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Community News

The 4th Solanaceae Genome Workshop

Ramada Plaza, Jeju Island, Korea
September 9 - 13, 2007

Dear Colleagues,

We are glad to announce that the online-registration for the 4th Solanaceae Genome Workshop is ready. You can register at <http://www.solanaceae2007.org/>. Faxed registrations to headquarters (Fax 82-2-873-5410) are accepted for wire transfer only. For "Early Bird" benefits, your registration and payment must be received no later than July 31, 2007. Registrations received after July 31, 2007 will be considered on-site registration and will be processed at the meeting.

We cordially invite you to participate in this exciting conference!

Sincerely yours,
Doil Choi and Byung Dong Kim
Chairs, The SOL 2007 Organizing Committee



First International Tomato Finishing Workshop

Contributed by Karen McLaren and Helen Beasley

On the 16th and 17th of April 2007, the First International Tomato Finishing Workshop was held at the Wellcome Trust Sanger Institute in Hinxton, Cambridge UK. Delegates from France, Italy, the Netherlands, Spain, the USA and the UK attended, giving representation for eight out of the twelve *S. lycopersicum* chromosomes being finished across the consortium.

The workshop started with a tour of the Wellcome Trust Sanger Institute (WTSI) campus followed by presentations on the main principles of mapping and finishing approaches at the WTSI. This opened the discussion to the recently updated tomato genome finishing standards document available on SGN at <http://www.sgn.cornell.edu/solanaceae-project/sol-bioinformatics/> and at http://docs.google.com/View.aspx?docid=dggs4r6k_1dd5p56.



Minimum attempts for gap closure and resolution of low quality sequence in BACs were discussed at length in conjunction with the finishing standards document. One of the key points raised from this discussion included the use of restriction digest data to confirm the assembly of finished BACs. Other discussion points included how each chromosome group is dealing with finishing overlaps between BACs, screening for contamination and other quality control steps.

New tools available on SGN for viewing map and finished sequence were also demonstrated. This led to a discussion on making available tile path format (TPF) and accessioned golden path (AGP) files for each chromosome, where the chromosome groups present at the workshop agreed to submit these files to SGN by June 2007.

Generally viewed as a success, the workshop provided a forum for both informal and formal discussions on the finishing process along with the opportunity to meet the people on the sequencing side of the tomato genome project who are all working towards the same goal. Proposals were made for holding a second workshop in February 2008.



The 3rd Japanese SOL Tomato Workshop Meeting Report **Kazusa, Japan, March 20 - 21, 2007** **By Koh Aoki, Kazusa DNA Research Institute**

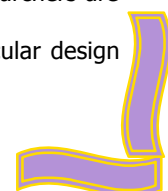
The 3rd Japanese (JSOL) Tomato Workshop, organized by Koh Aoki and Daisuke Shibata, was held at Kazusa Akademia Park (Okura Akademia Park Hotel) from March 20 to 21, 2007. One of the two main ideas of the workshop was to stimulate the use of currently available tomato genomic resources including a Micro-Tom transformation system, mutant lines, and cDNAs, and to discuss future directions of resource development. Thus, the workshop was entitled "Tomato Genomic Resources: Current Status and Things to Come". Three foreign invited speakers and seventy-four Japanese scientists from national institutes, universities, and private companies attended the workshop.

On March 20, three talks were presented by the foreign invited speakers. Giovanni Giuliano (ENEA, Italy) presented metabolic engineering of carotenoids in potato and tomato to produce "golden" crops, followed by the analysis of transgene-dependent pleiotropic effects that suggest the presence of unknown relationships between carotenoid accumulation and other aspects of fruit ripening. Rameshwar Sharma (University of Hyderabad, India) gave an overview of genome sequencing, mutant lines, and a TILLING platform in India, followed by analyses of an acetylene resistant mutant, tomato *short root*, and a non-phototropic shoot mutant. Yuval Eshed (Weizmann Institute of Science, Israel) demonstrated that tomato and Arabidopsis share the same molecular pathway but have diverged outcomes in leaf morphogenesis, by showing the analyses of *Lanceolate* and *wiry* orthologs (affecting miRNA regulation and siRNA biogenesis, respectively) in tomato and Arabidopsis. The next four talks were presented by Japanese invited speakers. Erika Asamizu (Kazusa DNA Res. Inst.) summarized the current status of chromosome 8 sequencing, and proposed several strategies towards finishing. Hiroshi Ezura (Univ. of Tsukuba) presented practical and detailed "tips" for successful tomato transformation. Daisaku Ohta (Osaka Prefecture Univ.) reported the analysis of CYP710A from Arabidopsis and tomato in the C-22 desaturation step of sterol biosynthesis. Koh Aoki (Kazusa DNA Res. Inst.) gave an update of Micro-Tom full-length cDNA sequencing.

On March 21, the development of Micro-Tom mutant lines was reported in the first session. Shunsuke Imanishi (NIVTS) reported on heavy-ion beam and gamma-ray induced mutant lines. Shin Watanabe (Univ. of Tsukuba) reported on development of EMS mutant lines and the phenotypic database, Tomato Mutant Archives. Tsuyoshi Mizoguchi (Univ. of Tsukuba) presented a preliminary result of T-DNA tagging of Micro-Tom, and an estimation of time required for generating saturated lines. Kentaro Yano (Univ. of Tokyo) presented an update on the full-length cDNA database KaFTom and a new unigene set available in MiBASE. In the second session, two talks concerning tomato plastids were presented. Mitsumasa Hanaoka (Univ. of Tokyo) reported on specific sigma factors associated with chloroplast development and chromoplast differentiation. Reiko Motohashi (Shizuoka Univ.) presented a proteomics analysis of Arabidopsis and tomato plastids, including chromoplast proteomics. In the third session, functional genomics and metabolomics studies using tomato genomic resources were presented. Yasutaka Kubo (Okayama Univ.) presented gene expression analysis of *rin*, *nor*, and *RiEIL* fruits to elucidate genes regulated by ethylene signaling pathway. Toru Fujiwara (Univ. of Tokyo) reported on a functional analysis of boron transporter genes in Arabidopsis, and preliminary results using Micro-Tom transgenics. Hideki Takahashi (Tohoku Univ.) reported on gene expression analysis of glycoprotein elicitor-induced genes, and suggested that the ubiquitin ligase E3 gene induced by glycoprotein elicitor may regulate JA-dependent response. Yoko Iijima (Kazusa DNA Res. Inst.) gave a comprehensive metabolite annotation of Micro-Tom using LC-FTICR-MS.

The conclusions of the workshop were: 1) Micro-Tom genomic resources developed by JSOL provide a uniform and consistent platform for tomato genomic research, 2) international exchange of the mutant resources will be beneficial to the community, 3) international collaboration will be desirable for developing saturated T-DNA tagging lines, and 4) many Arabidopsis researchers are interested in tomato with the increase of genomic resources.

This workshop was supported by Kazusa Akademia Park as a part of their 10th anniversary and JSPS plant molecular design 178th committee.





History and Iconography of the Solanaceae: 1. Mandrake, a Plant at the Intersection of Reason and Irrationality

Jules Janick & Marie-Christine Daunay

Plants of the Solanaceae (nightshades) throughout the ages have had complex relationships with human societies, as evidenced by the wealth of iconographic and text documents that have survived (Daunay et al, 2007, 2008), providing a dispersed but rich lode of information that we will mine. The period we review here covers antiquity up to the 17th century. This paper on mandrake is the first of a series that will outline the main historical and iconographic features of some well known and lesser known solanaceous species, for the enlightenment and pleasure of the readers of the SOL Newsletter.

Mandrake (*Mandragora* spp.) has been known as a powerful medicine since antiquity as attested by its presence in the *Ebers Papyrus* (ca. 1530 BCE), the earliest known Egyptian medical treatise; a carving of mandrake harvest (Fig. 1) which adorns an ivory casket of Tutankhamun (18th Dynasty of the New Kingdom, about 1323 BCE); and a painting in Tomb no 1 (19th Dynasty) illustrating the mandrake along with cornflower and poppy (Fig. 2). Mandrake, *Duda'im* in Hebrew (also the name for lovers), is referred to in the Bible as a fragrant plant (*Song of Solomon 7:13*) and aid for conception (*Genesis 30:14*). Medicinal properties of mandrake are referred to by Theophrastus (372-287 BCE), Dioscorides (20-70 CE), and Pliny the Elder (23-79 CE). The diverse properties of mandrake (disinfectant, anti-inflammatory, anesthetic, sedative, narcotic, hallucinogenic, paralytic, and supposed aphrodisiac) are due to the presence of various tropane alkaloids contained in its roots, leaves, and fruits, including hyoscyamine, hyoscyne (scopolamine), and atropine.

The frontpiece illustration in the earliest surviving illustrated manuscript of Dioscorides' *De Materia Medica* (512 CE) that now is the treasure of the national Austrian library of Vienna (*Aniciae Julianae Codex*), portrays the nymph Euresis (Discovery) presenting Dioscorides with a mandrake (in human form) attached to a dead dog (Fig. 3, left). On a second painting, the nymph Epinoia (Thought and Intelligence) holds up a mandrake to Dioscorides sitting at her left with a book while to her right Krateus [rhizotomist, physician, and famed



Figure 1. Mandrake in pharaonic Egypt: harvesting mandrake fruits on an ivory casket of Tutankhamun, 18th dynasty. Source: Manniche 1989.



Figure 2. Mandrake in pharaonic Egypt: mandrake along with cornflower and poppy, Theban Tomb no 1, 19th Dynasty. Source: Manniche 1989.

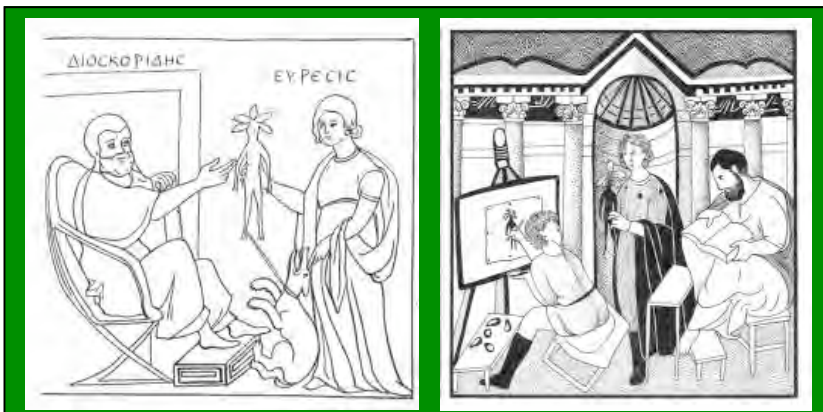


Figure 3. Mandrake in frontpiece paintings of *Aniciae Julianae Codex*, 512 CE: (Left) drawing by Singer (1927) of Dioscorides receiving mandrake from Euresis. (Right) drawing by M. Breen (Bredemeyer), from D'Andrea (1982), of Krateus painting mandrake held by Epinoia. Drawings based on the original (damaged) paintings, see <http://it.wikipedia.org/wiki/Imagine:ViennaDioscoridesAuthorPortrait.jpg>

herbal illustrator of Mithradates VI, Eupator (120-63 BCE), King of Pontus], paints a portrait of the plant (Fig. 3, right). These images testify to the early anthropomorphization of mandrake (hairy bifurcate root suggests human legs and rosette leaves suggest a crowned head), as well as the superstition about its harvest. The plant was believed to emit a fatal shriek when ripped from the soil; it was harvested by being tied to a starving dog, who when thrown some scraps, would rip it out, causing the demise of the dog but sparing the attendant with muffled ears. The human form and special harvest procedure of mandrake was the origin of countless folkloric tales, illustrated in manuscripts until the 17th century, and beyond. Furthermore, a "male" form (*Mandragora officinalis*) and a female form (*M. autumnalis*) were distinguished, as illustrated in *Hertensis*, a 9th century herbal (Fig. 4), on the basis of root color, leaf and berry morphology, as well as odor. The designation of the foul-smelling



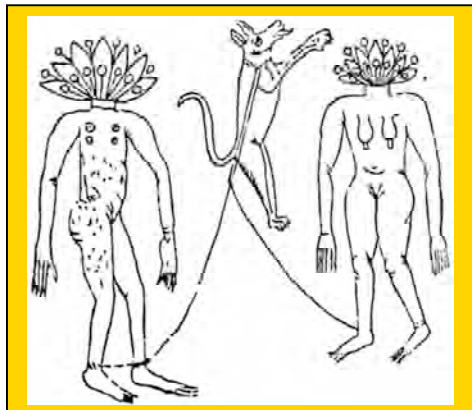
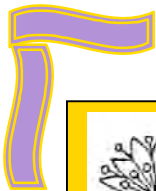


Figure 4. "Male" and "female" mandrakes and dead dog, *Hertensis*, 9th century. Source: Singer 1927.

species as "female" tells volumes about the status of women in the Middle Ages.

The plant morphology suggesting a human figure, the legs and torso of which grew underground, the home of Evil Forces, plus its powerful psychic effects when ingested, are at the origin of the very special status of this species that stands at the nexus between Good and Evil, Rationality and Superstition. This line could be crossed by changing the dosage and composition (addition of other plants), or by the addition of special incantations and ceremonies. Thus mandrake, widely used for curative medicinal purposes, was also widely used for black magic (the dark side of botany and medicine) as an ingredient of witches brews, flying ointments, and aphrodisiac philtres.

Mandrake is the classical example of a plant with a schizophrenic persona, having both benign and malevolent properties. The combination of human-like appearance and powerful physiological effects stimulated irrational fears and superstitious beliefs in Mediterranean and European societies. But for millennia, the human imagination was the arena for a wrestling match between logic vs. good sense since scepticism concerning these magical characteristics was as old as the dark and irrational legends. This special status of mandrake was

shared, to a lesser extent, by several other Old World nightshades (e.g. henbane, belladonna), which have similar physiological effects. These fears no doubt are the origin of the initial distrust of edible Old World solanaceous species, particularly eggplant, and later on New World species especially tomato, since some of the early introduced forms in Europe had round goldish berries as does mandrake (Fig. 5 and 6).



Figure 5. Mandrake. Aldrovandi, *Il Teatro della Natura*, vol.5-2, folio 222, 16th century, Source: <http://www.filosofia.unibo.it/aldrovandi/>

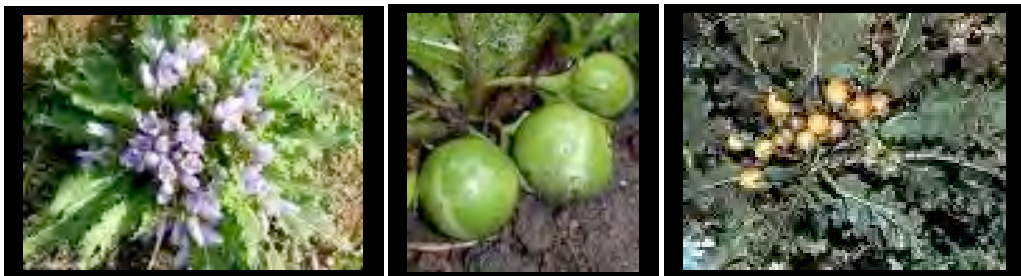
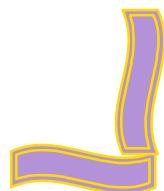


Figure 6. Photographs of mandrake plant with flowers, unripe fruit, and ripe fruit.

Literature References

- D'Andrea, J. 1982. Ancient herbs. The J. Paul Getty Museum. Malibu, California.
- Daunay, M.C., Janick, J., and Laterrot, H. 2007. Iconography of the Solanaceae from Antiquity to the 17th Century: A rich source of information on genetic diversity and uses. 6th International Solanaceae Conference, Madison (WIS, USA), 23-27th July 2006. Acta Hort. (in press).
- Daunay, M.C., Laterrot, H., Janick, J., 2008. Iconography of the Solanaceae: Antiquity to 17th Century. Horticultural Reviews 34 (in press).
- Manniche, L. 1989. An ancient Egyptian Herbal. Univ. Texas Press, Austin.
- Singer, C. 1927. The herbal in antiquity and its transmission to later ages. J. Hellenistic Studies 47:1-52.



Tomato Sequencing Updates

Chromosomes 1, 10, 11 (US)

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

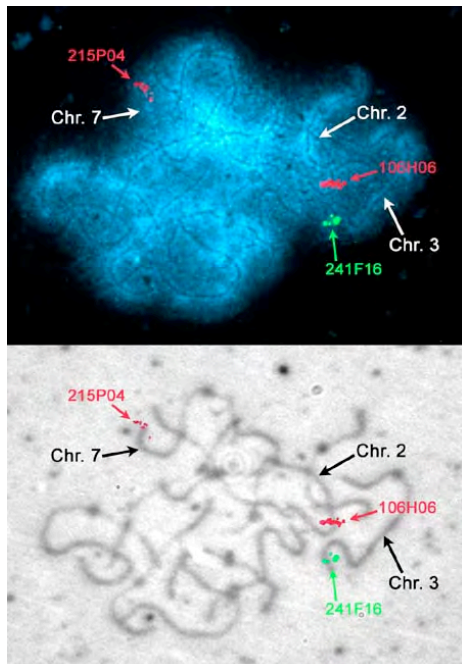
Two additional BACs have been sent for sequencing since our last report. We also plan to send 1,000 fosmid ends for sequencing to obtain preliminary information on the potential utility of the fosmid library.

In an effort to generate additional sequencing resources, we are doing hybridizations onto the MboI library with various markers. Lists of ten to twenty markers for hybridizations were submitted by sequencing partners from India, the Netherlands, France, Japan, and Spain. MboI hybridization filters were prepared, and the hybridizations are being done in different batches with ten markers being screened per batch. To date, we have sent six different batches of results to each sequencing partner.

Since the last report, the Stack lab at Colorado State University has localized an additional seven BAC clones using fluorescence in situ hybridization (FISH), bringing the total number of clones that we have positioned on tomato chromosomes to eighty-two. The recently positioned BACs include:

Chromosome Arm	BAC ID
2Q	LE_HBa0001M12
3Q	LE_HBa0241F16
5P	LE_HBa0157F14
5Q	LE_HBa0091D14
9Q	LE_HBa0245E05
11P	LE_HBa0168B23
11Q	LE_HBa0249E07

The figure below illustrates FISH labeling with three BAC clones on different chromosomes: LE_HBa0241F16 on chr 3, LE_HBa0106H06 on chr 2, and LE_HBa-215P04 on chr 7. The fluorescent signals have been superimposed on the phase image of the SCs to illustrate their positions on the chromosomes.



Chromosome 2 (Korea)

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

Currently, we have finished sequencing 109 BACs and twenty are in progress. We are focusing on filling the large gap at the 46 - 70 cM region. We selected new seed BACs and confirmed several newly identified BACs by IL mapping for filling the gap. One problem we encountered is when we read the extended BAC clones, some part was completely identical to the seed BAC clones, but the other part didn't match. We speculated this might be caused by segment duplication. To date, we have four BACs that showed this same problem, and we are trying to solve it. The next four clones showed identity to seed BAC clones.

Chromosome 3 (China)

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

Update pending.

Chromosome 4 (UK)

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

8,910,331 bp of sequence have been generated at the Wellcome Trust Sanger Institute for chr 4 as of April 3, 2007. Of this figure, 8,462,782bp are unique. The sequence has been produced from seventy-eight BACS originating from the LE_HBa and SL_MboI libraries. We intend to finish all BACS for chr 4 to HTGS phase 3. Currently, forty-one BACs that correspond to 4,678,895 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.

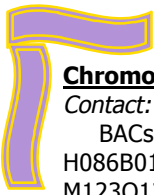
With a view to anchoring additional BACs and contigs from the FPC database to chr 4, we have been designing markers for a number of markers from the EXPEN-2000 map that are currently unanchored in the FPC map. A number of PCR hybridizations to filters of the fingerprinted libraries (LE_HBa & SL_MboI) are underway and we will conduct colony PCR verifications to determine if further chromosome markers hybridize to any additional clones and contigs in the FPC.

BAC selection continues as suitable sequencing candidates are identified. 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 and the AGP provides assembly information.

Chromosome 5 (India)

Contact: Akhilesh Tyagi (akhilesh@genomeindia.org)

The Indian Initiative on Tomato Genome Sequencing is currently working on forty BAC clones from chr 5. Nine BAC clones have reached Phase III level of sequencing, while nineteen and seven BAC clones are at Phase II and Phase I, respectively. Five BAC clones are in either the early phase of sequencing or library preparation. In addition, certain BACs associated with markers shown earlier belonging to chr 5 have now been confirmed on other chromosomes using ILs and/or FISH data. Some of these clones have been sequenced. Extension in the tiling path is slow as several seed BACs have been rendered redundant in the MTP due to the presence of more than one marker in them. Screening for more BACs on new markers is in progress by performing overgo hybridizations on the filters available for the MboI library.



Chromosome 6 (The Netherlands)

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

BACs H229B01, H309F14, H020O17, H049I02, H059D21, H086B01, H217M17, H222J18, E045F21, E093P23, M059G17, M123O13 have been phase 2 sequenced. BAC H021K07 has been closed. BACs H026E06, H242H19, and E129O21 are currently in the sequence pipeline. Furthermore, twenty-four BACs have entered the finishing pipeline for gap closure. From the Syngenta anchoring initiative, ten candidate BACs have been identified which will be screened by FISH analysis. Additionally, three BACs showing strong hits in the first two overgo screen hybridizations will be analyzed by FISH to verify their chr 6 location.

Chromosome 7 (France)

Contact: Farid Regad (regad@ensat.fr)

Since our last report, fourteen new seed BACs have been validated and five BACs have been finished. Currently, fifty-six BACs are in different sequencing phases and twenty-six finished BACs will be submitted to the SGN repository. Overgo hybridization results provided by Cornell are currently being analyzed in order to identify new seed BACs.

Chromosome 8 (Japan)

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

We finished fifty-six clones to Phase 3 (total non-overlapping length 6,052,565 bp) of which twenty-nine are seed and twenty-seven are extended clones. Shotgun sequencing of the selected low-copy BACs is in progress, and we have already generated 300,000 reads producing 200 Mb in length. We have been screening new tomato EST SSR markers on the parent strains of EXPEN-2000. So far, we have identified 500 co-dominant markers by testing 1400 primer pairs. In parallel, we are mapping these new markers using the IL comprised of eighty lines. We were able to obtain six new markers on chr 8 and this work would provide additional seed points for other chromosomes.

Chromosome 9 (Spain)

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

As of today, the sequencing of thirty-one BACs for chr 9 has been completed and another eighteen BACs are in progress.

Out of the eighteen BACs, thirteen are in different finishing stages, four are in the sequencing phase (libraries done), and one is in the library construction phase (BAC confirmed, DNA extracted and subcloning in progress).

Extension is still a problem as we have only ordered four new BACs to extend from only two positions. Indeed most of the progress has been the result of the new seed BACs selected *in silico* by BLASTing new chr 9 markers against the BAC end sequence (BES) database (seven out of the thirteen) and only six corresponded to extension BACs.

Overgo hybridizations conducted by Cornell for a number of chr 9 markers have so far produced three new marker-BACs associations that are pending mapping against IL or FISH. Two new markers were assigned to single BACs that were ordered. A new set of BACs are currently being FISHed by labs of our colleagues Stephen Stack's and Hans de Jong.

The recent release of information from Syngenta to SGN (FPC data) has allowed the identification of nine candidates for new seed BACs, which are distributed throughout chr 9. These BACs are in the same contig as other seed BACs already sequenced by us, and they do not overlap with our sequenced BACs, but must be close.

BACs for new chr 9 markers provided by Syngenta have been selected in eight new positions along the euchromatic regions of chr 9 based on BLAST against BES, and hopefully will provide additional seed BACs. These BACs have also been ordered from Cornell and will be mapped as soon as they are confirmed.

Chromosome 12 (Italy)

Contact: Mara Ercolano (ercolano@unina.it)

Currently, the sequences of ten BACs have been completed and fifty BACs are in different sequencing phases. Three BACs are in phase 3, thirty-five in phase 2 or 1 and an additional twenty-two BACs are in the sequencing pipeline. Italy participated in the workshop on Tomato Finishing and agrees with the sequencing and finishing guidelines discussed. In this way, the finishing phase will be much simpler, and as a result, the release of complete BAC sequences will be more straightforward.

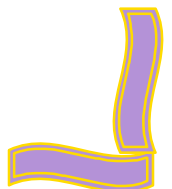
Announcements

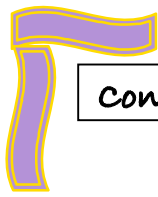
New Online Resources

MiBASE and KaFTom update

- (1) New unigene set in MiBASE. KTU2 (Kazusa Tomato Unigenes 2) containing 43,000 unigenes, built from 280,913 tomato ESTs, is now available in MiBASE (<http://www.kazusa.or.jp/jsol/microtom/indexj.html>).
- (2) 1942 new High-Throughput cDNA sequences (2268 HTC sequences, total) of Micro-Tom full-length clones will be available in KaFTom (<http://www.pgb.kazusa.or.jp/kaftom/>) with InterProScan and similarity search results (to Arabidopsis, rice, and tomato BAC sequences) on June 1, 2007.

Contact Kentaro Yano (yanoken@kazusa.or.jp) or Koh Aoki (kaoki@kazusa.or.jp) with questions and requests.





Conferences

First International Symposium on Chili Anthracnose Seoul, Korea September 17 - 19, 2007

<http://www.avrdc.org/anthracnose/index.html>
Contacts: Paul Gniffke at gniffke@avrdc.org and Dae-Geun Oh at daegeun@rda.go.kr



Chinese Medicinal Plant --- *Lycium barbarum*

by Ying Wang



Lycium barbarum

Seven *Lycium* species and three variations have been reported in the flora of China: *Lycium chinense*, *Lycium chinense* var. *potaninii*, *Lycium barbarum*, *Lycium barbarum* var. *auranticarpum*, *Lycium dasystemum*, *Lycium dasystemum* var. *rubricaulium*, *Lycium ruthenicum*, *Lycium truncatum*, *Lycium yunnanense*, *Lycium cylindricum*. But only *Lycium barbarum* is listed in the Pharmacopoeia of the People's Republic of China (2005). "Goqi", or wolfberry, is the fruit of *Lycium barbarum* L., which has been used as traditional Chinese medicine for over 2000 years and was recorded in the ancient Chinese medicinal books, "Shen Nong Ben Cao Jing" and "Ben Cao Gang Mu". "Goqi" contains beta-carotene, vitamin C, vitamins B₁ and B₂, polysaccharides, betaine, beta-sitosterol, sesquiterpenoids, tetraterpenoids, etc. Traditionally, it has been known as having the properties of enhancing eyesight, enriching the yin, tonifying the kidney and liver, moistening the lungs, and improving immunity.

The main production areas for *Lycium barbarum* are Gansu and Ningxia provinces, with a total planting area of 13,000 hectare. Many commercial products have been developed besides the traditional dry fruit, such as Goqi wine, *Lycium* young leaves, Goqi tea, Goqi beverage, Goqi milk powder, Goqi polysaccharides, and Goqi seed oil. In 2006, the domestic consumption of "Goqi" was more than 30,000 tons, and the export was over 4,500 tons with a market value of over 15 million USD, which ranks fifth in exports of traditional Chinese medicines after ginseng, cinnamon, cordyceps, and pepper.

Lycium barbarum is diploid (2n=24), and has a large portion of pericentromeric heterochromatin in the genome, which is similar to the model species in *Solanaceae* - tomato. However, the genome of *Lycium barbarum* is about twice the size of tomato. Molecular genetics and genomics of *Lycium* have been carried out in China for better understanding the heritability of phytochemical contents and the expression and regulation of related genes.

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Dried fruit of *L. barbarum*



What's new on SGN?

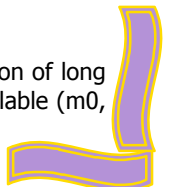
1. Improved Alignment Analyzer and Tree Viewer

Improved versions of the Alignment Analyzer and the Tree Browser are available. The Alignment Analyzer (Fig. 1) can now calculate alignments on the fly, using the MUSCLE program on the SGN cluster. It also supports zoom levels through clicking, exclusion of sequences, re-aligning any section of the alignment and automatic display of Interpro domains for known sequences. Trees can be calculated from any alignment section on the fly, using the QuickTree program.

The Tree Browser (Fig. 2) now has the capability of showing the alignment next to the tree, and sports a significantly improved user interface.

2. Advanced BLAST

An advanced BLAST interface has been introduced that allows better control of BLAST options and the submission of long multi-fasta files. The BLAST is run on the SGN cluster. Most of the native BLAST output formats are directly available (m0, m8, etc.).



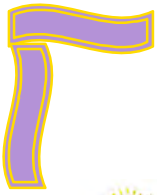


Figure 1. The SGN Alignment Analyzer.

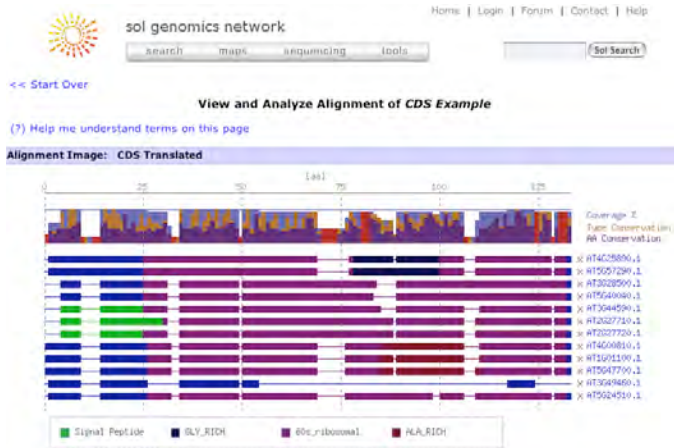
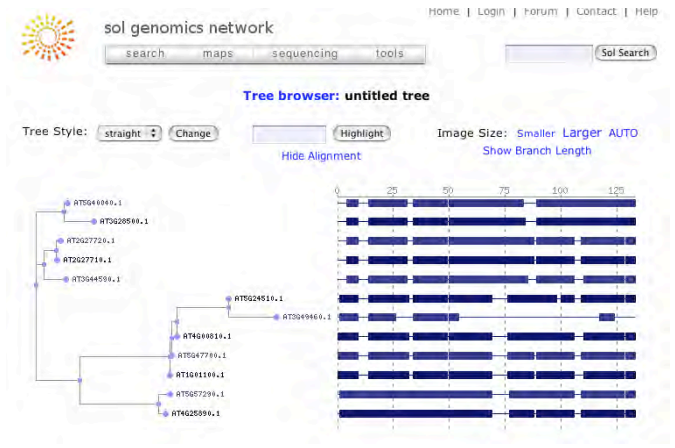


Figure 2. The SGN Tree Browser, displaying an alignment along the phylogenetic tree.



3. New and Improved Maps

New maps have been added to the SGN comparative mapviewer, and the appearance of some maps has been improved. New maps include the IL map, which shows the position of IL lines on the EXPEN1992 map (soon positions on the F2-2000 will be also available), the AGP map, which shows the positions of the sequenced chromosomes, and the Contig map, which shows the position of the Sanger FPC contigs on the F2-2000 map. Improved maps include the physical map, which now shows all the anchored clones as small glyphs. Click on the maps menu to see any of these maps at <http://sgn.cornell.edu/>.

For feedback and suggestions, please email sgn-feedback@sgn.cornell.edu.



Solanaceae Recipes

MANGO AND TOMATILLO SALSA From: foodreference.com

- 2 mangos, peeled and diced
- 10 tomatillos, husked and sliced
- 1 jalapeno pepper, seeded and sliced
- 1/4 cup lime juice
- 1/4 cup onion, diced
- 1/4 cup cilantro, chopped
- 1/2 cup tomatoes, diced

Combine all of the ingredients in a large bowl.

Cover and let sit for at least 2 hours before serving.

Makes 8 servings.

