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Editor: Joyce Van Eck

The Sol Newsletter

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Community News

Genome Sequencing Goes Wild

We have heard about developments in genome sequencing of key *Solanaceae* family members, but now it is the wild species turn. Wild species provide a rich resource of genetic diversity and have been integral parts of breeding programs, especially for tomato. The following two articles highlight recent developments in the sequencing of two tomato wild species, *Solanum pimpinellifolium*, the closest wild progenitor of cultivated tomato, and S. pennellii, an important source of research tools and alleles for breeding.

Genome Sequence of the Wild Tomato Species, *Solanum pimpinellifolium*

Doreen Ware, W. Richard McCombie, Z. B. Lippman
Cold Spring Harbor Laboratory

The research groups of Doreen Ware, W. Richard McCombie, and Zach Lippman at Cold Spring Harbor Laboratory in New York have generated and assembled the genome sequence of the wild tomato species *Solanum pimpinellifolium* (LA1589). *S. pimpinellifolium* is the proposed wild progenitor of domesticated tomato, and its elucidated genome provides a rich resource for biological discovery on the processes of plant domestication and evolution. The sequence was generated using Illumina sequencing technology consisting of paired-end 100 base pair reads, which resulted in an estimated 20- to 30-fold genome coverage. The data have been assembled using the ABySS short read sequence assembly algorithm. Provided below are a selection of statistics resulting from de novo assembly of the Illumina data only:

N50	3303
n>=1000nt	136086
n>=10000nt	13082
Total contig length: 899.84 Mb	

Solanum pimpinellifolium fruit

Additional data has been generated, including two 3kb mate-pair linker libraries sequenced on Illumina and 454, which will enable a much improved de novo assembly, and these additional sequencing reads are currently being incorporated into the existing assembly.

Initial usage of the data has indicated excellent coverage and depth: of more than 100 loci analyzed, all have been located in the *S. pimpinellifolium* genome assembly. This analysis includes both genes and promoter sequences. Furthermore, polymorphisms (SNPs and indels) are apparent and are abundant enough to achieve molecular markers for genes of interest. With a *S. pimpinellifolium* genome in hand, there is now the opportunity to exploit the germplasm of closest wild relative of domesticated tomato for gene and QTL discovery.

The biological comparison of *S. pimpinellifolium* with *S. lycopersicum* cv. Heinz will provide rich knowledge on the evolution and domestication of tomato, and will provide the foundation for future tomato genome sequencing efforts on more distantly related species. The Ware group has begun an analysis of the *S. pimpinellifolium* genome, including annotation and alignment to the reference Heinz genome. Preliminary analysis indicates that greater than 50% of the *S. pimpinellifolium* raw sequence reads align to Heinz, suggesting a very close genomic relationship. The *S. pimpinellifolium* contigs from the first assembly have been aligned to Heinz, and a diversity analysis comparing *S. pimpinellifolium* with *S. lycopersicum* has been initiated to determine SNP and indel frequency.

Sequencing of the *Solanum pennellii* Genome as a First Approach to Investigate Diversity in the Tomato Clade

By Alisdair Fernie

Solanum pennellii leaves and fruit

The previously announced sequencing of *S. pennellii* - a joint effort mainly coordinated between the Potsdam-Golm and Tübingen Max Planck Research Institutes, INTA-Buenos Aires and the Boyce Thompson Institute and the USDA, Ithaca, NY, is relatively close to completion. A coverage of approximately 100-fold has been obtained and assembly is in progress. In parallel we have begun work on M82, the other parent of the much used "Zamir pennellii introgression lines", which we anticipate to sequence at between 20- and 30- fold coverage.

Solanaceae Resources

Illumina Potato and Tomato Arrays

Provided by Cindy Lawley

SolCAP (http://solcap.msu.edu/) is making SNP genotyping tools for potato and tomato widely available to the Solanaceae community. An Illumina genotyping array targeting approximately 9,000 SNPs is being developed for potato. The anticipated availability of the potato array is August 2010 with initial orders due by June 15, 2010. An Illumina array targeting 7,000-9,000 SNPs is also being developed for tomato. Orders for the tomato genotyping tool will be accepted later in the summer with availability of the tool anticipated in the Fall 2010. For any questions related to these tools, please contact David Douches (douchesd@msu.edu) regarding the potato array and David Francis (francis.77@osu.edu) for the tomato array.

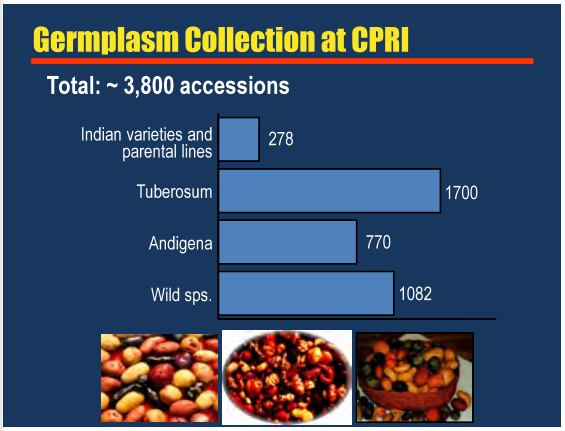
Biodiversity

Potato Genetic Resources in India

By J. Gopal
Central Potato Research Institute, Shimla-171 001
Email: jai_gopal@rediffmail.com

Potato though an introduced crop for India, is now the third most important food crop of the country after rice and wheat. Presently it is grown over an area of 1.4 million hectares with an average yield of 19-20 tons per ha. Lower productivity of potato in India as compared to European and American countries is due to the fact that in India 90% of the potato area is in plains where it is grown as a short duration crop of 70-90 days under 8-10 h photoperiod of sub-tropical winters. In temperate regions of the world potato is grown during summer under long photoperiods of 14-16 h and the crop duration is more than 120 days. Since the start of an organized research program on potato in India in 1949 at the Central Potato Research Institute, Shimla (CPRI-the only national institute in the country devoted to potato research and development), the area, production and productivity of potato have increased by 6, 16 and 3 times, respectively. Development of improved potato cultivars adapted to varying agro-climatic conditions of the country has contributed significantly to this increase. The genetic resources program of potato has been the backbone of all potato improvement programs of the country.

Potato is generally believed to have been introduced in India in the late 16th century, possibly by the Portuguese or the British missionaries. By the end of the 19th century, potato cultivation spread throughout northern India, which covers the main potato belt of Indo-Gangetic plains. In India, the first attempt to collect variability of potato was made in the 1940s, and about 400 indigenous samples were collected. In this mass of variability, 16 varieties were identified as known exotic cultivars, while the rest were grouped into 16 distinct morphotypes, whose original identity could not be established. These cultivars represented some of the earliest introductions or their clonal variants and were termed as *desi* varieties. During 1983-1992, several explorations were conducted. A total of 621 samples were collected. These samples were studied for various morphological characters and



grouped into 125 distinct morphotypes. These were mostly susceptible to various diseases and pests and stocks were highly degenerated. Thus this material was not enough to have a robust potato breeding program. Acquisition of exotic germplasm from different countries has, therefore, been a continuing activity of the CPRI since its establishment. The CPRI now has a collection of nearly 3,800 accessions belonging to cultivated species (*S. tuberosum* ssp. *tuberosum* and ssp. *andigena*) as well as wild or semi-wild species. These germplasm accessions have been imported from 30 countries based on our requirements of resistance or tolerance to various biotic and abiotic stresses. The major source of this collection has been the International Potato Center (CIP), Lima, Peru and the USA Potato Genebank, Sturgeon Bay, Wisconsin. Prior to the establishment of the CIP, maximum import of potato germplasm was made from the Commonwealth Potato Collection, Dundee, Scotland.

The germplasm collection at the CPRI is being maintained by three methods, i) *in vivo* clonal propagation, ii) *in vitro* clonal propagation, and iii) true seeds. *In vivo* clonal propagation is carried out in duplicate sets in fields. All *tuberosum* and a part of *andigena* accessions are being maintained and multiplied by this method to facilitate their evaluation for adaptability to different agro-climatic regions as well as for resistance/tolerance to various biotic and abiotic stresses. A part of the accessions belonging to *andigena* and wild species are being maintained in true seed form. True seeds are produced by selfing and/or sibmating.

Sibmating is often resorted to in the case of diploid species most of which are self-incompatible. To date, about 1700 *tuberosum* and some wild accessions have been conserved employing *in vitro* approach. Minimal growth strategy is used in which nodal cuttings are cultured on Murashige and Skoog's medium containing 20g/l sugar and 40g/l sorbitol under a 16-h photoperiod at 6 °C. Under these conditions potato plantlets can be preserved up to 24 months without sub-culturing. This medium when used under normal propagation temperature reduces the plantlets life to only 9-12 months. A protocol based on chemo-cum thermotherapy has been developed for virus elimination and it is now routinely used for eliminating even the most difficult viruses namely PVX and PVS from the infected accessions. Testing for virus freedom of all *in vitro* conserved accessions is followed as a routine activity.

In the early stages of potato research in India, evaluation of a large number of European varieties was undertaken to identify cultivars adapted to Indian conditions. These efforts were, however, largely unsuccessful because the exotic cultivars being adapted to temperate long-day growing conditions in the west were unsuitable under the sub-tropical short-day conditions prevailing in India. Attention was, therefore, focused to identify suitable parental lines for Indian potato breeding programs. The germplasm accessions were thus evaluated for economic characters like resistance to late blight (*Phytophthora infestans*), bacterial wilt (*Ralstonia solanacerum*), wart (*Synchytrium endobioticum*), root-knot nematodes (*Meloidogynae* sps.), cyst nematodes (*Globodera* sps.), potato tuber moth (*Phthorimaea operculella*), powdery scab (*Spongospora subterranea*), charcoal rot (*Macrophomina phaseoli*), hopper burn (*Amrasca devastans*) and viruses, besides maturity, tuber dormancy, storage quality, tuber dry matter and protein content, etc.

The accessions are also evaluated for adaptability under varying thermo-photoperiods. The results of evaluation have been compiled and the catalogs of potato germplasm collection have been published. The electronic databases are also maintained and updated regularly so that breeders are able to use this information for selecting the parents as per their requirements. To identify good general combiners among the germplasm accessions found promising for various characters, combining ability studies have been conducted. Evaluation as well as breeding value estimation is a regular process and are being continued to confirm as well as generate new information.

Evaluation and pre-breeding of wild species is also undertaken. Similarly, a program on improvement of *andigena* is underway so as to develop clones with early bulking and acceptable tuber characters. Good progress in this regard has already been made and efforts are being continued to improve *andigena* as a population. A core collection of *andigena* germplasm has been developed and this group of germplasm is particularly suitable to Indian conditions being adapted to short–days for tuberization. The use of *andigena* has resulted in the development of some clones, which have been released as varieties for general cultivation.

To date, the CPRI has released 47 potato varieties by using the potato collection available in its germplasm repository. Presently more than 90% of the area under potato production in India is grown with the varieties developed by the CPRI. Some of these varieties are also popular in neighboring countries and demand is also being received from far off countries e.g. Australia and South Africa. All this has been possible due to systematic work on collection, conservation, evaluation, documentation and parental lines development undertaken under the potato genetic resources program of the country.

Genome Updates

Progress of Pepper Genome Sequencing

As an aim to make a reference genome sequence of pepper, we launched a pepper genome sequencing project in Korea. On the basis of a haploid genome, pepper has the largest genome size (2.7 – 3.3 Gb) among well-known *Solanaceae* species. In this project, we used the *Capsicum annuum* CM334 as the sequencing material. CM334 is known as the wild species, which has strong resistance against diverse diseases. It also contains diverse phenotypes such as trichome and pungency. The genome size of CM334 is estimated at approximately 2.7 Gb.

As a major strategy for the pepper genome sequencing project, we are using Illumina/Solexa Genome Analyzer 2 to generate massive raw sequences. To date (May, 2010), we have generated a total of 306 Gb raw sequences corresponding to above 100x coverage of the CM334 genome. Currently, a total of 156 Gb raw sequences corresponding to 57x coverage have been successfully assembled, and the results are as follows. The total assembled contig length is 2.57 Gb and the contig number is 1,876,612. N50 size and average length are 3,890 bp and 1,370 bp, respectively. The assembly results will be improved by including the remaining raw sequences.

Our current effort for pepper genome sequencing is focused on making longer scaffolds. To make scaffolds we will collaborate with BGI. By cooperation with BGI, we will generate long mate-pair sequences, and the scaffolds will also be assembled.

Along with the whole genome shotgun sequencing, we used pepper BAC clones to make longer contigs. We have a pepper BAC library of CM334 corresponding to 12x coverage of the genome and approximately 120 Kb insert size. By BAC library screening, we selected a total of 2,382 pepper BAC clones and sequenced them. Among them, 1,270 BAC clones were sequenced using Roche/454 FLX and the others were sequenced using Illumina/Solexa Genome Analyzer 2 by BAC pooling. The BAC clones were screened by labeled cDNA of pepper or tomato mRNA (tomato mRNA was used to avoid the screening by retrotransposons). In addition, a total of 435 BAC clones containing NBS-LRR were found by BAC screening using the NBS-LRR gene sequences as probes. Recently, we have assembled the 1,270 pepper BAC clone raw sequences generated by Roche/454 FLX, resulting in 34,743 of contigs, 2,707 bp of average contig size, and 0.94 Gb of total length. The remaining BAC clone sequences will also be assembled soon.

Progress of the pepper genome sequencing will be keep updated through the SOL Genomics Network (http://solgenomics.net/). For additional information, contact Mr. Minkyu Park (minkju@hanmail.net) or Prof. Doil Choi (doil@snu.ac.kr).

Tomato Genome Sequencing

India: Contact - Akhilesh Tyagi (akhilesh@genomeindia.org)

At the Indian Initiative on Tomato Genome Sequencing, we have confirmed positions of ninety-seven BACs on chromosome 5. Till now, seventy BACs have been sequenced to phase III level, fifteen BACs are at phase II level and six BACs are at phase I level of sequencing. The remaining six BACs are in the early phase of sequencing or library preparation. Emphasis has been given to finish the in-hand BACs and the search is on to find new nucleation points on chromosome 5 by mapping BAC ends on the tomato WGS data followed by confirmation using introgression lines.

UK: Contact - Gerard Bishop and Rosa Lopez-Cobollo (g.bishop@imperial.ac.uk, r.lopez-cobollo@imperial.ac.uk*)*

We are using PCR to assess the nature of the gaps between contigs in the scaffolds. Sixteen scaffolds from the assembly version 1.03 have been mapped to Chr 4 with a total length of 63,09 Mb. In a first approach, we selected the five largest scaffolds from this assembly and integrated the Chr4 sequences produced by the BAC-by-BAC sequencing. This gave us a total of 269 gaps. We have used ~1-2 kb upstream and downstream of each gap to design primers and fill the gaps by PCR. In summary, the results show that the gaps are smaller than expected and a number of non-specific products have been found. Certain products have generated suitable sequence information to fill the gaps. See the table on the next page.

We intend to continue this strategy to improve the quality of Chr4 sequence.

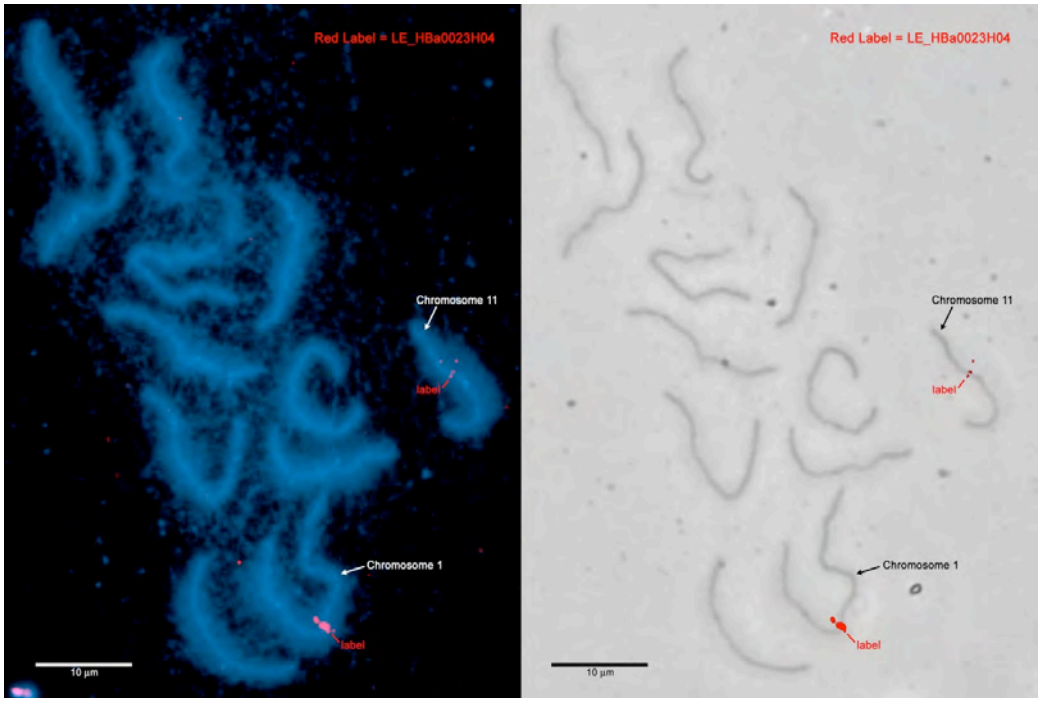
Scaffold number	# gaps in the scaffold	Pair primers assessment	Checked	Results
00103	6	6	6	2 good PCRs smaller size than expected, 2 multiple bands but one high intensity, 2 no PCR product
01260	14	14	14	2 good PCRs one band expected size; 2 PCRs one band smaller size than expected; 10 PCRs multiple bands, the intensive is smaller size than expected or not intensive band
00192	143	6	6	5 good PCRs one band expected size; 1 no PCR product
00077	106	8	-	-

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

We have continued to sequence chromosome 1 and 10 BACs with over 180 completed and many more in the pipeline. Current efforts are directed toward utilization of the tomato physical map to identify minimal tiling paths across these two chromosomes that will allow selection of BAC contigs, which will be sequenced to fill gaps in the current assembly.

Since the last SOL newsletter, the Stack lab at Colorado State University has localized an additional 32 BACs using FISH on pachytene synaptonemal complex spreads. This brings the total number of BACs placed on the SGN FISH map to 246. The 246 BACs are distributed among the chromosomes as follows: 1 - 55; 2 - 19; 3 – 17; 4 – 19; 5 – 13; 6 – 11; 7 – 25; 8 – 9; 9 – 20; 10 – 34, 11 – 15, 12 – 10. The recently positioned BACs include (all from the HindIII library, listed by chromosome arm): 1Q-256E08, 174H02, 024H04, 289N16, 330O05, 140O23, 123A07, 169H23, 057C07, 159C14, 010F03, 005L21, 001H15, 302G11, 111D21, 164M23, 057J16, 037D10, 239E07, 231M15, 3P-162G22, 3Q-276M05, 4Q-007D04, 291H22, 078E04, 013P02, 6Q-188N10, 146O07, 7P-293I23, 325D07, 111F22, 007H24, 095C18, 002D20, 193E01, 8P-270A17, 8Q-213E05, 9P-072G22, 9Q-061J21, 10P-091N19, 176H22, 10Q-115K16, 044O20, 022B11, 181E17, 11P-023H04, 291F03, 12P-163O04, 146I19, 049J09, 206N09, and 12Q-148K11. BAC 023H04 has two loci, one on 1Q and one on 11P.

The figure below illustrates FISH labeling on tomato chromosomes 1 and 11 with BAC LE_HBa0023H04, which localized to two places in the genome. This BAC contains marker T1524, which mapped to chromosome 1 at 34.5 cM. This genetic position is consistent with the cytogenetic position of the locus on chromosome 1.



Announcements

Publications

Ament K, Krasikov V, Allmann S, Rep M, Takken FLW, Schuurink RC (2010) Methyl salicylate production in tomato affects biotic interactions. Plant J 62:124-134.

Colón AM, Sengupta N, Rhodes D, Dudareva N, Morgan J (2010) A kinetic model describes metabolic response to perturbations and distribution of flux control in the benzenoid network of *Petunia hybrida*. Plant J 62:64-76.

D'Ambrosio C, Stigliani AL, Giorio G (2010) Overexpression of *CrtR-b2* (carotene beta hydroxylase 2) from *S. lycopersicum* L. differentially affects xanthophyll synthesis and accumulation in transgenic tomato plants. Transgenic Res DOI 10.1007/s11248-010-9387-4.

de Kochko A, Akaffou SI, Andrade A, Campa C, Crouzillat D, Guyot R, Hamon P, Ming R, Mueller LA, Poncet V, Tranchant-Dubreuil C, Hamon S (2010) Advances In Coffea Genomics. In: Advances in Botanical Research, 53 (Kader JC, Delseny, eds.) Elsevier Inc. (http://www.elsevier.com/wps/find/bookdescription.cws_home/722900/description#description).

EU-SOL Newsletter, no. 6, April 2010 (www.eu-sol.net), editor: Huib de Vriend.

Kelley BS, Lee S-J, Damasceno CMB, Chakravarthy S, Kim B-D, Martin GB, Rose JKC (2010) A secreted effector protein (SNE1) from *Phytophthora infestans* is a broadly acting suppressor of programmed cell death. Plant J 62:357-366.

Koltai H, LekKala SP, Bhattacharya C, Mayzlish-Gati E, Resnick N, Wininger S, Dor E, Yoneyama K, Yoneyama K, Hershenhorn J, Joel DM, Kapulnik Y (2010) A tomato strigolactone-impaired mutant displays aberrant shoot morphology and plant interactions. J Exp Bot 61:1739-1749.

Kosma DK, Parsons EP, Isaacson T, Lü S, Rose JKC, Jenks MA (2010) Cuticle development in tomato ripening mutants. Physiologia Plantarum 139:107-117.

Loebenstein G, David DR, Leibman D, Gal-On A, Vunsh R, Czosnek H, Elad Y (2010) Tomato plants transformed with the inhibitor-of-virus-replication gene are partially resistant to *Botrytis cinerea*. Phytopathology 100:225-229.

Tieman D, Zeigler M, Schmelz E, Taylor MG, Rushing S, Jones JB, Klee HJ (2010) Functional analysis of a tomato salicylic acid methyl transferase and its role in synthesis of the flavor volatile methyl salicylate. Plant J 62:113-123.

Web Resources

Interactive Sequencing Puzzle

An international consortium of research groups from ten different countries including the US is sequencing the tomato genome. The US team's tomato sequencing efforts are funded by the National Science Foundation (NSF). In addition to funding the research, NSF also provides funds for educational outreach. As part of their outreach activities, the US group has devised an interactive sequencing puzzle activity in collaboration with Boyce Thompson Institute's web designer. The activity includes background information on tomatoes and various molecular biology terms and techniques. Give the puzzle a try at http://www.bti.cornell.edu/multimedia/puzzleComplete.html.

Tomatoes Having Sex

Contributed by Huib de Vriend, LIS Consult

To attract the attention of a wider audience to EU-SOL's achievements and objectives, we have asked two Austrian students in video and animation arts to make a nice videoclip about EU-SOL. It can be viewed on YouTube (http://www.youtube.com/watch?v=33YMYOAuDiQ) and Vimeo (http://www.vimeo.com/10630076); better quality! <http://www.vimeo.com/10630076%20;%20better%20quality!>). You may find it fun to use this in your presentations. If you like to have a version in full resolution, please send an email to devriend@lisconsult.nl and I'll send you a DVD.

Tomato Processing Industry Newsletters

Tomato Land - http://www.tomatoland.com/index.php
Tomato News - http://www.tomatonews.com/index.php

Conferences

Metabolomics 2010
June 27 - July 1, 2010
Amsterdam, The Netherlands
http://www.metabolomics2010.com/

XXI International Congress of Sexual Plant Reproduction
August 2 - 6, 2010
University of Bristol, Bristol, UK
http://www.sebiology.org/management/meetings/SexualPlantReproduction.html

Potato Association of America
August 15 - 19, 2010
Corvallis, Oregon
http://potatoassociation.org

Capsicum and Eggplant Breeding 2010, Working Group Meeting
August 30 - September 1, 2010
Valencia, Spain
e-mail: jprohens@btc.upv.es
www.comav.upv.es/capsicumeggplant

SOL2010
7th Solanaceae Conference
September 5 - 9, 2010
Dundee, Scotland
http://www.sol2010.org/

ASIC 2010
The 23rd International Conference on Coffee Science
October 3 - 8, 2010
Bali, Indonesia
http://www.asic2010bali.org/index.htm

43rd Tomato Breeders Roundtable Meeting
March 20 - 23, 2011
El Cid Resort
Mazatlan (Sinaloa), Mexico
Information will be posted within the next month at
http://tombreeding.ifas.ufl.edu

Solanaceae Recipes

Cape Gooseberry Chutney

Contributed by Owen Hoekenga

Ingredients

1 lb Cape Gooseberries/Husk Cherries (*Physalis pruinosa*), such as http://www.johnnyseeds.com/p-5883-goldie-og.aspx or 450 g
¼ lb raisins (prefer golden) or 115 g
½ oz chillies (14 g)
½ oz garlic (14 g)
1/16 oz fresh ginger (2 g)
12 oz white sugar (340 g)
5/8 c white vinegar (150 ml)
¼ oz salt (7 g)

Makes 3 half-pint jars as described, but can be scaled up.

Cape gooseberries (*Physalis pruinosa*)

1. Wash and rinse half-pint canning jars; keep hot until ready to use. Prepare lids according to manufacturer's directions.
2. Husk, wash and dry cape gooseberries. Rinse raisins and leave to drain. Core and seed the chillies. Peel garlic.
3. Place cape gooseberries, raisins and ginger into food processor and chop to relish-like consistency. Tip mixture into saucepan with the sugar. Stir under low heat until sugar dissolves.
4. Place vinegar, garlic, chillies and salt in the food processor and chop to very fine consistency. Add this mixture to fruit/sugar. Increase to boil but then reduce to simmer, stirring occasionally for 5-10 minutes or until 220F/104C temperature is reached. Remove from heat.
5. Add hot chutney with ladle to hot, sterile jars, leaving ¼ inch/5 mm headspace. Wipe rims of jars with a damp, clean cloth; adjust two-piece metal canning lids. Process in a Boiling Water Canner for appropriate amount of time for your elevation (generally 5 minutes for sea level to 1000 ft, 10 minutes for 1,001 to 6,000 ft and 15 minutes for above 6,000 ft; see food preservation websites such as that operated by USDA's National Center for Home Food Preservation for more detailed instructions: http://www.uga.edu/nchfp/publications/uga/using_bw_canners.html).
6. Check the seals 1-2 days later. Use homemade chutney within 12 months of canning.

Adapted from "The Complete Book of Curries" by Harvey Day (1970).

Eggplant Rolls with Spicy Tomato Sauce

http://www.gourmet.com

1 garlic clove, minced
1/4 teaspoon dried hot red pepper flakes
7 tablespoons olive oil
1 1/2 lb plum tomatoes, chopped
1/2 teaspoon sugar
1 teaspoon salt
1 (1 1/4-lb) eggplant
12 1/2 oz ricotta (preferably fresh; 1 1/2 cups)
1 1/2 oz finely grated Parmigiano-Reggiano (1/2 cup)
3 tablespoons finely chopped fresh basil
1/4 teaspoon black pepper

Make sauce:

- Cook garlic and red pepper flakes in 1 tablespoon oil in a 2-quart heavy saucepan over moderate heat, stirring, until garlic is golden, about 30 seconds. Add tomatoes, sugar, and 1/2 teaspoon salt and simmer, uncovered, stirring occasionally, until slightly thickened, 15 to 20 minutes.

Grill eggplant while sauce cooks:

- Heat grill pan over high heat until hot.
- Peel 2-inch-wide strips of skin from opposite sides of eggplant and discard. Holding a knife parallel to a peeled side, cut eggplant lengthwise into 8 (1/3-inch-thick) slices. Brush both sides of slices with 3 tablespoons oil (total), then season with salt and pepper.
- Grill slices in batches, turning over once and brushing grilled sides with some of remaining oil, until golden brown and tender, about 4 minutes, then transfer to a tray.

Assemble eggplant rolls:

- Stir together cheeses, 2 tablespoons basil, pepper, and remaining salt. Divide cheese mixture among slices (3 to 4 tablespoons per slice), leaving an 1/8-inch border along edge. Roll up each slice, beginning with a short end, and serve rolls topped with sauce and sprinkled with remaining basil.

Cooks' note: Eggplant can be grilled using a gas grill. Preheat all burners on high, covered, 10 minutes, then reduce heat to medium. Grill eggplant on lightly oiled grill rack, covered with lid, turning over once, until tender and grill marks appear, 4 to 5 minutes total.