Sol Newsletter

Issue number 31
October 2011
Editor: Joyce Van Eck

In this issue

Community News

Afri-SOL: A New Network of Researchers Working on African Solanaceous Plants

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Solanum retroflexum

A group of scientists working on African solanaceous plants have come together to form Afri-SOL. The need to create this network stemmed from the realization that a number of African solanaceous plants are increasingly playing an important role in meeting the nutritional and health needs of many households globally. Breeders also continue to look for novel traits from wild plants of the Solanaceae family that are native to the African continent. Research interest on the rich source of diversity present within the African continent, however, does not match the potential value of these plants. There has been very little consolidated research effort towards proper conservation, management, and improvement of the valuable germplasm. Afri-SOL brings together a multidisciplinary team of stakeholders with the following aims:

1. To undertake extensive collection and characterization of all solanaceous plants found in Africa; proper maintenance of native African Solanaceae genetic resources will ensure availability of basic material for selection and crop improvement. Exploration and exhaustive collection of all diverse Solanaceae germplasm found in Africa will be the first step towards understanding the extent of diversity and potential contribution towards crop improvement, better health and food security.
2. To collate information on geographic distribution of solanaceous species within Africa and their uses; there will be need to create a comprehensive database with details on various solanaceous plants found in different regions of the continent in order to enhance the correct identification of priority target areas for sources of both cultivated and wild germplasm. Such information will also help highlight target areas threatened by genetic erosion.
3. To promote the benefits of solanaceous crops grown in Africa; unknown to many, some African nightshades, including *S. scabrum* and *S. villosum* are edible and very nutritious with medicinal and industrial value. The increasing concerns on narrowing food diversity and the recognition of the potential role of vegetables in combating micronutrient deficiencies, call for renewed research interest in underutilized nutritious vegetables such as those of Solanaceae family.
4. To develop research tools for the improvement of beneficial African solanaceous crops; it will be necessary to enhance knowledge and the breeding process of beneficial African solanaceous plants in order to increase their commercial value within the farming and market industry. With the current advances in genomics technologies, it will be possible to generate a lot of valuable data on these underutilized plants within a relatively short period of time.
5. To facilitate technology dissemination for the improvement of solanaceous crops in Africa; existing research information on native plants and other closely related species will be made available through member interactions and collaborations with other *Sol* communities. Afri-SOL will enable proper coordination of activities in order to eliminate research duplication that is likely to reduce progress in varietal and product development.
6. To seek joint funding from various institutions geared towards the improvement of solanaceous crops in Africa; consolidation of the region's research efforts will result in more focused research objectives and enhanced research impacts. It is hoped that the likely comprehensiveness of research activities within the network will make it particularly attractive for major funding as well as in creating collaborations with other existing successful on-going Solanaceae research networks.
7. To enhance sharing of information and germplasm among researchers; research progress within the continent will be significantly increased through effective pooling of valuable genetic resources.

The network is open to all researchers based in Africa and working on solanaceous plants, or scientists based elsewhere with an interest in African solanaceous plants. Afri-SOL will strive to enhance better exchange of ideas, enhance access to information and publications, and find potential collaboration partners.

Afri-SOL members welcome any suggestions from other *Sol* communities.

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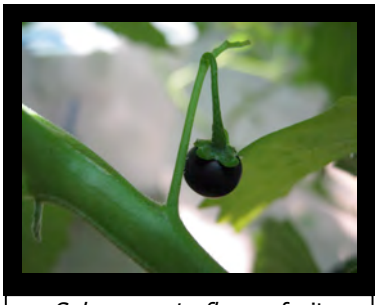

Solanum retroflexum fruit

Photos were kindly provided by Ms. Erika Viljoen.

SOL "Down Under"

Sandra Knapp
NHM London

A Solanaceae symposium entitled "Recent advances in Solanaceae research: biodiversity to genomics" was held recently at the XVIII International Botanical Congress in Melbourne, Australia (http://www.ibc2011.com/). International Botanical Congresses are only held every six years, so this was a good opportunity to showcase how our community is progressing to a very broad cross-section of the botanical community. Despite being scheduled on the last morning of the congress, the talks were well attended, and as usual for Solanaceae folk, good discussions were had. Speakers were (abstracts can all be found on the IBC2011 website at http://www.ibc2011.com/downloads/IBC2011_Abstract_Book.pdf, all except Lynn's which somehow went missing):

Rachel Levin (Amherst, MA) - *Lycium* (Solanaceae): diversity, dispersal, and dating
Stephen Stern (University of Utah) - Prickly phylogenies: unraveling relationships in *Solanum* subgenus *Leptostemonum*
Amy Litt (New York Botanical Garden) - Comparative gene function in the development of fleshy and dry fruits in Solanaceae
Simon Renny-Byfield (Queen Mary, University of London) - Genome downsizing in allopolyploid *Nicotiana tabacum*: how does next generation sequencing depth influence results?
Bicheng Yang (BGI, Shenzhen) -The potato genome and its comparison with other plant genomes
Lynn Bohs (University of Utah) - Progress on global *Solanum* taxonomy

We began with an overview of global evolution in the genus *Lycium*, including the rationale for the inclusion of the small genera *Phrodus* and *Grabowskia* in a monophyletic but much larger *Lycium* (recently published in Levin et al. 2011. A new generic circumscription in tribe Lycieae (Solanaceae). *Taxon* 60: 681-690). Then Stephen showed us how the relationships in the spiny solanums were slowing becoming more clear using a combination of molecular and morphological approaches, coupled with a lot of very exciting field work. Fruit development is well studied in tomato, but Amy Litt described comparative work in flowering tobacco and showed how fruit development differs in this non-fleshy-fruited species. The tobaccos are a model group for the study of polyploidy, and Simon explored genome downsizing using 454 pyrosequencing; it turns out paternal sequence is preferentially eliminated! Bicheng Yang outlined the results of the potato genome sequence that had been published in *Nature* just in time for our meeting (The Potato Genome Sequencing Consortium 2011. Genome sequence and analysis of the tuber crop potato. Nature 475: 189-195). Lynn Bohs wrapped things up with an overview of progress in understanding the taxonomy of the hyperdiverse genus *Solanum*; she showed how this has been a combination of increasing synonymy in over-described groups (like the potatoes, see Ovchinnikova et al. 2011. Taxonomy of cultivated potatoes. *Botanical Journal of the Linnean Society* 165: 107-155) and the discovery of many new species in other groups such as section *Gonatotrichum*

Symposium speakers and organizers (L to R) – Bicheng Yang, Sandy Knapp, Simon Renny-Byfield, Stephen Stern, Rachel Levin, Amy Litt, Lynn Bohs.

(check it out on Solanaceae Source!! http://www.solanaceaesource.org – try *Solanum turneroides*) whose species number has tripled following in-depth study. Comparative SOL research is alive and well, and our community was seen as one that is truly bringing genomics and biodiversity closer together. Long may it continue! The next International Botanical Congress will be held in the city of Shenzhen, China, in July 2017 – let's try to have a few SOL symposia there.

Highlight Article

Activity Report of Tsukuba-INRA Joint Lab (TIL)

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Assistant professor residing at INRA Bordeaux from 2009
http://til.gene.tsukuba.ac.jp/index.html

Brief history

In 2007, the Gene Research Center in University of Tsukuba was positioned as a core institution of the Tomato National Bio-Resource Project, and has been playing a key role in the tomato study in Japan. At the same time, a cooperation agreement was signed between INRA and the University of Tsukuba. Prof Hiroshi Ezura (Univ Tsukuba) and Dr Christophe Rothan (INRA Bordeaux) carried out JSPS-INRA Bilateral Joint Research Program "Use of tomato mutant resources for functional studies of target genes in tomato by TILLING" during 2007-2008. This collaborative project developed a useful research resource, platform of TILIING*, which is high-throughput screening method to find mutations of target gene (the joint laboratory name "TIL" is also named after TILLING). On the basis of these collaborations, we established a joint laboratory with aims at the realization of a high quality research environment by integrating mutual resources, and training of young researchers by personnel exchange. Joint labs were opened at the Gene Research Center, University of Tsukuba and INRA Bordeaux in October 2008 and in January 2009, respectively.

Organization

The Bordeaux Joint Lab is based in the UMR619 Fruit Biology laboratory (reorganized as UMR1332 Fruit Physiology and Pathology from January 2011), in INRA Bordeaux Research Centre located 30 minute drive from Bordeaux downtown. UMR stands for a joint laboratory, consisting of staffs from INRA and University of Bordeaux. By grace of the UMR structure, we can efficiently promote collaborations for research activities as well as educational activities like student exchanges. The Tsukuba Joint Lab is set up in the Gene Research Center, University of Tsukuba. Tsukuba city is called "Tsukuba science city" because there are many research institutes such as Riken, National Institute of Agrobiological Sciences, and the National Institute of Advanced Industrial Science. Therefore, the Tsukuba Joint Lab can benefit from these partners. Although we usually communicate by e-mail due to geographical distance between Tsukuba and Bordeaux, once a month we have a regular meeting using a video conferencing system to discuss face to face. In addition, once a year, the activities of the joint lab are evaluated by the external advisory board composed of Japanese, French and American scientists. The first round was held at Bordeaux, the second was held at Tsukuba. Using those opportunities, we also held workshops for students and young researchers.

Research activities

Before setting the joint lab, we have developed tomato mutant collections separately in Tsukuba and Bordeaux. INRA Bordeaux has developed 8500 EMS-mutagenized M2 families of Micro-Tom. There are 2200 EMS-mutagenized M2 lines and 2700 gamma-ray irradiated M2 lines in Tsukuba. These mutant collections cover the entire tomato genome and can be used to discover new genes and alleles by a forward genetics approach, and also by reverse genetics using TILLING. The use of mutant collections and TILLING represents a large part of the research activities of the joint lab. Many young researchers and students have participated in this collaboration. For example, the mutant collection has been screened for mutated alleles of genes related to GABA (γ-aminobutyric acid) metabolism and to ascorbic acid biosynthesis and the corresponding mutants are being investigated.

Efforts are also combined for the generation of transgenic tomato lines in which the expression of target genes is modulated in order to study their function. Generation of transgenic tomato is time-consuming and often requires experienced skills. In addition, transgenes often need to be targeted precisely to specific tissues. Common projects therefore benefit from the efficient method for tomato transformation developed at University of Tsukuba and from the series of vectors having tomato fruit-specific and developmental stage specific promoters available at INRA Bordeaux. These resources make it possible to produce various transgenic tomato lines according to the research objectives of the joint lab. Also, INRA Bordeauxhas has in-house access to well-established experimental facilities including cytology (electron microscopy, confocal laser microscopy, and analysis FISH), transcriptome (Illumina sequencer, microarray and quantitative PCR), TILLING and metabolome (1H-NMR, LC range-MS, GC-MS, high throughput enzyme activity assays). By combining mutual resources in both labs, we succeeded in creating an excellent research environment from preparation of biological materials to phenotypic analysis.

Activities in Education

The main educational activity is the exchange of students. Obviously research experiences in foreign countries bring various advantages, new knowledge, new experimental techniques, different ways of thinking and improved language skills, etc. In addition, people who understand the cultural background in Japan and France can contribute to develop education and research

activities in two countries by working as a bridge between Japan and France. By taking advantage of the framework of a joint lab, graduate students and undergraduates have stayed in each joint lab to perform experiments or to take a short-course. Most of the Japanese students have no experience abroad, therefore in the beginning they often had difficulties in the unfamiliar environment. However, they adapted well eventually and finished their scheduled work. After this short experience, some students started to consider longer experiences as postdoctoral associates in foreign countries. In the short-course, undergraduates spend about ten days taking lectures on French agriculture including grape and wine science at Bordeaux. The program also includes study tours of agricultural facilities and research institutes.

As for French students wishing to study in Japan, so far one PhD student has spent one year in Tsukuba by the French-Japanese joint supervised "cotutelle" program. For French Master students, they are required to do work experience for six months. There are five students who have studied master research in Tsukuba. Similar to Japanese students, French students had difficulties in language and with the way of life. Nevertheless, each year there are students are highly motivated to study in Japan. In both cases, students are free from most of the problems with administrative procedures for arranging housing during their stay because of the help of support staff and members of the laboratories. Therefore, they can easily jump into another environment and concentrate on their study.

Conclusion

The Joint Lab gives us the opportunity to accelerate synergistic and interactive research utilizing our Micro-Tom resources. In addition, TIL joint lab introduced new a new collaboration with Cornell University in 2011. Cornell University is a leading institution for tomato research in bioinformatics and genetic resources. The concerted efforts of these three joint labs are expected to develop research and educational activities.

Acknowledgement

This Joint Lab project is supported by the Special Educational Research Budget from the Ministry of Education, Culture, Sports, Science and Technology (MEXT), Japan and the JSPS-INRA Bilateral Joint Research Project.

***Reference**

Okabe Y, Asamizu E, Saito T, Matsukura C, Ariizumi T, Brès C, Rothan C, Mizoguchi T, Ezura H (2011) Tomato TILLING technology: Development of a reverse genetics tool for the efficient isolation of mutants from Micro-Tom mutant libraries. Plant and Cell Physiology. (In press)

Research Updates

Sexual Distinctions on Frequency of Crossing Over in Tomato

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In higher plants, sexual distinctions on a recombination level are poorly studied despite the large theoretical value and importance for practical selection. The estimation of distinctions $rf_{♀}$ and $rf_{♂}$ is possible only for objects with well developed particular genetics since cytologic comparison on the basis of frequency of chiasmata for the majority of plants is complicated because of technical complexity due to chiasmata in macrosporogenesis. Even for genetically well-investigated economically important objects such as a tomato, peas, barley, rice, and cotton the $rf_{♀}$ and $rf_{♂}$ distinctions are still not completely understood. Rick (1972) has shown recombination distinctions in micro- and macrosporogenesis for tomato with the use of markers of a chromosome 3. It turned out that in a segment sy-bls, which contains the centromere, frequency of crossing over is essentially higher, when the heterozygote is used for analyzing crossing as a female component, and in a segment bls-sf distinctions are practically absent. Frequency of double exchanges in a considered zone in macrosporogenesis was two times higher than in microsporogenesis.

In our experiments $rf_{♀}$ and $rf_{♂}$ values for four zones of the tomato genome were compared, two of them contained the centromere (e-ful, hl-a in chromosomes 4, 11) and two were distal (aw-d and m-2–c in chromosomes 2, 6). For segments aw–d and m-2–c the analysis was carried out on six F_1 hybrids obtained from crossing of marker line aw, d, c, m-2 with various forms of the genus Lycopersicon (Table 1). From the results it is followed that at genotypic variations the value of rf in a segment aw-d changes poorly, the variability of rf is more significant. The correlation between them is positive, but a difference changes a sign from a genotype to a genotype. Many combinations between them are positive, but a difference changes a sign from a genotype to a genotype. In many combinations of crossing, precise distinctions are found between male and female meiocyte on rf level. In these cases, frequency of exchanges in female meiosis on the order is reduced in comparison with the normal level corresponding to a map distance. So, because of insufficiency of amount of BC populations these results should be considered as preliminary. For a segment m-2–c at three of six hybrids significant distinctions between $rf_{♀}$ and $rf_{♂}$ also are found: in two cases $rf_{♀} > rf_{♂}$, and in one $rf_{♀} < rf_{♂}$. Correlation between changes of $rf_{♀}$ and $rf_{♂}$ is absent.

The analysis of sexual distinctions on rf for segments (ful-e, hl-a) of chromosomes 4 and 11 was carried out by us with hybrids between marker line Mo 628 and *L. racemigerum* and *L. pennellii* species (Table 1). For both segments, a strong "sex x genotype" interaction as defined by a recombination level is observed between marker genes. Distinctions $rf_{♀}$ and $rf_{♂}$ in a zone hl-a at a hybrid with *L. racemigerum* are especially strong. By the obtained estimations, here specifically in macrosporogenesis it is completely suppressed. It is necessary to also note that for this hybrid there is a typically sharp decrease of rf in a zone aw-d. The results in Table 1 show that genotypic variations, which are connected with interspecific hybridization in tomato, can cause significant alternate changes of a crossing over level in male and female meiosis. Thus, the submitted data on sexual distinctions on a level of crossing over (rf) in male and female meiosis in tomato essentially depend on a genotype of F_1 plants and marker segment under investigation. However for the majority of sites, $rf_{♂}$ is significantly higher than $rf_{♀}$. These distinctions have strongly pronounced segment-specific character.

Table 1: Variability of crossing over frequencies in tomato in aw-d и m-2–c, ful-e и hl-a segments subject to sex and genotype of heterozygotes F_1.

Hybrid of line aw, d, m-2 with tomato species	$F_1(♂)$			$F_1(♀)$		
	N	rf (%) in segment		**N**	rf (%) in segment	
		aw-d	**m-2–c**		**aw-d**	**m-2–c**
L.esculentum	171	9,36±0,80	25,73±1,20	2492^{+}	14,12±2,00*	29,11±3,11
L.pimpinellifolium	162	7,41±0,59	24,69±0,96	3832^{+}	10,60±1,45*	24,60±2,48
L.racemigerum	135	11,11±0,87	24,44±1,18	2501^{+}	0,64±1,73***	29,89±3,06
L.cheesmanii var.minor	104	14,42±1,64	27,88±2,10	812^{+}	13,65±3,93	13,93±5,42**
L.minutum	95	8,42±1,11	34,74±1,90	1163^{+}	0,76±2,16***	20,12±5,33**
L.hirsutum var. glabratum	95	9,47±0,81	14,74±0,98	2501^{+}	0,93±1,61***	32,44±2,61***
Hybrid of line ful, e, hl, a with forms	**N**	**ful-e**	**hl-a**	**N**	**ful-e**	**hl-a**
L.racemigerum	247	30,77±1,79	24,33±1,67	1078^{+}	15,07±4,79***	0,01±3,95***
L.pennellii	464	26,29±1,75	18,10±1,43	803^{+}	50,00±4,46***	43,06±4,01***

The sign + means, that the estimation rf is obtained on the basis of joint analysis F_2 and BC2;
*, **, *** - distinctions $rf_{♂}$ and $rf_{♀}$ are significant at P <0,05; 0,01 and 0,001 correspondingly.

References

Rick C.M. 1972. Further studies on segregation and recombination in backcross derivatives of a tomato species hybrid. Biol. Zbl. Bl. 91(2): 209–220.

Variability of Crossing Over in F_2 Populations of Interspecific Hybrids of Tomato

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The degree of inhibition of crossing over in marker segments in the later generations of BC as it has been shown by Rick (1972), can amplify in comparison with the level of the F_1. Earlier similar results were obtained for interspecific hybrids of cotton (Stephens, 1961). Not excluding the importance of the specified position for introgressive selection, we have carried out an experiment with hybrids hl-a x *L. hirsutum* var. *glabratum* and hl-a x *L. racemigerum*. It has compared rf_{hl-a} values of genotypes F_1 and F_2 of each hybrid (Table 1).

Table 1 Frequency of crossing over (rf_{hl-a}) in F_1 and F_2 interspecific hybrids of a tomato.

Hybrid	hl–a x *L. hirsutum var. glabratum* :		hl–a x *L. racemigerum*	
	N	rf,%	N	rf,%
	163	21,90 ± 3,75	870	11,10 ±1,14
	651	21,16 ± 1,89	552	18,74 ± 1,88
	159	8,68 ± 2,36	572	11,20 ± 1,41
F_2	133	19,55 ± 3,91	325	10,19 ± 1,79
	243	27,18 ± 3,45	496	14,86 ± 1,76
	147	10,44 ± 2,69	362	10,31 ± 1,70
	228	10,01 ± 2,12	412	15,79 ± 1,99
	188	8,30 ± 2,12	576	21,45 ± 3,94
	205	25,58 ± 3,63	364	15,46 ± 2,09
	average F_2	15,19 ± 2,52	average F_2	12.96 ± 1,23
	rf (CV,%)	57,2 (49,8)	rf (CV,%)	13,2 (28,5)
F_2	χ^2 (heterogeneity) = 65,6 (P<0,001)		χ^2 = 26,2 (P< 0,01)	
F_1	566	12,60 ± 1,95	1078	7,96 ± 1,06

High variability in the F_2 on frequency of crossing over in the investigated zone has been revealed. Thus the hybrid between the more distant form (*L. esculentum* x *L. hirsutum glabratum*) has also given more variable progeny (Table 1). At all 9 heterozygotic F_2 genotypes for both markers of chromosome 11, triple distinctions – 8.3 up to 27.2 % are obtained. It specifies particularly of selection on rf in the progeny of F_2 hybrids. We have made conclusions about a higher level of crossing over at F_1 hybrids of line hl-a, a cultural tomato with wild species *L. hirsutum glabratum* in comparison with F_1 hybrid - hl-a x *L. racemigerum* has proved to be true on F_2 - rf F_2 (hl-a x *L. hirsutum glabratum*) > rf F_2 (hl-a x *L. racemigerum*).

A comparison of rf_{hl-a} values in F_1 and F_2 genotypes of each of hybrid follows that restriction of frequency particularly (in intraspecific hybrid hl-a x *L. esculentum* rf = 20,6 %) in F_1 can be stronger than in F_2. Formally it is equivalent to the domination of the rec genes, which have reduced crossing over.

Thus, results of the value of rf in F_2 and F_1 allow us to challenge the universally established result by Rick (1972) for hybrid *L. esculentum* x *S. pennellii* that in the later generations the level of exchanges is reduced in comparison with F_1. For two hybrids investigated by us, the average frequency of exchanges in F_2 is higher than in F_1, and genotypes from F_2 with the maximal value more than twice surpass the corresponding value for F_1. These data show that selection in progenies of interspecific hybrids, and genotypes with high recombination ability can have not only theoretical, but practical value as well.

References

Rick C.M. 1972. Further studies on segregation and recombination in backcross derivatives of a tomato species hybrid. Biol. Zbl. Bl. 91(2): 209–220.

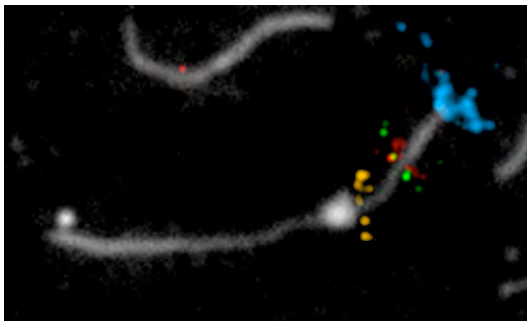
Stephens S.G. 1961. Recombination between supposedly homologous chromosomes of *Gossypium barbadense* L. and *G. hirsutum* L. Genetics. 46(11): 1483–1500.

Update from Steve Stack's Lab at Colorado State University

Lindsay Shearer

The Stack lab at Colorado State University has now placed a total of 379 BACs on the tomato FISH map using fluorescence in situ hybridization on pachytene synaptonemal complex spreads. This total includes 56 BACs added since the last SOL Newsletter. These new BACs (all from the HindIII library unless otherwise noted), listed by chromosome arm, are: 1P – SL_s0083L21, SL_s0053P14, SL_MboI0034D03, SL_s0090M22 ; 1Q – SL_EcoRI0016I11, SL_s0006A13, 033N15, SL_s0042B18, SL_MboI042O02, 037N04, SL_s0040G18, SL_EcoRI0021C24, SL_s0022L14, SL_s0121I01, SL_s0071P10, SL_s0024J19, SL_MboI0028C09; 2P – 111L05; 3P – SL_MboI0103M17, SL_FOS0082H20; 3Q – 154B13; 4P – 323C04; 4Q – 059C20, 030F21, SL_MboI0120F05, 303A06, SL_MboI0078A08; 5P – 116D11; 5Q – 100I16; 6P SL_MboI0134P07, 024L21, 068M22, 176D13, 097D13; 7P – SL_MboI0024O10; 8Q – 076I13; 9P – SL_MboI0080E11; 10P – SL_EcoRI0029F05, SL_s0071N16, 023E16, SL_MboI0009D07, SL_EcoRI0027L04, 205L07, 105C09; 10Q – SL_MboI0011N01, SL_x0042K13, SL_s0121P17, SL_EcoRI0036N16, SL_EcoRI0013B18, SL_EcoRI0008A07; 11P – SL_MboI0121I03, 080C09; 12P -- 012P02; 12Q – 012E19, 093P12. The 379 localized BACs are distributed at 387 loci among the chromosomes as follows: 1 - 107; 2 - 23; 3 – 25; 4 – 28; 5 – 20; 6 – 19; 7 –33; 8 – 10; 9 – 24; 10 – 55, 11 – 21, 12 – 22. The total number of loci reflects the fact that there are now eight BACs that have each been localized to two positions.

Many of the new BACs are on the borders of the sequenced scaffolds on chromosomes 1 and 10. By using two of these BACs as probes on the same slide, we were able to measure the distance of unsequenced DNA between each pair of adjacent scaffolds. Those distances, along with estimates of the Mb/micrometer in the euchromatin and heterochromatin were used to estimate gap sizes in base pairs. This lab will be doing similar measurements and calculations for tomato chromosomes 2, 3, 5, 8, and 11 in the near future. We will also be using fiber FISH to more accurately measure very small gap sizes.



The figure on the right illustrates FISH labeling of four BACs on the short arm of chromosome 10. BACs SL_EcoRI0027L04 (blue) and SL_EcoRI0009D07 (red) are at the borders of scaffold 1. BACs SL_s0071N16 (yellow) and LE_HBa0023E16 (green) are at the borders of scaffold 2. We have estimated the unsequenced area between these two scaffolds to be approximately 1 Mb.

Resources

fitTetra Software

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The Netherlands

We have developed fitTetra: software for automatically scoring data from SNP genotyping assays from tetraploid samples (such as potato) into the five tetraploid genotypes: nulliplex, simplex, duplex, triplex and quadruplex. This is described in the article: Voorrips RE, Gort G, Vosman B (2011) Genotype calling in tetraploid species from bi-allelic marker data using mixture models. BMC Bioinformatics 2011, 12:172.

The software is available from http://www.plantbreeding.wur.nl/UK/software_fitTetra.html.

Job Announcements

Faculty Position in Plant-Biotic Interactions

Boyce Thompson Institute for Plant Research

The Boyce Thompson Institute (BTI), an independent affiliate of Cornell University, invites applications for a tenure-track faculty position at the Assistant or Associate level. We seek candidates whose research addresses fundamental questions in plant biology and is synergistic with current research at BTI and Cornell University. Areas of interest include interactions of plants with pathogenic or symbiotic microorganisms, insects, nematodes, or parasitic plants at the molecular, organismal or community level. The successful candidate is expected to establish an outstanding extramurally-funded research program and is encouraged to develop links to relevant departments at Cornell University. BTI is located on the Cornell University campus in Ithaca, a culturally diverse and vibrant town in the Finger Lakes region of New York. Our faculty members have access to state-of-the-art mass spectrometry, cell imaging, and plant growth facilities at BTI, as well as extensive infrastructure through the Cornell University Life Sciences Core Facilities. Applicants should submit a single PDF document that includes a cover letter, detailed *curriculum vitae,* the names of three references, and a statement of research accomplishments and future research interests (2-3 pages) to Gregory Martin, Chair, BTI Faculty Search Committee at: **BTI_Faculty_Search@cornell.edu.** Review of applications will begin November 15, 2011. Please visit http://bti.cornell.edu for additional information about BTI.

BTI has a shared- and split-faculty position policy; candidates applying for such a position should indicate this in their cover letter (see http://bti.cornell.edu/SSP.pdf for more information).

Boyce Thompson Institute is an affirmative action, equal opportunity employer and is committed to increasing the diversity of its faculty and staff.

Postdoctoral Position in the Area of Tomato-Spider Mite Interaction

University of Western Ontario, London, Canada

A two-year postdoctoral position (with the possibility of extension) for studying tomato-spider mite interaction is available in the group of Drs. Miodrag and Vojislava Grbic at the University of Western Ontario, London, Canada. The position is available immediately.

Our group is using genomic tools developed for tomato and spider mites to study the molecular mechanisms underlying tomato-spider mite interaction. Our group is part of the larger GAP-M international consortium http://devbiol.zoo.uwo.ca/spidermite/, with current funding available for next four years.

We are seeking a highly motivated person capable of working independently and with experience in tomato biology and genetics, and/or bioinformatics. To qualify for the position you should have a PhD degree or equivalent obtained, preferably, no longer than three years ago.

Interested parties should email a cover letter outlining interests, complete CV, and contact information for two individuals willing to supply letters of recommendation to vgrbic@uwo.ca and mgrbic@uwo.ca.

Publications

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Scholthof HB, Alvarado VY, Vega-Arreguin JC, Ciomperlik J, Odokonyero D, Brosseau C, Jaubert M, Zamora A, Moffett P (2011) Identification of an *ARGONAUTE* for antiviral RNA silencing in *Nicotiana benthamiana.* Plant Physiol 156:1548-1555.

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Zhong S, Joung J-G, Zheng Y, Chen Y-R, Liu B, Shao Y, Xiang JZ, Fei Z, Giovannoni JJ (2011) High-throughput Illumina strand-specific RNA sequencing library preparation. Cold Spring Harb Protoc, doi:10.1101/pdb.prot5652.

Conferences and Workshops

SOL & ICuGI 2011
8th Solanaceae and 2nd Cucurbitaceae Joint Conference
November 28 - December 2, 2011
Kobe, Japan
www.sol2011.jp

Plant and Animal Genome Conference
January 14 - 18, 2012
Town and Country Hotel
San Diego, California
www.intlpag.org/web

EUCARPIA
Plant Breeding for Future Generations
May 21 - 24, 2012
Budapest, Hungary
www.mgki.hu/index.php?conference=30&lang=en

Potato Association of America
August 11 - 15, 2012
Denver, Colorado
www.paa2012.colostate.edu

Solanaceae Recipes

Grilled Eggplant Pepper Sandwiches

www.tasteofhome.com

Ingredients – Olive mixture
- 1/2 cup pitted ripe olives
- 2 to 3 tablespoons balsamic vinegar
- 1 garlic clove, minced
- 1/8 teaspoon salt
- Dash pepper
- 1/4 cup olive oil

Sandwiches
- 1/4 cup olive oil
- 3 garlic cloves, minced
- 1 teaspoon pepper
- 1/2 teaspoon salt
- 1 large eggplant, cut lengthwise into 1/2-inch slices
- 2 large sweet red peppers, quartered
- 8 slices firm white bread (1/2 inch thick)
- 1/4 cup fresh basil leaves, thinly sliced

Directions
1. Place the first five ingredients in a food processor; cover and process until pureed. While processing, gradually add oil in a steady stream; process until blended. Set aside.
2. For sandwiches, in a small bowl, combine the oil, garlic, pepper and salt; brush over eggplant and red peppers. Prepare grill for indirect heat, using a drip pan. Arrange vegetables on a grilling grid; place on a grill rack over drip pan.
3. Grill, covered, over indirect medium heat for 10-12 minutes or until tender. Remove and keep warm. Grill bread over medium heat grill for 1-2 minutes on each side or until toasted.
4. Spread olive mixture over toast. Top four slices with vegetables and basil; top with remaining toast.

Yield: 4 servings.

Editor's Note: If you do not have a grilling grid, use a disposable foil pan. Poke holes in the bottom of the pan with a meat fork to allow liquid to drain.

Nutrition Facts: 1 sandwich equals 463 calories, 31 g fat (4 g saturated fat), 0 cholesterol, 844 mg sodium, 44 g carbohydrate, 8 g fiber, 7 g protein.

Tomatillo Mary

www.marthastewart.com

Ingredients

- 1 pound tomatillos, husked, rinsed, and chopped
- 1 medium English cucumber, peeled and chopped
- 1 jalapeno chile, seeded and chopped
- ¾ cup cold water
- 3 tablespoons fresh lime juice (about 2 limes)
- 1 tablespoon sugar
- Lime wedge
- Coarse salt
- Cayenne pepper
- 1 cup chilled vodka
- Ice cubes

Directions

1. Puree tomatillos, cucumber, jalapeno, water, lime juice, sugar, ½ tsp salt, and a generous pinch of cayenne pepper in a blender until smooth.
2. Stir in vodka.
3. Refrigerate until chilled, about 2 hours.
4. Meanwhile, stir together 2 teaspoons salt and ½ teaspoon cayenne pepper on a small plate.
5. Wet the rims of 4 glasses with lime wedge, and dip each in the salt mixture, turning to coat.
6. Stir Tomatillo Mary mixture well, and divide among 4 ice-filled glasses.

Make ahead: Tomatillo Marys can be refrigerated for up to 4 hours. Pour over ice just before serving.