

# Sol Newsletter

April 2013 Issue Number: 35 Editor: Joyce Van Eck Assistant editor: Ruth White

# Community News

# The 10th Solanaceae Conference — Genome versus Phenome Beijing Friendship Hotel, Beijing, China October 13 - 17, 2013

# Dear Colleagues,

You are cordially invited to the 10th Solanaceae Conference (SOL 2013) to be held at the Beijing Friendship Hotel in Beijing, China, from October 13 - 17, 2013. As in past years, SOL 2013 would bring together a spectrum of scientists working on different aspects of Solanaceae ranging from biodiversity, genetics, development and genomics. With the availability of the high-quality genome sequences of tomato and potato, studies of the SOL community have extended from structural genomics into virtually every aspect of functional genomics. SOL 2013 would be a forum to discuss the impact of the reference genome on different aspects of Solanaceae studies. Meanwhile, a battery of high throughput technologies, including transcriptomics, proteomics and metabolomics, are leading the way in providing new insights into the inner workings of plant cells. Importantly, the cell biology toolbox, which is previously mainly restricted to animal and yeast cells, has finally been built up in the Solanaceae allowing researchers to establish the fundamental linkage between genotypes versus phenotypes. The conference would also provide a forum to sit together and create a roadmap for the future of the Solanaceae Community.

The proposed program lists 37 confirmed invited speakers who will be distributed through 12 sessions. Each session will include these invited speakers and 15-minute shorter talks, which will be chosen from the submitted abstracts. Each chair will introduce the subject of the session and will encourage discussion.

Online abstract submission and online registration are open now! For more information, please refer to the conference website: http://www.sol2013.org/

#### **Organizer**

Institute of Genetics & Developmental Biology, CAS The State Key Laboratory of Plant Genomics

#### **Conference Co- chairs**

- Jiayang Li (Institute of Genetics and Developmental Biology, CAS)
- Zhiyuan Fang (Institute of Vegetables and Flowers, CAAS)
- Yongbiao Xue (Institute of Genetics and Developmental Biology, CAS)
- Chuanyou Li (Institute of Genetics and Developmental Biology, CAS)

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- Zhibiao Ye (Huazhong Agricultural University)
- Yuhe Sun (Tobacco Research Institute, CAAS)

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FISH Update

#### **Members**

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Zhibiao Ye (Huazhong Agricultural University)

Wengui Yu (Vegetable Research Institute, Jiangsu Academy

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Chuanyou Li (China) Lukas Mueller (USA) Graham Seymour (UK) Akhilesh Tyagi (India) Allen Van Deynze (USA) Joyce Van Eck (USA)

Richard Visser (The Netherlands)

Dani Zamir (Israel)

#### **Scientific Sessions**

Session I. Hormone Signaling and Development

Session II. Fruit Biology

Session III. Biotic Interactions

Session IV. Abiotic Interactions

Session V. Systems Biology

Session VI. Metabolomics and Proteomics

Session VII. Translational Genomics and Breeding

Session VIII. Biodiversity and Evolution

Parallel Session IX. SOL Genomics and Beyond: Tomato Parallel Session IX. SOL Genomics and Beyond: Medicinal

Plants & Pepper

Parallel Session X. SOL Genomics and Beyond: Potato &

Egaplant

Parallel Session X. SOL Genomics and Beyond: Tobacco &

Coffee

### **Keynote Speakers**

**Jiayang Li** (Institute of Genetics and Developmental Biology, CAS)

Topic: TBA

Dani Zamir (Hebrew University of Jerusalem, Israel)

Topic: Yield Canalization in Crop Plants

Harry Klee (University of Florida, USA)

**Topic:** The Chemistry and Genetics of Good Tomato

Flavor

#### **Confirmed Speakers**

**Alan Andrade** (Embrapa Recursos Genéticos e Biotecnologia, Brazil)

**Yuling Bai** (Wageningen University, The Netherlands) **Christian Bachem** (Wageningen University, The Netherlands)

**Ian T. Baldwin** (Max Planck Institute for Chemical Ecology, Germany)

Gerard Bishop (East Malling Research, UK)

**Mondher Bouzayen** (Institut National de la Recherche Agronomique, INRA, France)

**Glenn Bryan** (James Hutton Institute, Invergowrie, UK) **Mathilde Causse** (Institut National de la Recherche Agronomique, INRA, France)

**Doil Choi** (Seoul National University, Republic of Korea) **Yuval Eshed** (Weizmann Institue of Science, Israel)

**Aaron Fait** (Ben-Gurion University of the Negev, Israel) **Zhangjun Fei** (Boyce Thompson Institute for Plant Research, USA)

Jim Giovanoni (Cornell University, USA)

**Giovanni Giuliano** (ENEA, Italian National Agency for New technologies, Energy and Sustainable Development, Italy)

**Antonio Granell** (Instituto de Biología Molecular y Celular de Plantas, Spain)

**Joseph Hirschberg** (Hebrew University. of Jerusalem, Israel)

Jim Giovannoni (Cornell University, USA)

**Topic:** Genetic and Epigenitic Regulation of Tomato Fruit Ripening

**Yongbiao Xue** (Institute of Genetics and Developmental Biology, CAS)

Topic: TBA

Klaus Palme (Freiburg University, Germany)

Topic: Plant Growth and Yield Control by Hormones

**Sanwen Huang** (The Institute of Vegetables and Flowers, CAAS, China)

**Jeanne Jacobs** (The New Zealand Institute for Crop & Food Research, New Zealand)

**Byung-Dong Kim** (Seoul National University, Republic of Korea)

Harry Klee (University of Florida, USA)

Robert Last (Michigan State University, USA)

**Chuanyou Li** (Institute of Genetics and Developmental Biology, CAS, China)

**Jiayang Li** (Institute of Genetics and Developmental Biology, CAS, China)

Mary Beth Mudgett (Stanford University, USA) Lukas Mueller (Boyce Thompson Institute for Plant Research, USA)

**Klaus Palme** (Freiburg University, Germany)

**Graham Seymour** (The University of Nottingham, UK) **Yuhe Sun** (Tobacco Research Institute, CAAS, China)

Ying Wang (Wuhan Botanical Garden, CAS, China)

Esther van der Knaap (Ohio State University, USA)

**Yunbi Xu** (Institute of Crop Sciences/International

Maize and Wheat Improvement Center, CAAS, China)

Yongbiao Xue (Institute of Genetics and

Developmental Biology, CAS, China)

**Zhibiao Ye** (Huazhong Agricultral University, China)

Dani Zamir (Hebrew University of Jerusalem, Israel)

# Highlight Article

# Improving Potato Production for Increased Food Security of Indigenous Communities in Colombia

Teresa Mosquera<sup>1</sup>, Ajjamada Kushalappa<sup>2</sup>, Merideth Bonierbale<sup>4</sup>, David Cuéllar<sup>1</sup>, Sara Del Castillo<sup>1</sup>, David DeKoeyer<sup>3</sup>, Cecilia Delgado<sup>1</sup>, Diana Duarte<sup>1</sup>, Alejandra Guateque<sup>1</sup>, Patricia Heredia<sup>1</sup>, Deissy Juyó<sup>1</sup>, Stan Kubow<sup>2</sup>, Sonia Navia<sup>4</sup>, Philip Oxhorn<sup>2</sup>, Leonor Perilla<sup>1</sup>, Clara Piñeros<sup>1</sup>, Patricia Restrepo<sup>1</sup>, Clara Bianeth<sup>1</sup>, Ernesto Rodríguez<sup>1</sup>, Felipe Sarmiento<sup>1</sup>, Helen Tai<sup>3</sup>, Sonia Tinjaca<sup>1</sup>, Diana Vargas<sup>1</sup>, Thomas Zum Felde<sup>4</sup>

<sup>1</sup>Universidad Nacional de Colombia Carrera. 30 40-05. Bogotá, Colombia; <sup>2</sup>McGill University, Montreal, Canada; <sup>3</sup>University of New *Brunswick,* Fredericton, Canada; <sup>4</sup>International Potato Center, CIP, Lima-Perú; <sup>5</sup>Fundelsurco, San Juan de Pasto, Colombia

McGill University and Universidad Nacional de Colombia are leading a comprehensive project involving seven components: potato breeding, genomics and metabolomics, nutritional potato quality, food security and nutrition, family roles and gender studies, agricultural education through participative research in Field Farmers' Schools (ECAs) and involving policy makers. The project seeks to impact on food security and nutrition (FSN) by selecting potato cultivars with high yield and better nutritional qualities. The indigenous population of Nariño province in

Colombia is the second highest undernourished people in Colombia. The indigenous communities' food security status will be assessed and the communities will be educated on improved potato production practices and daily diet.

In the short term, we are characterizing the daily diet of the population to determine nutritional deficiencies, analyzing the nutritional qualities of potato cultivars and selecting the best cultivars through participative research. Along with these processes we are studying and empowering women as nutritional decision makers within the family to facilitate recovering of good ancestral nutritional habits (Fig. 1) and for women to become valid interlocutors with governmental agencies. We are also developing participatory research on Good Agricultural Practices (GAP) to enhance sustainability of potato crops.

In the long term, we are getting basic nutritional information to incorporate criteria for breeding potato genotypes with higher nutritional quality and high late blight resistance to mitigate potential risks of climate change. We are also increasing the autonomy of communities to face change.

An in-depth study is being conducted on dietary intake and household consumption pattern, adapting to local conditions the 24-hour Dietary Recall method (Fig. 2). Formative modules have been designed and implemented. We have advanced in the design of the methodological guide for the development of dialogue

Figure 1. Women from Carlosama community preparing

Carlosama community preparing locro, soup based on peeled potatoes and vegetables. Photo: FSN team

**Figure 2.** Using neutral modules simulators food portions in 24-hour Dietary Recall methodology. Photo: FSN team

encounters for the recovery of the nourishing memory, habits of the population and recommendations of good nourishing practices.

We have obtained the following plant material: phureja genotypes from the Colombian Core Collection, commercial phureja genotypes and advanced breeding clones. Potato genotypes sown in two localities have been harvested, cooked and being analyzed for nutritional composition based on UHPLC (Dionex 3600). The methodology to identify and quantify various nutritional components has been standardized (Fig. 3). We also have validated methodologies for the determination of moisture, ash, fat, protein, dietary fiber, starch, sugars and phenolic compounds.

The trials to register new cultivars are being carried out. Eight advanced clones and two commercial controls in eight localities in the department of Nariño are being evaluated under the supervision of Colombian Agrarian Institute (ICA). Selection with community participation takes into account: yield, color and tuber shape (Fig. 4). These results contribute to the selection of the optimal clones for cultivation and consumption in indigenous communities in the department of Nariño.

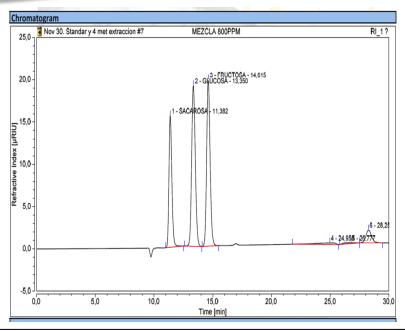


Figure 3. Separation and identification of sugars in potato by UHPLC. Photo: Nutritional quality team

Along with potato trials, nine ECAs were established to support the indigenous participation in breeding research and to adopt GAP. Smallholders registered in the ECAs answered a baseline survey.

An advanced training program was agreed with ECAs' participants. Technological needs were identified for designing training programs trough the baseline survey. The educational program includes: training workshops; workshops following breeding trials; organized purchase of inputs; practical training for GAP with participatory approach; knowledge exchange tours and field days.

To build bases for strengthening the breeding program with nutritional criteria and to anticipate climate change a collection of native materials has been executed, acquiring more than 170 native potato genotypes (Fig. 5) and we are identifying potato genotypes with broad genetic resistance to late blight based on metabolomic and genomic technologies.



**Figure 4.** Harvesting breeding potato trials with community participation. Photo: Potato breeding team



**Figure 5.** Female custodian of potato seeds harvesting native potatoes. Photo: Potato breeding team

In order to identify potato clones with broad genetic resistance based on metabolomic and genomic technologies pilot tests were made for metabolomics analysis. The methodology for the inoculation of diploid genotypes under controlled conditions was standardized (Fig. 6). Putative late blight resistance genes have been identified based on metabolomics. This is a breakthrough technology that shows promising results towards improving late blight resistance of potato genotypes through cisgenics technology. Association mapping is in progress and we have determined population structure for *S. phureja* and characterized the population for late blight resistance. Thirty-six novel candidate genes were validated for *S. phureja* in collaboration with Christiane Gebhardt in the Max Planck Institute for plant breeding.

All activities are being carried out following wide advocacy strategies for the incorporation of the results of the project to public policies in Colombia.

This project is undertaken with the financial support of the International

Development Research Centre (IDRC: http://www.idrc.ca), and the Canadian International Development Agency
(CIDA: http://www.acdi-cida.gc.ca). This project has genetic resources access from the Colombian government under contract No. RGE0069 of Ministerio de Ambiente y Desarrollo Sostenible.



Figure 6. Phytophthora infestans lesion in stem 72 hours after inoculation. Photo: metabolomic and genomic team

Resources



# Save Time and Increase Quality of Data by using RFID

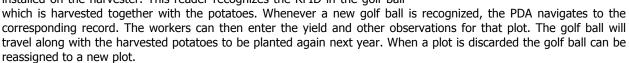
By Evert Keuken

Separating between plots in potato field trials can be a nuisance. Many breeders work with sticks that hold a label, with plot information and possibly a barcode. Problem is, these labels are not durable and information needs to be transferred from the crate to the field. This process is time consuming and prone to errors.

One of our customers of the E-Brida breeding software (more info: e-brida.com) came up with an innovative solution. They have injected RFID tags<sup>1</sup> in golf balls. Every golf ball has its own unique RFID tag which corresponds with a number. Now, they place a golf ball in every crate. Each crate corresponds with one plot (usually one genotype) in the field trial. A PDA with RFID scanner is used to connect the golf ball to the right crate.

Once this is done, the golf ball is planted in the field as the first "tuber" of the plot. When observations need to be taken, a reading stick (also used in livestock breeding) is used to read the RFID tags. The PDA then navigates to the corresponding plot in the observation form and you can enter observations. The observation data is automatically synchronized with the breeding software E-Brida.

The last step in this process is harvesting the trial. A RFID reader is installed on the harvester. This reader recognizes the RFID in the golf ball



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Agri Information Partners provides IT solutions for plant breeding and research companies.

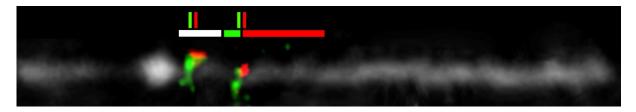
<sup>&</sup>lt;sup>1</sup> Radio Frequency Identification. These are actually small antennas that, when approached with the proper device, send out a unique code that identifies the tag. RFID tags are most commonly known as the tags used in stores to prevent customers from stealing products.

# Research Updates

# **Update from Steve Stack's Lab at Colorado State University**

## Lindsay Shearer

Since the last edition of the SOL Newsletter, 119 new BACs have been added to the tomato FISH map by the Stack lab at Colorado State University, bringing the total to 618 BACs. A majority of the new BACs are on the borders of sequenced scaffolds on chromosomes 6, 9 and 12. The gap distance between scaffolds has been estimated for each of these chromosomes. In addition, many of the new BACs are Chromosome 0 BACs, which are BACs that cannot be associated with the sequence on any existing scaffolds. By FISH, we have observed that these Chromosome 0 BACs are usually in gaps between scaffolds. The 618 localized BACs are distributed at 630 loci among the chromosomes as follows: 1 - 116; 2 - 64; 3 - 63; 4 - 40; 5 - 28; 6 - 50; 7 - 51; 8 - 32; 9 - 45; 10 - 55, 11 - 36, 12 - 50. The total number of loci reflects the fact that there are now twelve BACs that have each been localized to two positions.



The figure illustrates a small duplication on the long arm of chromosome 6 on a reverse phase contrast image of the synaptonemal complex (SC). The large white spot is the centromere. Three scaffolds are represented above the SC: SL2.40sc04279 (white), SL2.40sc05188 (green), and SL2.40sc05732 (red). The two BAC probes are SL\_MboI0034N10 (red) at the end of scaffold SL2.40sc05732 and LE\_HBa0031J01 (green) at the end of scaffold SL2.40sc05188. Each BAC shows a second signal in the heterochromatic interior of scaffold SL2.40sc04279, indicating an area of duplication.

# Publications

Chalivendra SC, Lopez-Casado G, Kumar A, Kassenbrock AR, Royer S, Covey PA, Dempsey L, Stack SM, Rose JKC, McClure B, Bedinger PA (2013) Developmental onset of reproductive barriers and associated proteome changes in stigma/styles of *Solanum pennellii*. J Exp Bot 64:265-79 (front cover).

Chambonnet D (2012) In situ induction of haploid gynogenesis in tomato. Report of the Tomato Genetics Cooperative 62:5-22. Note: within the coming year, online access to this paper is possible only for people subscribing to TGC. In one year time, TGC 62 will be of free access (as for all issues of TGC).

Chevalier E, Loubert-Hudon A, Matton DP (2013) ScRALF3, a secreted RALF-like peptide involved in cell-cell communication between the sporophyte and the female gametophyte in a solanaceous species. Plant J 73:1019-1033.

Guyot R, Lefebvre-Pautigny F, Tranchant-Dubreuil C, Rigoreau M, Hamon P, Leroy T, Hamon S, Poncet V, Crouzillat D, de Kochko A (2012) Ancestral synteny shared between distantly-related plant species from the asterid (*Coffea canephora* and Solanum Sp.) and rosid (*Vitis vinifera*) clades. BMC Genomics 13:103.

Joshi RS, Mishra M, Tamhane VA, Ghosh A, Sonawane U, Josh R, Gupta VS, Giri AP (2013) The remarkable efficiency of a Pin-II proteinase inhibitor sans two conserved disulfide bonds is due to enhanced flexibility and hydrogen-bond density in the reactive site loop. J Biomol Struct Dynam (In Press).

Mishra M, Joshi RS, Gaikwad SM, Gupta VS, Giri AP (2013) Structural-functional insights of single and multi-domain *Capsicum annuum* protease inhibitors. Biochem Biophy Res Co 430:1060-1065.

Mishra M, Mahajan N, Tamhane VA, Kulkarni MJ, Baldwin IT, Gupta VS, Giri AP (2012) Stress induced proteinase inhibitor diversity in *Capsicum annuum*. BMC Plant Biology 12:217.

Mohanan S, Gowda K, Kandukuri SV, Chandrashekar A (2013) Involvement of a novel intronic microRNA in cross regulation of *N*-methyltransferase genes involved in caffeine biosynthesis in *Coffea canephora*. Gene 519:107-112.

Munger A, Coenen K, Cantin L, Goulet C, Vaillancourt L-P, Goulet M-C, Tweddell R, Sainsbury F, Michaud D (2012) Beneficial 'unintended effects' of a cereal cystatin in transgenic lines of potato, *Solanum tuberosum*. BMC Plant Biology 12:198.

Naz AA, Raman S, Martinez CC, Sinha NR, Schmitz G, Theres K (2013) Trifoliate encodes an MYB transcription factor that modulates leaf and shoot architecture in tomato. PNAS 110:2401-2406.

Sun P, Kao T (2013) Self-incompatibility in *Petunia inflata*: The Relationship between a self-incompatibility locus F-box protein and its non-self S-RNases. Plant Cell 25: 470–485.

Rai GK, Rai NP, Kumar S, Yadav A, Rathaur S, Singh M (2012) Effects of explant age, germination medium, preculture parameters, inoculation medium, pH, washing medium, and selection regime on *Agrobacterium*-mediated transformation of tomato. In Vitro Cell Dev Biol-Plant 48:565-578.

Shi JX, Adato A, Alka N, He Y, Lashbrooke J, Matas AJ, Meir S, Malitsky S, Isaacson T, Prusky D, Leshkowitz D, Schreiber L, Granell AR, Widemann E, Grausem B, Pinot F, Rose JKC, Rogachev I, Rothan C, Aharoni A (2012) The tomato SISHINE3 transcription factor regulates fruit cuticle formation and epidermal patterning. New Phytol 197: 468-480.

# Conferences

# European Association for Potato Research and Eucarpia Potato Congress

June 30 – July 4, 2013 Hévíz, Hungary http://www.hutton.ac.uk/eapr-eucarpia2013

# The Potato Association of America

July 21 – August 8, 2013 Quebec City, Quebec, Canada http://www.paa2013.com/

# 9th Annual Canadian Plant Genomics Workshop

August 12 - 15, 2013 Halifax, Nova Scotia http://cpgw2013.org/

# **EUCARPIA: Capsicum and Eggplant Working Group Meeting**

September 2 - 4, 2013 Turin, Italy http://e20.unito.it/XVth\_EUCARPIA/

## **Current Opinion Conference: Plant Genome Evolution**

September 8 - 10, 2013
Amsterdam, The Netherlands
http://www.plantgenomeevolution.com/

## **SOL 2013**

October 13 - 17, 2013 Beijing, China http://www.sol2013.org/

# Solanaceae Recipes

# **JUANESCA**

# Provided by Theresa Mosquera

Juanesca is an ancestral soup from native communities in Southern Colombia (Nariño). Juanesca is a special dish to be served in Holy Week and shared with a large family.

This recipe is a part of the study for recovering the ancestral culinary memory in the framework of the project, *Improving Potato Production for Increased Food Security of Indigenous Communities in Colombia,* led by the Universidad Nacional de Colombia and McGill University and funded by IDRC and CIDA from Canada.

25 servings

Time of preparation: 2 hours

### **Ingredients**

Toasted peanut ½ pound
Lima beans (*Vicia faba*) ½ pound
Corn cob (*choclo*) 5 pounds
Green pea (shelled) ½ pound
Green beans (shelled) ½ pound
Yellow potato (*S. phureja*) 3 pounds
Common potato (*S. tuberosum* subsp. *andigena*) 5 pounds
Pumpkin (bare, without seeds) 5 pounds
Onion 4 stems ¼ pound
Cabbage ½ pound
Ollocos (Ollucus tuberosus) ½ pound
Vegetable oil 2 spoonfuls
Coriander
Salt



#### **Directions**

- Wash all the ingredients.
- Peel and shell lima beans and corn cobs.
- Peel and cut in small cubes yellow potatoes, common potatoes, pumpkin and onion stems.
- Chop the *ollocos* in small pieces or in strips.
- Wash and break off by hand the cabbage leaves.
- Mill the toasted peanut until it becomes a smooth mass.
- Boil water in a pot. Fill the pot with capacity for 25 servings, up to the half.
- When the water boils for the first time add the green beans, the corn cob, half of the onion stems, vegetable oil, the *ollocos* and salt.
- After the water boils for the second time, add the peas and the yellow potato.
- After the second boiling add the pumpkin, the cabbage, the lima beans and the common potato.
- Remove from the fire and add the peanut milled and toasted.
- Let cool and add a mixture of onion stems and fresh coriander.

Nutrition per serving: 356 calories; 6.1 g fat; 63.4 g carbohydrates; 11.8 g protein.