contracting Parties and in the public domain. A standard Material Transfer Agreement (MTA), to be used for facilitated access of genetic resources that are part of the multilateral system, was adopted in June 2006 by the Governing Body of the IT. For the other Solanaceous crops, reference international legislation regulating access is the Convention on Biological Diversity (CBD). Under this convention, requests of germplasm are usually dependent on bilateral agreements between the requesting party and the provider with conditions for access dependent upon on specific MTAs proposed by the party providing the genetic resource(s). Details about international policies on genetic resources for food and agriculture are available on the FAO web site (http://www.fao.org/AG/cgrfa/default.htm).

Photo acknowledgements

Tree tomato: Jaime Prohens (Departamento de Biotecnología-genética, Universidad de Politécnica E.T.S.I.A., Valencia, Spain)
Husk tomato: Wolfgang Palme, (Hoehere Bundeslehr- und Forschungsanstalt (HBLFA) für Gartenbau - Schoenbrunn, Wien)

Highlights of the General Assembly of the International Coffee Genome Network

Provided by Florent Engelmann

The General Assembly of the International Coffee Genome Network (ICGN) took place in Montpellier on September 16, 2006, back to back with the 21st ASIC International Conference on Coffee Science. The following three main items were on the agenda: i) renewal of coordination and secretariat; ii) review of working groups; and iii) review of the steering committee.

i) *Renewal of coordination and secretariat:* it was decided to change the role of the ICGN Coordinator to Executive Secretary to place more emphasis on the execution of the tasks of the network, as decided by the Steering Committee. F. Engelmann (IRD, France) was nominated Executive Secretary of the ICGN.

ii) *Review of working groups:* the renewal of the six working groups for the next two years was discussed. The coordinators of the working groups gave brief overviews of the activities performed within their respective groups over the past two years.

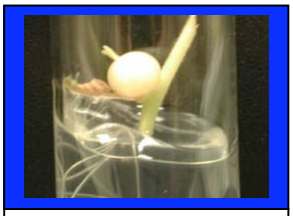
iii) *Review of the steering committee*: the Assembly agreed to give the following new composition to the Steering Committee: one coordinator of the six working groups (among whom one WG coordinator will serve as chairperson of the SC on an annual rotation basis); one representative of IPGRI; two representatives of the Industry; one Grower representative; one Consumer representative.

The full minutes of the ICGN General Assembly can be accessed from the ICGN Website (http://www.coffeegenome.org/).

OUTREACH

Micropotatoes in the Classroom

by Joyce Van Eck



Micropotato on stem nodal segment cultured in a test tube

As part of our NSF-funded tomato sequencing project, we have an educational outreach program that includes different activities geared for kindergarten – 12th grade, college undergraduates, and educators. One of the activities developed for a high school level biology class is based on *in vitro* potato cultures. An Ithaca High School biology teacher, Linda Knewstub, and I designed this activity to complement the following aspects of the required curriculum content: traits of living organisms (life functions), requirements of photosynthesis and respiration (cell energy), scientific method and experimental design, and cell division (mitosis, asexual reproduction, vegetative propagation, stem cells). For this class exercise, stem internode sections are cut from sterile, *in vitro* potato plants, cultured on two different media, and maintained in two different environments (under lights and in the dark). One medium promotes plant growth from the internode, whereas, a second medium contains the anti-gibberellin ancymidol, which promotes micropotatoes to develop. The students work together in small groups, and each group prepares cultures for both plant growth and micropotato production. They record their observations several times a week, and after four weeks the data is compiled into one large chart that is drawn on the blackboard. For the past two years, I visited the classes on the last day of the experiment to observe the results and interact with the students as they evaluate the data. Each year, there have been approximately 120 students that participated in this exercise. It is always a pleasure to visit the classes and see the critical thinking and scientific inquiry of these students who are 14 – 15 years old. The teacher and I plan to publicize information about this activity by posting instructions and a list of materials on web sites commonly used by teachers and we also plan to do presentations at teacher workshops. If you would like to learn more, contact Joyce Van Eck (jv27@cornell.edu).

Students taking data on their potato cultures

Additional information for this outreach activity and others has recently been posted on our outreach page on SGN at http://www.sgn.cornell.edu/outreach/.

AVRDC – World Vegetable Center

AVRDC – the World Vegetable Center is the leading international institute for vegetable research and development worldwide. It is a not-for-profit research institute aimed at reducing malnutrition and alleviating poverty in developing countries through improved production and consumption of vegetables. Founded in 1971 as the Asian Vegetable Research and Development Center with a mandate to enhance vegetable production in the Asian tropics, the Center's renaming as the World Vegetable Center reflects its widened global role in promoting and supporting vegetable research and development in Africa and other regions of the world.

Headquartered in Taiwan, the World Vegetable Center has established regional centers in Thailand, India and Tanzania, and offices in six other developing countries. In recent years, programs have expanded into West Africa and networks of partners forged in Northeast and Central Asia, Central America, and in Afghanistan. The Center is governed by an international Board of Directors and receives funding from governments (United States, Germany, United Kingdom, France, Republic of China and others), foundations, and donors from the private sector (e.g. Asian Development Bank, Rockefeller Foundation, Asia & Pacific Seed Association).

Vegetables: Health, prosperity and diversity benefiting the poor

It is commonly recognized that vegetables are vital for stronger economies and healthier diets, which is of enormous importance especially in developing countries. Vegetable production creates more jobs and income than other food crops. In addition, vegetables are also the most sustainable source of micronutrients, affordable even for the poorest. Over the past 30 years, scientists at the World Vegetable Center have successfully bred cultivars and designed technologies to help increase yields and incomes in developing countries. Millions of farmers today grow vegetable crops using seed or technologies that have been developed at the Center. In Asia alone, more than a third of tomatoes grown are based on lines developed at the World Vegetable Center.

Research at the World Vegetable Center

Dealing with all relevant steps from production to consumption of vegetables, the Center's activities range from breeding vegetable lines to socio-economic impact analyses. Among the research units are those specialized in breeding of tomatoes, peppers, cucurbits, crucifers, bulb Alliums, and legumes. Scientists at the World Vegetable Center are also active in identifying and disseminating superior cultivars of indigenous vegetables, many of them originating from Africa. The Genetic Resources and Seed Unit at AVRDC's headquarters currently maintains more than 55,000 accessions of diverse vegetables, making it the biggest genebank for vegetable germplasm worldwide.

In addition to germplasm conservation and varietal development, other core activities include genetic enhancement using molecular technologies, nutritional security and human health, safe and sustainable production systems and crop protection, post-harvest management, market opportunities, and income generation.

The World Vegetable Center forms alliances with partners from both the public and private sectors, which have complementary expertise. Engagement in regional and supra-regional networks for research and development helps increase outreach and impact. Capacity building is enhanced through training, backed up by extensive web and library services.

For more information visit www.avrdc.org or contact Dr. Warwick Easdown, Head of Communications: w.easdown@avrdc.org.

TOMATO SEQUENCING UPDATES

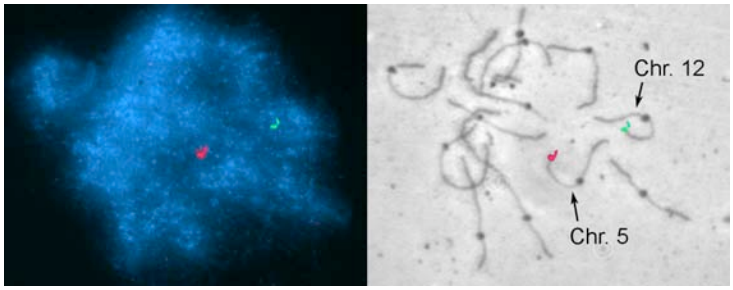
Chromosomes 1, 10, 11 (US)

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

To date, we have sequenced a total of seventeen BACs for all three chromosomes, and two additional BACs are in the sequencing pipeline. The Stack lab has used FISH to localize a total of fifty-six BAC clones on various tomato chromosomes, including six that have been positioned since our last report. Among these new BACs are three located near the telomeres of the long arms of chr 3, 5 and 8; one located close to the centromere of chr 2; one on the long arm of chr 7; and one near the euchromatin/heterochromatin border on the long arm of chr 8. With the localization of our first BAC on chr 5, we now have markers that can be used to identify all twelve tomato chromosomes. The recently positioned BACs include:

Chromosome Arm	BAC ID
2Q	006P20
3Q	159C06
5Q	251J13
7Q	130B18
8Q	005L01
8Q	160L02

The figure below illustrates FISH labeling of BACs Le_HBa 251J13 on chr 5 (red) and Le_HBa 045N22 on chr 12 (green). Since these two chromosomes cannot be distinguished by relative length and arm ratio alone in SC spreads, a marker has been used to identify chr 12.



Chromosome 2 (Korea)

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

We obtained sequences for six additional BACs since our last report. Currently, ninety-two BAC sequences have been completed, and seven BAC clones are in the sequencing pipeline. We found some chimeric clones, which showed exact matches with two different seed BACs that are located several Mb away. From now on, this chimeric clone could cause a problem. Also, I want to share an experience regarding BAC extension. Please be careful when using the results from a BLAST of the BAC end sequences (BES). I did a BLAST search using our BAC sequence into the current sequences in the SGN database. Surprisingly, I found two clones, but both sequences were generated from another chromosome. One was close to a 100% match with our clone. The other showed 100% in 40KB of 100KB. Therefore, we need additional verification methods (e.g. IL mapping, FISH, etc.) for BES BLAST. For the selection of additional seed BAC clones, we asked the sequencing group in Japan to send the 3-D pooling library, which will arrive soon.

Chromosome 3 (China)

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

Update pending.

Chromosome 4 (UK)

Contact: Christine Nicholson (ckb@sanger.ac.uk)

3,268,730 bp of sequence have been generated at the Wellcome Trust Sanger Institute for chr 4 after sequencing twenty-nine BACs from the LE_HBa and SL_MboI libraries. 3,111,616 bp of this sequence are unique, i.e. they exclude the overlapping sequence. Fourteen BACs have been fully finished to HTGS phase 3, contributing 1,638,552 bp of sequence. The other accessioned BACs are at HTGS phases 0 to 2 and remain active in Finishing.

Tilepath selection continues across the FPC contigs containing confirmed chr 4 markers and BACs are progressing through the mapping, subcloning and shotgun stages of our sequence pipeline prior to their release into the public databases at EMBL/Genbank/DDBJ where they are accessioned. The development of the chromosome contigs can be viewed via the TPFs and AGP assemblies of chr 4 that we are posting monthly at SGN.

A number of markers from the tomato EXPEN-2000 map are un-anchored in the FPC database. Therefore, we plan to anchor additional chr 4 markers to this map via hybridizations to library filters. This is with a view to obtaining further coverage across chr 4.

Chromosome 5 (India)

Contact: Akhilesh Tyagi (akhilesh@genomeindia.org)

Presently, the Indian Initiative on Tomato Genome Sequencing is involved in sequencing thirty-eight BAC clones from chr 5, anchored to chromosome specific markers (CT101, C2-At1g60440, T1252, C2-At1g60200, cLET-8-B23, T0564, cLED-8-G3, T1592, Bs4, TG432, T1360, cLEX-13-G5, T1746, T1777, T1584, TG69, CT130, TG185, TG597 and CT138). Sequencing of BACs has progressed to various stages. Six BAC clones are at phase 1, sixteen BAC clones are at phase 2, and six BACs have reached phase 3. Ten BAC clones are at different stages of library preparation and sequencing. All the BAC clones that are being sequenced have been confirmed using Introgression Lines (ILs) specific for chr 5. Seed BAC clones at new marker positions, as nucleation points, are being validated and confirmed. The marker T0876 and its associated BACs (C05MBa0077G20, C05HBa0179K09 and C05MBa0032F07) at 12.0 cM were reallocated to chr 7 by using chr 5 and chr 7-specific IL lines.

Chromosome 6 (The Netherlands)

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

To extend the number of chr 6 seed BACs, we have started additional FISH screening of HindIII BAC candidates. These BACs have been selected according to the chr 6 marker mapping information available at SGN. FISH labeling on chr 6 for BACs H167M06, H251G05, H261A18, H288L16, H301C21, H302A23, H302K01, H309K01, and H310B09 has been obtained. After BAC end sequence verification, these BACs will enter the sequencing pipeline. BACs H003K02 and H336O09 produced multiple signals, and BACs H32F01, H155K09, and H267E16 have their signals on other chromosomes. Therefore, these BACs were rejected for sequencing.

Currently, five BACs (M118M03, M017O21, H261A18, H309K01, and H310B09) are in the sequencing pipeline. In addition, extension BACs E123G17, M124M03, and H146A12 have been sequenced and assembled to phase 2. BAC E123G17 shows overlap with seed BAC H215M16. Seed BAC H012A08 is extended in both directions by M124M03 and H146A12, respectively. Overlaps between seeds and extension BACs show a 100% sequence match.

In the SOL newsletter issue no. 5, 2005, the EU-SOL strategic objectives were presented by Willem Stiekema (Centre for Biosystems Genomics, Wageningen, The Netherlands). One of the objectives is to link the EU-SOL data resources and research to the efforts of the SOL initiative. On November 22, 2006, the kick-off meeting for the Bioinformatics part (Module 6, coordinated by Dr. Heiko Schoof, Max Planck Institute for Plant Breeding Research Plant Computational Biology, Koeln Germany) will start in Wageningen. Workpackage 6 consists of three parts. WP6.1 (wp leader Dr. Yves van de Peer, Bioinformatics and Evolutionary Genomics Division, Department of Plant Systems Biology, Flanders Interuniversity, Institute for Biotechnology, Ghent, Belgium) is dedicated to tomato genome bioinformatics. In WP6.2 (wp leader Dr. Roeland van Ham, Plant Research International, Wageningen, The Netherlands) functional genomics (transcriptomics, proteomics, and metabolomics), data management and analysis will be addressed. WP6.3, headed by Heiko Schoof, concentrates on integration of *Solanaceae* data resources and analysis. Part of the work within WP6 will be directed to phase 3 completion of tomato BACs, building a *Solanaceae* genome annotation platform, and provide an automated functional annotation.

Chromosome 7 (France)

Contact: Farid Regad (regad@ensat.fr)

Update pending.

Chromosome 8 (Japan)

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

We finished forty-six BACs to phase 3 (total non-overlapping length 3,922,329 bases) of which twenty-two are seed BACs and twenty-four are extended clones. Two BACs are being assembled and eighteen are in the sequencing pipeline. Extension from the southernmost markers TG294 and TG346 at 87 cM has led us to discover a possible subtelomeric repeat of 180-bp unit. We are planning to perform FISH to identify its localization on chr 8 as well as on other chromosomes.

To complement the ongoing sequencing project, we have launched Selected BAC Mixture (SBM) shotgun sequencing. In this method, BAC clones whose end sequences do not contain repeat sequence are selected, then the selected BACs are mixed and shotgun sequencing is performed. This may be effective for filling in gene spaces at the later stage of the project. To select clones to mix, we performed a search against the repeat dataset using the BAC end sequences as query. According to the result, 54,000 out of 177,000 clones had unique sequence on both ends. Currently, we are picking up 20,000 clones among the 54,000 non-repeat BACs. If we estimate the length of euchromatin to be 300 Mb, these clones could cover more than six times.

Another effort is the development of novel microsatellite markers from tomato unigene and full-length cDNA sequences. We identified 2,500 SSR of which 2,000 have not been mapped. We will map these markers using IL lines to develop new seed points for chr 8 sequencing.

Chromosome 9 (Spain)

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

So far, we have deposited sequences corresponding to eighteen BACs, and we have nine additional BACs in the finishing process. Of the eighteen BACs, eight are in phase 3 that are without gaps and ten are in phase 2 with less than 6 gaps. We now face the problem of a lack of BACs overlapping with the ones sequenced. The new FPC from the MboI library has not been very useful in our case to find new extension BACs. We are looking forward to a more complete FPC. Our efforts are currently oriented to identify new seed BACs. We have found BES containing sequences from chr 9 markers in five cases. We are also trying to do our own FISH localization in-house. We have asked to use part of our budget for sequencing from EUSOL to screen the libraries for new seed BACs using chr 9 markers, however, so far, none have assigned to any BACs.

Chromosome 12 (Italy)

Contact: Mara Ercolano (ercolano@unina.it)

Since our last report, three new seed BACs have been validated and ten new extension BACs are under evaluation to select minimal tilling paths. Sequencing of six BAC clones has been completed to phase 3 and twenty are in phase 1 or 2. Five clones are in the production phase, and four are in the shotgun phase. Processing of the additional five clones is underway. The chromosome walking to move out as small contigs has been initiated. In particular, the seed BAC LE_HBa026C13 has been merged with BAC LE_HBa0073O10 and LE_HBa0090D09, the seed BAC 032K07 with BAC SL_MboI0126D24 and SL_EcoRI0082A18, the seed BAC LE_021L02 with BAC Le_HBa0149G24, SL_EcoRI0004H16, and SL_EcoRI0004H16. Currently, we are assessing our data to reduce the overlaps between successive clones to obtain a more efficient chr 12 sequence scaffold.

International Tomato Annotation Group (ITAG)

Contributed by Lukas Mueller

The International Tomato Annotation Group (ITAG) met in Ghent, Belgium, from October 23-25, 2006, to establish an annotation protocol for the tomato genome. The ITAG consists of computational biology groups from Germany (MIPS, Max Planck Cologne), Great Britain (Imperial), India (Genome India), Korea (KRIBB), Spain (IMIM Barcelona), Italy (University of Naples), France (INRA Toulouse), the Netherlands (University of Wageningen), USA (Cornell University), Japan (Kazusa), China and Belgium (VIB Ghent). The annotation pipeline is a distributed effort between these centers and will result in an automated, high-quality, uniform annotation for the entire tomato genome. Initially, the annotation will be based on BAC sequences, and in a later stage of the genome project on large contigs approximating chromosome arms. The annotation will incorporate ab-initio prediction as well as evidence-based annotation. A centerpiece of the annotation pipeline is Eugene, a genome annotation program developed at INRA Toulouse and Ghent, that has been successfully run on many other plant genomes, such as *Arabidopsis*, *Medicago* and rice. Additional information on the ITAG and the meeting is available at http://sgn.cornell.edu/solanaceae-project/sol-bioinformatics/.

ANNOUNCEMENTS

NEW WEBSITE

eusol The EU-SOL has launched its website which can be found at www.eu-sol.net.

PUBLICATION

There is a newly published molecular marker for the discrimination of the original San Marzano tomato, which is the typical and famous peeled tomato grown for processing in Italy, particularly in the Campania region. A pdf of the publication will be posted along with the pdf of this newsletter on SGN at http://www.sgn.cornell.edu/solanaceae-project/index.pl#SOL_news.

CONFERENCES/MEETINGS

eusol The kick-off meeting of the EU-SOL project will take place in Wageningen from November 21 – 22, 2006. For additional information, contact René Klein Lankhorst at rene.kleinlankhorst@wur.nl.

Plant and Animal Genome XV Conference
January 13 – 17, 2007
Town and Country Convention Center
San Diego, California
http://www.intl-pag.org/

SOL 2007

The 4th Solanaceae Genome Workshop
September 9 – 13, 2007
Ramada Plaza, Jeju Island, Korea
http://www.solanaceae2007.org/

SOLANACEAE RECIPES

Since many of us live in regions that are now in the cold weather seasons, I thought it would be good to include recipes for soup and bread, which is my favorite combination for a meal on a cold, blustery day. Remember, if you have any *Solanaceae* recipes to share, send them to me, Joyce Van Eck, at jv27@cornell.edu. Enjoy!

Potato, Spinach and Tomato Soup

From the Food Network (www.foodnetwork.com)

3 cloves crushed or finely chopped garlic
1 large onion, chopped
2 tablespoons extra-virgin olive oil
2 quarts chicken broth
3 pounds all purpose potatoes, peeled and thinly sliced
1 pound fresh triple washed spinach, stems picked and coarsely chopped
1/4 teaspoon nutmeg, grated or ground
Salt and pepper
1 (28-ounce) can chunky-style crushed tomatoes or diced tomatoes in puree
1/2 cup grated Parmigiano-Reggiano or Romano

In a deep pot, sauté garlic and onion for 2 or 3 minutes. Add broth and bring liquid to a boil. As you slice potatoes, add them carefully to the broth. Cook potatoes 20 minutes, stirring occasionally. The potatoes will begin to break up and thicken broth as the soup cooks. Stir in spinach in bunches as it wilts into soup. Season soup with nutmeg, salt and pepper, to your taste. Stir in tomatoes and heat through, 1 or 2 minutes. Remove pot from the stove. Stir grated cheese into the soup and serve.

Potato Bread

From the Food Network (www.foodnetwork.com)

1 baking potato, peeled and cut into large chunks, or 1 cup leftover mashed potatoes
1 cup milk
1 1/2 tablespoons shortening
1 1/2 tablespoons unsalted butter
1 1/2 teaspoons salt
1 tablespoon granulated sugar
1 tablespoon dry yeast
1/3 cup warm water
5 cups bread flour

Boil potato until soft. Drain and save the cooking liquid. Mash the potato well.

Scald milk and combine with 1/2 cup of the saved liquid from cooking the potato. Combine liquids and potato with shortening, butter, salt, and sugar in a large bowl. Set aside to cool to room temperature.

Meanwhile combine yeast and warm water, and set aside until foamy. When potato mixture has cooled, add yeast mixture. Add flour and knead need by hand or in an electric mixer fitted with a dough hook until smooth and glossy, about 7 minutes.

Transfer to a buttered bowl, cover with plastic wrap, and set aside in warm place to rise about 1/2 hour. Punch dough down and briefly knead. Butter a 9 x 5 x 3-inch loaf pan. Place dough in pan, cover with plastic, and let rise until doubled, about 45 minutes.

Preheat oven to 350 degrees. Bake 30 minutes, or until bread sounds hollow when tapped.