

# THE SOL NEWSLETTER

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## Community News

### Announcement for 8<sup>th</sup> SOL and 2<sup>nd</sup> ICuGI Joint Conference

"Completion of Reference Genomes and Application"

Tohru Ariizumi and Hiroshi Ezura  
Graduate School of Life and Environmental Science  
University of Tsukuba, Japan

#### **What is the next step in plant research and how can we utilize genome sequence information?**

We are pleased to announce that the 8<sup>th</sup> Solanaceae genome conference (SOL) will be jointly held with the 2<sup>nd</sup> Cucurbitaceae genome workshop (ICuGI) in 2011. The Solanaceae and Cucurbitaceae families include many important species for basic plant science as well as edible crops. This conference will provide many opportunities for scientists to interact with colleagues working in diverse areas of research in this area, and will hopefully guide us in revealing both the evolutionary history and genetic diversity of the Solanaceae and Cucurbitaceae. We also believe that this joint conference will give us new perspectives on "what is the next step in plant genomics research?" and "what can we learn from large volumes of sequencing data?"

Thanks to the latest technical advancements in sequencing technology and bioinformatics, we are now able to complete the genome sequences of key Solanaceae family members and related wild species and to investigate comprehensive gene fluctuations using whole transcriptome shotgun sequencing (also called RNA-seq). In addition, genome sequencing projects of several key Cucurbitaceae members are underway. One of the major goals of this conference is to develop a complete reference sequence for the Solanaceae genomes and to explore the ideas, strategies or methodologies we can use to make this information a benefit for new research that will both improve our fundamental understanding of plant biology, while solving challenges of maintaining the global food supply including disease, drought, salinity, and nutritional limitations.

The SOL & ICuGI 2011 joint conference will be held on October 16 – 20, 2011 at the Tsukuba Convention Center (EPOCAL), Tsukuba, Japan. Please consider attending the SOL & ICuGI 2011 joint conference and immediately mark the date in your calendar. The programs of the conference include many areas (see the conference website below). On behalf of the organizing committee, we are looking forward to seeing all of you in Tsukuba, Japan!



Conference website: <http://www.sol2011.jp>  
Contact: [sol2011@gene.tsukuba.ac.jp](mailto:sol2011@gene.tsukuba.ac.jp)

## SCRI Welcomes SOL2010 Delegates to Dundee, Scotland

Contributed by Gerard Bishop, Glenn Bryan, Anne Rendall, Graham Seymour



Conference delegates on the grounds of the Guthrie Castle where the conference dinner was held.

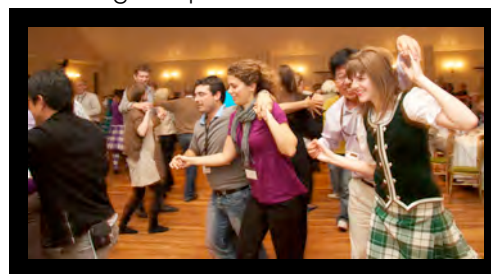
Approximately 280 SOL scientists from over 30 countries attended the 7<sup>th</sup> Solanaceae Conference in Dundee, Scotland at the beginning of September.

SCRI, in conjunction with UK-SOL, were the hosts and organizers of the conference, for this, its first visit to the UK. The meeting opened on Sunday evening with a keynote speech by Professor Sir David Baulcombe, who, in 2009, chaired a Royal Society policy study on the contribution of biological research to sustainable food crop productivity. Delegates then attended a civic reception at Discovery Point and had the opportunity to tour the Royal Research Ship Discovery.

The formal scientific program covered a wide range of topics from Biodiversity and Evolution, through Plant Development, Abiotic and Biotic stresses, Solanaceae Genomes and Systems Biology. There were separate sessions on the major Solanaceous crops including potato, tomato and pepper. Talks were from both established and early career scientists and there were around 100 posters in addition to the oral presentations. The meeting also provided a forum for

discussing the recently released draft genomes of tomato and potato and how research groups were taking advantage of this exciting new data.

The conference dinner was held at Guthrie Castle, in Angus, and Scotland delivered a perfect romantic autumn mist to add just the right atmosphere to the venue! Guests were treated to some traditional 'sword' dancing and violin music, plus a very chaotic but extremely entertaining Scottish ceilidh, in which many SOL scientists participated with great enthusiasm, if little technique!



Students from a Scottish dance school and SOL scientists participating in the ceilidh.

## Highlight Article

### Genetic collection of tomato and its use in genetic and breeding investigations

*Nadezhda I. Bocharnikova*

Russian Agricultural Academy of Sciences, Krzhizhanovskogo Str. 15/2, 117218 Moscow  
e-mail: gametas@mail.ru

Creation and conservation of identified genetic collections is increasing the efficiency of genetic and breeding investigations. A collection of tomato mutants is a unique scientific tool for solving applied and theoretical problems of genetics and breeding (broadening the spectrum of available genotypic variability, the introduction of genes into breeding lines, and so on).

Among dicots, tomato is one of the most informative objects of investigations. There are well-characterized genetic maps and tomato is very plastic and easy to multiply, which makes it possible to grow tomatoes in the field as well as in a greenhouse. Researchers have provided very important practical information about the genetics of tomato and in return, fundamental investigations have contributed to tomato breeding. That is why the tomato is often used as a model in various types of investigations. In the latter decades, there have been considerable contributions from molecular-genetic investigations of tomato, including sequencing of the genome.

Nevertheless, even today, geneticists and breeders frequently use a collection of tomato mutants that is of interest for theoretical investigations as well as applied breeding. Collections of mutants are a part of an identified gene pool for tomato, which are subdivided into different groups according to displayed marker traits in ontogenesis.

Characterized mutants are valuable for solving various theoretical and applied problems of breeding. We suggest the following possible ways to use the phenotypic markers of tomato in genetic and breeding investigations:

1. Investigation of biochemical and physiological processes.
2. Genetic mapping.
3. Investigation of quantitative traits heritability.

4. Control of introgression for interspecific hybridization.
5. Investigation of gene dose effect, allele interaction and other events.
6. Using mutants in evolutionary genetic investigations.
7. Using mutant forms in breeding programs.
8. Investigation of the selective elimination processes based on post-meiotic phases.
9. In molecular-genetic investigations.

Such approaches using phenotypic markers of well-investigated mutant genes of tomato allows a broad field of potential applications in genetic and breeding investigations.

Of great interest is the question of how mutant traits are manifested in changeable environments (ecological genetics) and how different combinations of genes can influence genome interactions. Our data show that the stability of phenotypic expression of mutant traits of tomatoes, which were grown in different environments, should be a question of investigation in genetic and breeding investigations. The degree of trait manifestation and reliability of mutant identification depends on environments where they are grown.

Our evaluation of the degree of expression of a mutant trait was carried out in both the field and greenhouse. Along with mutants (*atv*, *cy*, *Tor*, *dip*, *cb-2*, *cjf*, *tf*, *mult*, *fa*, *atn*, *mon*, *Me* and some others) where trait manifestation was stable in different growing conditions, there were some mutants that had good expression only in specific growing conditions.

It is important to note the influence of different genotypic backgrounds on phenotype manifestation of mutant traits. Markers (*c*, *d*, *aw*) in different genotypic backgrounds, especially for interspecific hybridization, manifested different degrees of trait expression. Moreover, it is possible to change the phenotypic expression of traits based on epistatic gene action.

Additional limitations of using mutants could be related to their fertility. Our results showed that some mutants (*cit*, *Fw*, *Lpg*, *ful*, *clau*, *ht*) have reduced pollen fertility. However, the majority of mutant accessions had normal pollen fertility. Nevertheless, even high pollen fertility of some mutants (*mup*, *mult*, *yv*, *coa*) cannot guarantee normal seed set because of the high failure of reproductive organs.

More recent investigations have focused on the processes that take place within pollen grains based on the influence of different environmental effects on their cytological characteristics. In connection with this and based on investigations of morphological peculiarities of pollen grains, we have paid attention to their shape. It was observed that the shape of tomato pollen grains can be ellipsoidal, spherical, and three pore-shaped. In addition, the size of pollen grains for each accession was specific to the accession. Nevertheless, within different groups of marker genotypes it was observed that the variation of pollen grains was square. From these observations and the collection of photographs of pollen grains (their shapes, sizes, pictures of exine and so on), it is possible to use this information for genotype identification of plants.

The large diversity of marker genes in these tomato mutant collections allows researchers to more readily solve a greater number of problems. For instance, multimarker mutants can be used to investigate the problems of interspecific hybridization, induction of form-building processes, and play an important role in cytological investigations. In our investigations, we have synthesized chains of markers with associated genes, which are manifested in the early stages of seedlings and growth (color of hypocotyls and cotyledons, pubescence of stem, shape and color of leaves). Based on the selection of markers, we have taken account of their positions on chromosomes – distal or around the centromere. We have determined the optimal number of markers in a chain that are manifested in one stage of development. Four is the optimal number when there is no loss of viability of a plant and no pleiotropic effects. However, it is possible to synthesize the chains with five or more markers, but that they have to be manifested in late stages of development.

Additionally by means of RAPD analysis, we have obtained spectrums of amplified DNA with unique bands from accessions within a mutant collection. The data showed the possibility of using RAPD analysis for the saturation of multimarker forms along with molecular markers, which allow experiments to be carried out more efficiently on recombinant variability not only on a morphological basis, but also on a molecular level.

Thus it is possible to conclude that creation and conservation of identified genetic collections increases the efficiency of genetic and breeding investigations.

## Biodiversity

### Georg Bitter's bitter tomatoes 2: an elusive group of intrusive weeds

John Samuels

Trezelah Barn, Trezelah, Gulval, Penzance, TR20 8XD, Cornwall, UK  
correspondence: john.samuels@virgin.net

#### Introduction

Across the world there are twenty-five cultivated food species of *Solanum*, including the potato, tomato, and various eggplants (Samuels, 2009a). The brinjal eggplant, *Solanum melongena* L., together with its wild and weedy relatives in Asia (*S. melongena sensu lato*), and those in Africa and the Middle East (*S. incanum sensu lato*), comprise the brinjal eggplant complex.

The various species comprising *S. incanum* s.l. are known as bitter tomatoes (Burkill, 2000; Matu, 2008; Samuels, 2009b, 2010; Tindall, 1983). They have also been referred to as "African eggplants" (Weese & Bohs, 2010) but this term is best reserved for the

more distantly related *S. aethiopicum* L. (scarlet eggplant) and *S. macrocarpon* L. (Gboma eggplant), domesticated in Africa. Bitter tomatoes are to be found across much of eastern and southern Africa, and parts of western Africa, south-west Asia and south Asia (Samuels, in press). They are typically ruderal shrubs or sub-shrubs with yellow berries, and often have a dense covering of hairs, and prickles (Fig. 1). They may colonize roadsides (Matu, 2008), recently disturbed land such as cultivated fields (Samuels, 2009b) and over-grazed areas (Le Houerou, 2003; Matu, 2008), often becoming intrusive weeds.



**Figure 1:** *S. incanum* L. (herbarium specimen NIJ-H00162) from Sudan-detail of flowering branch. (photo: courtesy of Radboud University Botanical & Experimental Garden, Netherlands).

*S. incanum* L. is believed to be the wild ancestor of the brinjal eggplant, *S. melongena* L. (eg. Daunay *et al.*, 2001; Lester & Daunay, 2003; Lester & Hasan, 1991; Matu, 2008) and along with its close relatives continues to be the subject of research associated with this species (eg. Behera & Singh, 2002; Behera *et al.*, 2006; Furini & Wunder, 2004; Isshiki *et al.*, 2008; Lester & Daunay, 2003; Meyer & Litt, 2010; Singh *et al.*, 2006; Vilanova *et al.*, 2010; Weese & Bohs, 2010).

#### Taxonomy of *S. incanum* s.l.

The taxonomy of species related to the eggplant remains a challenge (Daunay, 2008)-several groups are well known for being taxonomically elusive. In particular, the bitter tomatoes have caused taxonomic difficulty since the earliest collections. The highly variable nature of this group has caused many problems with identification (Samuels, 2009b) and species delimitations been difficult to establish. There is also considerable interfertility amongst the component taxa (Jaeger, 1985; Lester & Daunay, 2003; Lester & Hasan, 1990, 1991; Pearce, 1975; Samuels, 2010, in press). Historically, both in herbaria and in the field, *S. incanum* L. s. str. has been confused with the closely related *S. melongena* L., as well as *S. coagulans* Forssk., *S. torvum* Sw., and other more distantly related taxa (Samuels, unpubl.). The taxonomy of the bitter tomatoes has consequently challenged many authors (eg. Bitter, 1923; Deb, 1989; Furini & Wunder, 2004; Karihaloo *et al.*, 2002; Lester & Daunay, 2003; Lester & Hasan, 1990, 1991; Mace *et al.*, 1999; Weese & Bohs, 2010).

Georg Bitter, working in Germany around one hundred years ago, was the last botanist to attempt a detailed survey of the taxonomy of the bitter tomatoes and their allies. He classified them as part of series *Incaniformia* Bitter (1923), which is in turn part of section *Melongena* (Miller) Dunal in subgenus *Leptostemonum* (Dunal) Bitter, the "spiny solanums." Since then the tendency has been to organize the *S. incanum* complex into informal groups (eg. Jaeger, 1985; Lester & Hasan, 1991; Whalen, 1984). Further taxonomic progress on the bitter tomatoes was only made possible by the much-needed typification of *S. incanum* L. s. str. and *S. insanum* L. (Hepper & Jaeger, 1985), and *S. campylacanthum* Hochst. ex A. Rich and *S. panduriforme* E. Meyer ex Dunal (Lester, 1997). There is still a lack of clarity over species identities of some of the taxa associated with *S. panduriforme* (Lester, unpubl.).

Added to this, there have been difficulties over the precise distinction between *S. incanum* and *S. insanum* L. (see Fig. 2). Conspecificity of the two taxa was proposed by De Candolle (1904) and has been discussed more recently by Deb (1989), Lester & Hasan (1990), Karihaloo & Gottlieb (1995), Karihaloo & Rai (1995), Karihaloo *et al.* (1995), Karihaloo *et al.* (2009), Lester & Hasan (1990), Sakata & Lester (1997). The relationship of *S. insanum* to *S. melongena* remains unclear. Some authors consider *S. insanum* to be a feral form of *S. melongena* landraces (eg. Lester & Hasan, 1991). However, such feral forms rarely conform to the nomenclatural type of *S. insanum* L. (Samuels, unpubl.).

Furthermore, the taxonomic affinities of taxa such as *S. cumingii* Dunal, *S. undatum* Lam., *S. trongum* Poir. and many others have long been in question. The distinction between Lester & Hasan's group E ("*S. insanum*") and their group F ("*S. cumingii*") is also unclear (Karihaloo & Gottlieb, 1995; Samuels unpubl.). These problems have been exacerbated by a complex but, as yet, unresolved synonymy, which has arisen as a result of over three hundred years of collecting expeditions in various parts of Africa and Asia.

Recent genomic studies have proved to be a useful adjunct to descriptive taxonomy, and have generally confirmed earlier findings on the *S. incanum* s.l. group (Samuels, 2009b). However, few studies have effectively combined "taxonomic information about wild species of *Solanum* with the genomic information being generated about the economically important species of the genus"-an alliance promoted by Knapp *et al.* (2004).

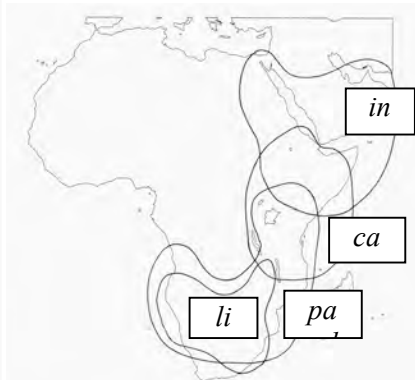
Of the dozen or so species in section *Melongena*, several have been considered to be close allies of the *S. incanum* s.l. group. *S. marginatum* L.f., originating from Ethiopia, and *S. aculeastrum* Dunal from central, eastern and southern Africa were included in Whalen's (1984) "*S. incanum* group." Jaeger (1985) retained both in section *Melongena* but omitted them from his *S. incanum* agg. Weese & Bohs (2010), in their study based on molecular markers, proposed that *S. linnaeanum* Hepper & P-M. L. Jaeger, originating from South Africa, is a close ally of *S. lichtensteinii* and part of the brinjal eggplant complex. There is no published information to date on the crossability relationships between these two species, and only limited information on their respective levels of interfertility with *S. melongena*. Until this data, along with additional genomic data gained from larger sample sizes of African accessions becomes available, judgement on this relationship should be postponed.

There are several endemic species (eg. *S. aureitomentosum* Bitter) distributed across central and eastern Africa, that, like *S. linnaeanum*, are undoubtedly part of section *Melongena*. They appear to be close relatives of the bitter tomatoes, but their precise affinities have yet to be clarified.



**Figure 2:** *Solanum melongena* s.l. (Lester & Hasan's [1991] *S. melongena* group E/"*S. insanum*" from India). (photo: courtesy of Radboud University Botanical & Experimental Garden, Netherlands).

Recent studies on *S. incanum* s.l. (eg. Karihaloo & Gottlieb, 1995; Karihaloo *et al.*, 2009; Mace *et al.*, 1999; Samuels, 2010, in press) have tended towards a broader species concept. Samuels (in press) performed an investigation into the taxonomic relationships within *S. incanum* s.l., provisionally designated as groups A-D by Lester & Hasan (1991). This involved a study of interfertility between *S. campylacanthum*, *S. panduriforme*, *S. incanum* and *S. lichtensteinii* Willd. from Africa and the Middle East, and the morphometric analysis of vegetative characters in African *S. campylacanthum* and *S. panduriforme*. The findings of Samuels' study confirmed several of those of Lester & Hasan (1991). It also showed that *S. panduriforme* is a subspecies of *S. campylacanthum*, and that *S. incanum* and *S. lichtensteinii* are distinct species.



**Figure 3:** Simplified Distribution of *S. incanum* s.l. in Africa and the Middle East; *inc*: incanum/cam; *ca*: campylacanthum/pan; *pa*: panduriforme; *li*: lichtensteinii (from Samuels, 2010).

#### Distribution of *S. incanum* in Africa and the Middle East

There have been varying views on the distribution patterns of the bitter tomatoes, resulting in inconsistencies (cf. Daunay *et al.*, 2001; Lester & Hasan, 1991; Samuels, 1996; Weese & Bohs, 2010). A consensus on precise distribution patterns is essential to the descriptive taxonomy of this group, and contributes to the correct identification of accessions of both in situ and ex situ sources. Furthermore, correct identification of experimental accessions is vital to the validation of conclusions based on non-descriptive methodologies.

Fig. 3 shows the distribution of the bitter tomatoes based on information to date. The common ancestor of *S. incanum* s.l. may have originated in tropical East Africa and resembled *S. campylacanthum*, believed to be a more ancient taxon (Mace *et al.*, 1999; Sakata & Lester, 1994; Samuels, in press).

The evolving *S. incanum* migrated away from East Africa, moving north-eastwards to the Middle East (Samuels, 2010). Recent studies (Samuels, in preparation; Thomas *et al.*, 2008; Zubaida, 2007) show that the range of *S. incanum* s. str. extends into Pakistan and north-western India, further eastwards than previously noted. If domestication of brinjal eggplant from *S. incanum* did take place in the Indian subcontinent, as suggested by various authors (eg. Arora, 1991; Anon, 2009; Chen & Li, 1996; Isshiki *et al.*, 1994; Swarup, 1995; Zeven &

Zhukovsky, 1975), then it is likely to have been in this region. This may help to explain the suggestion of Weese & Bohs (2010) that there may have been a "single introduction" of eggplants into Asia; this would have been mediated through the natural occurrence of *S. incanum* in this region. The Indus Plains agro-ecological region (Arora, 1991) is the likely area in which initial domestication by early agricultural populations such as the Harappan (or Indus River Civilisation) around 1750-2300 BC may have occurred. This pre-dates the earliest record of cultivation of brinjal in the Far East, of 59 BC (Wang *et al.*, 2008) by about two thousand years.

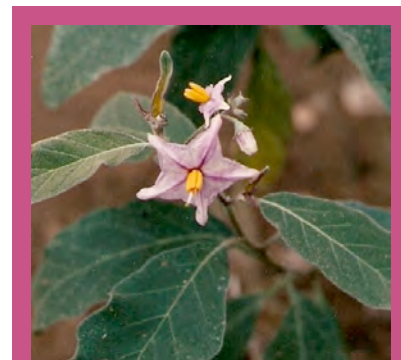
#### General characteristics of the species and subspecies

*S. campylacanthum* A. Rich. subsp. *campylacanthum* subsp. nov. Polymorphic group of mostly pubescent, mostly armed shrubs, with curved prickles, reaching 2 m or more high, with lanceolate, more or less lobed leaves. Inflorescence with up to 50 violet or purple flowers, up to 15 or more of which may be hermaphrodite. Yellow fruits up to 3.5 cm diameter. Tropical eastern Africa.

*S. campylacanthum* A. Rich. subsp. *panduriforme* (Dunal) comb. nov. (Fig. 4). Uniform group of finely pubescent, sparsely armed with straight prickles, or unarmed shrubs, sub-shrubs or herbaceous perennials, up to 2 m high, with elliptic, entire to sub-entire, occasionally sinuately lobed leaves. Inflorescence with up to 12 violet flowers, up to 3 of which may be hermaphrodite. Yellow fruits up to 2.5 cm diameter. Eastern and south-eastern Africa.

*S. incanum* L. (Fig. 1). More or less uniform group of densely pubescent, strongly armed, shrubs, with robust, curved prickles, reaching 2 m high, with broadly ovate, sub-entire to lobed leaves. Inflorescence with up to 15 purple or violet flowers, up to 3 of which may be hermaphrodite. Yellow fruits up to 3.5 cm diameter. Northeast Africa and Middle East to Iran and northwest India.

*S. lichtensteinii* Willd. More or less uniform group of densely pubescent, shrubs or sub-shrubs, strongly armed with robust, curved prickles, reaching 0.5-1m high, with narrowly ovate, lobed leaves. Inflorescences with up to 5 white (rarely violet) flowers, up to 3 of which may be hermaphrodite. Yellow fruits, up to 4.5 cm diameter. Southern Africa.



**Figure 4:** *S. campylacanthum* subsp. *panduriforme*-detail of single hermaphrodite flower.

#### Future research prospects

*S. incanum* s. str. is presumed to be the closest wild relative of the brinjal eggplant. Further studies on the taxonomy, distribution and phylogeny of *S. melongena* and its wild and weedy relatives in Asia are urgently needed.

#### Acknowledgements

I would like to thank the International Scientific Committee and Local Organizing Committee for the opportunity to participate in the XIVth. Eucarpia Meeting on Genetics and Breeding of *Capsicum* and Eggplant, Universidad Politecnica, Valencia, Spain, 30 August-1 September, 2010. This paper is partly based on Samuels (2010) presented at this meeting.

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## Genome Updates

### *Solanum pennellii*

Contact - Alisdair Fernie (Fernie@mpimp-golm.mpg.de)

The assembly of *S. pennellii* presented at the SOL conference in Dundee has recently made major progress. After stringent filtering of the original sequencing data, coverage of about 75x high quality data was obtained. Using these data, the latest assembly has reached a contig N50 size of nearly 9kb before scaffolding (i.e. half of the sequence data is in a contiguous sequence of 9kb or more). Based on these data first downstream analyses have begun.

### Tomato

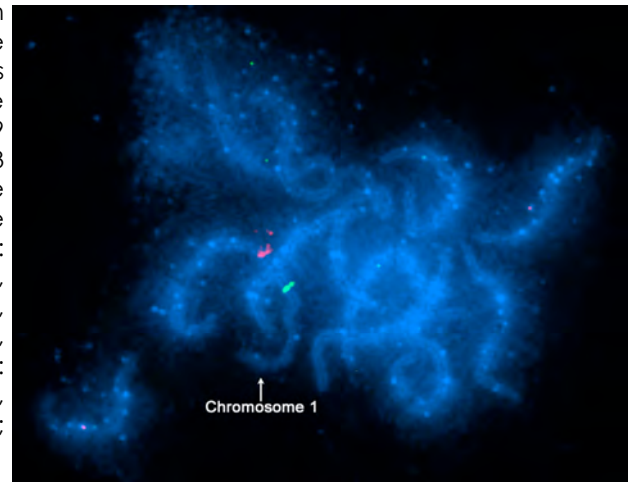
The latest developments on the international tomato genome project since the last Sol Newsletter involve efforts related to assembly and annotation. Assembly version 2.3 was released in August and is accessible from the SOL Genomics Network (<http://solgenomics.net/>). This version of the assembly covers 781 Mb, which is 87% of the revised tomato genome size of 900 Mb. There are 3,232 scaffolds with 97.2% of the assembly being in 91 chromosome-anchored scaffolds and 2.8% is in 3,141 "loose" scaffolds. Annotation is in progress.

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

We have continued to sequence chromosome 1 and 10 BACs with nearly 200 completed comprising over 20 Mb of sequence and many more are in the pipeline. Current efforts are directed toward utilization of the tomato physical map to identify minimal filling paths across these two chromosomes that will allow selection of BAC contigs, which will be sequenced to fill gaps in the current assembly. We have also been mapping sequences from the unassigned "chromosome 0" sequence assembly scaffolds and have tentatively assigned over 700 kb of this sequence to chromosomes.

Since the last edition of the SOL Newsletter, 54 new BACs have been localized using FISH on pachytene synaptonemal complex spreads at the Stack lab at Colorado State University. This brings the total number of BACs placed on the FISH map to 300. The 300 BACs are distributed among the chromosomes as follows: 1 - 80; 2 - 22; 3 - 21; 4 - 20; 5 - 15; 6 - 11; 7 - 32; 8 - 9; 9 - 21; 10 - 36, 11 - 17, 12 - 19. The total for the distribution above equals 303 instead of 300 because there are now 3 BACs with two positions each. The recently positioned BACs include (from the HindIII library unless otherwise noted, listed by chromosome arm): 1P: 008A081Q, SL\_Mbol0012120; 1Q: 203E06, 079N04, 210F09, 055E23, 035M19, 053C22, 049F03, 043D23, 067M04, 039M19, 080J18, 234D05, 125A09, 058O13, 165M11, 243A15, 049P09, 033M02, 048O19, 087D19, 029G15, 182E16, 002F21; 2Q: 189G15, 118M12; 3P: 130G19, SL\_FOS0097P22; 3Q: 142A05, 197O22; 4Q: 105J24; 5P: 011G20; 5Q: 033M02; 7P: 150H03, SL\_Mbol0137E08, SL\_EcoRI0042G10; 7Q: 224G23, 041L08, 106F06, 034B22; 9Q: 075M11; 10P: 028O04, SL\_EcoRI0076M19; 11P: 024K09; 11Q: 158K02; 12P: 180J10, 075A23, 150C12, 154D06; and 12Q: 079O22, 326K10, 152A18, 153L10, 047D08. BAC 033M02 has two loci, one on 1Q and one on 5Q.

The figure to the right illustrates FISH labeling on the long arm of tomato chromosome 1. The green label is BAC LE\_HBa0182E16 and the red label is BAC LE\_HBa0029G15.



## Announcements

### Publications

Chakravarthy S, Velasquez AC, Ekengren SK, Collmer A, Martin, GB (2010) Identification of *Nicotiana benthamiana* genes involved in pathogen-associated molecular pattern-triggered immunity. *Mol Plant Microbe In* 23:715-726.

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Velasquez AC, Chakravarthy S, Martin GB (2009) Virus-induced gene silencing (VIGS) in *Nicotiana benthamiana* and tomato. *Visualized Experiments* 28:1292.

## Conferences

### Plant Breeding in Postgenomic Era: Trends and Perspectives

November 22 - 23, 2010  
National University of Colombia  
Bogotá - Colombia  
tmosquerav@unal.edu.co

### International Conference on Solanaceae Resistance

February 17 – 19, 2011  
Le Meridien Hotel  
Chiangmai, Thailand  
<http://www.sol-symposium2011.com/>

### 43rd Tomato Breeders Roundtable Meeting

March 20 - 23, 2011  
El Cid Castilla Beach Resort Hotel  
Mazatlan (Sinaloa), Mexico  
<http://www.tbtr2011.eventbrite.com>

### XVIIth EUCARPIA Meeting of the Tomato Working Group

April 11 – 14, 2011  
Hotel Beatriz Palace & Spa  
Fuengirola (Málaga), Spain  
<http://www.eucarpiatomato2011.org>



## Solanaceae Recipes

### Tangy Tasty Tomatillo Soup

<http://www.recipezaar.com/member/382071>

Serves 8

#### Ingredients

3 boneless skinless chicken breast halves, cooked and shredded  
2 tablespoons olive oil  
1 red onion, chopped  
1 white onion, chopped  
5 garlic cloves, minced  
2 lbs tomatillos, whole hulled and rinsed (No need to chop)  
3 jalapeno peppers, seeded and minced  
6 cups chicken broth  
1/2 teaspoon garlic salt, more to taste  
ground black pepper, to taste  
cayenne pepper, to taste

2 red onions, chopped  
2 green bell peppers, chopped  
1 red bell pepper, chopped  
1 yellow bell pepper, chopped  
1 yellow jalapeno, minced  
1 (7 ounce) can mild green chilies, diced  
1 (10 ounce) bag frozen corn  
1 cup frozen baby peas  
1 cup frozen chopped spinach  
2 lemons, juice of  
sugar, to taste if too acidic  
sour cream, to serve  
cilantro, chopped to serve

Directions

- Cook and shred chicken. Set aside.
- Heat oil over medium high heat in a large pot or dutch oven. Ingredients 3-8: add 1 red onion and 1 white onion, saute until golden. Add garlic and saute 1-2 minutes. Stir in tomatillos, 3 jalapenos and broth. Bring to a boil. Reduce heat, cover and simmer for about 15 minutes until the tomatillos start to burst.
- Puree in pot with an immersion blender. Stir in garlic salt, black pepper and cayenne pepper to taste.
- Add reserved shredded chicken and the rest of the ingredients up to the chopped spinach and cook until heated through.
- Stir in lemon juice and sugar if desired and remove from heat.
- Serve in bowls topped with sour cream and cilantro to taste. Tortilla chips are also good with this.

## Chile and Bell Pepper Frittata

Serves 6

<http://www.gourmet.com>Ingredients

- |  |                                       |
|--|---------------------------------------|
| 8 bacon slices, cut into 1-inch pieces   | 1 yellow bell pepper, cut into strips |
| 3/4 lb waxy potatoes such as fingerlings, Peruvian purple, or Yukon Gold,<br>sliced crosswise into 1/4-inch-thick rounds                   | 1 green bell pepper, cut into strips  |
| 4 to 6 assorted hot and sweet chiles such as Hungarian wax, Cubanelle<br>(Italian green frying pepper), habanero, serrano, and/or jalapeño | 3 garlic cloves, finely chopped       |
|  | 1 cup sour cream                      |
|  | 12 large eggs                         |

Directions

- Preheat oven to 350°F with rack in middle.
- Cook bacon in an ovenproof 12-inch heavy skillet (preferably cast-iron) over medium heat until beginning to brown, about 5 minutes. Add potatoes, 1/2 tsp salt, and 1/4 tsp pepper and cook, stirring occasionally, until potatoes are tender, about 10 minutes.
- While potatoes cook, stem, seed, and devein chiles, then finely chop.
- Add chiles and bell peppers to potatoes and cook, stirring occasionally, until peppers are softened, 10 to 12 minutes. Add garlic and cook, stirring occasionally, until pale golden, about 3 minutes.
- Whisk together sour cream, eggs, 3/4 tsp salt, and 1/2 tsp pepper, then pour over vegetables in skillet.
- Transfer skillet to oven and bake until eggs are just set, 18 to 24 minutes. Serve warm or at room temperature.

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