# 13th Annual Solanaceae Conference

*SolGenomics: From Advances to Applications*

# CONFERENCE PROGRAM

## September 12 — 16, 2016

Davis, California USA

UCDAVIS

www.SolGenomics2016.ucdavis.edu

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## General Conference Information

- Conference Center building will open daily at 7:30 am.
- Conference Center restrooms are located adjacent to the registration desk; Additional restrooms are available on the second floor.
- Meal and drink tickets are placed in the plastic sleeve of the name badges.
- Drink tickets are needed for beer and wine at all evening social events. Non-alcoholic drinks and water available at no cost. Additional beer and wine drinks may be purchased (cash only, USD).
- All conference abstracts available at SolGenomics2016.ucdavis.edu/program
- Platinum and Gold level sponsor representatives are encouraged to be present at their company hosted lunch tables.
- Emergency help is available by dialing 911 from a land line or (530) 752-1230 from a mobile phone. Do not dial 911 from a mobile phone. For additional campus emergency and safety information, visit www.ucdavis.edu/emergency/. For status or information during an emergency, call the campus Emergency Status Line at (530) 752-4000.
- In case of emergency, conference attendees should gather on VanderHoef Quad.

### Conference Policies

- Name badges should be worn at all Conference functions.
- For all evening social events, guests may not leave event area with alcohol in hand.
- Lunch, reception and banquet tickets must be turned in at each meal.
- Cell phones should be turned off during all scientific sessions.
- Photos are discouraged during talks.
- Photos of posters may be taken only with presenter's permission.

# SESSION CHAIRPERSONS

### Session I • DIVERSITY-TAXONOMY/CROP GERMPLASM DIVERSITY

Ellen Dean, UC Davis • Irma Ortiz, UC Riverside

### Session II • BARRIERS TO BREEDING

Roger Chetelat, UC Davis • Benny Julissa Ordonez Aquinno, UC Davis

### Session III • GENOMES & GENOME TECHNOLOGIES

Massimo Delledonne, Univ. of Verona • Arsenio Ndeve, UC Riverside

### Session IV • HIGH-THROUGHPUT PHENOTYPING

Allen Van Deynze, UC Davis • Lav Yadav, West Virginia State Univ.

### Session V • GENE-EDITING AND NEW BREEDING TECHNOLOGIES

Anne Britt, UC Davis • Julie Pedraza, California State Univ., Fresno

### Session VI • EPIGENOMICS AND METHYLATION

Luca Comai, UC Davis • Brittany Davenport, West Virginia State Univ.

### Session VII • GENOMICS-ASSISTED BREEDING

Jeanne Jacobs, Plant & Food Res NZ • Kieu Nga Tran, Louisiana State Univ.

### Session VIII • SYSTEMS BIOLOGY AND NETWORKS

Siobhan Brady, UC Davis • Sophia Jinata, UC Davis

### Session IX • ABIOTIC STRESSES

Julin Maloof, UC Davis • Lumariz Hernandez-Rosario, Univ. of Puerto Rico

### Session X • RESISTANCE, PATHOGENS, PESTS AND MICROBIOMES

Gitta Coaker, UC Davis • Kevin Babilonia, Texas A&M

### Session XI • TUBERS AND ROOT SYSTEMS

Glenn Bryan, The James Hutton Institute • Justin Medina, Cal Poly Pomona

### Session XII • FLOWERS, SEEDS AND FRUIT

James Giovannoni, USDA/BTI/Cornell • Kimberly Rodriguez, New Mexico State Univ.

### Session XIII • PLANT DEVELOPMENT AND REGULATION

Neelima Sinha, UC Davis • Timothy Batz, Calif. State Polytechnic Univ., Pomona

### Session XIV • METABOLITES, FLAVOR AND QUALITY

Cathie Martin, John Innes Centre • Sassoum Lo, UC Riverside

Haploid induction can be used to rapidly introduce novel genetic combinations into crop varieties. We have previously demonstrated that haploid induction via uniparental genome elimination in *Arabidopsis* is able to create a range of novel karyotypes such as truncations, deletions, rearrangements, or minichromosomes derived from the haploid inducer genome. In the potato haploid induction system, residual fragments of *Solanum tuberosum* Group Phureja haploid inducer genome have been reported in haploid progeny, but these introgression events have not been characterized with genome sequencing approaches. Therefore, we plan to explore the extent of dosage variation produced by potato haploid induction crosses using whole-genome sequencing. We will test the hypothesis that some of the haploid progeny from the haploid inducing cross in potato will exhibit novel genome dosage variation, or may contain DNA fragments from the haploid inducer genome. Here, we report a pilot-scale chromosome dosage analysis of F1 haploids (n=6) produced from a *S. tuberosum* Group Andigena × *S. tuberosum* Group Phureja haploid induction cross. We found that one of the six analyzed lines exhibited a truncated chromosome 4, which suggests that chromosome remodeling can occur during *in vivo* haploid induction in potato. In order to characterize a broader range of chromosome dosage variation, including potential introgressions from the Phureja haploid inducer, we plan to generate and sequence 400 additional putative haploid lines.

### 308-TH. GENOME WIDE ASSOCIATION STUDIES CORRECTING POPULATION STRATIFICATION IN PEPPER CORE COLLECTION

Lee H-Y.[1], Han K.[1], Hur O-S.[2], Go H-C.[2], **Kwon J-K.**[1], Sung J-S.[2], Kang B-C.[1]
*[1]Department of Plant Science and Vegetable Breeding Research Center CALS, Seoul National University, Seoul 151-921, Korea; [2]National Academy of Agricultural Science, Rural Development Administration, Jeonju 560-500, Korea*
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Genome-wide association study (GWAS) is an effective approach for identifying genetic variants associated to useful agronomic traits. GWAS has emerged as a powerful approach for identifying genes underlying complex diseases or morphological traits at an unprecedented rate. In such studies, it is very important to correct for population stratification, which refers to allele frequency differences between cases and controls due to systematic ancestry differences. Population stratification can cause false positive findings if not adjusted properly. As we are performing GWAS for various agronomic traits in pepper, a genotyping-by-sequencing (GBS) approach was used to provide dense genome-wide marker coverage (>33,000 SNPs) for a 250 pepper core collection. Using GBS platform, a high density haplotype map was constructed and various stratification methods, including distance based phylogenetic methods, principal component analysis (PCA), and bayesian phylogenetic methods (STRUCTURE) were performed to show the genetic diversity and population stratification. MLM using Q values combined with kinship matrix estimated from stratification methods were used to identify quantitative trait loci controlling the variation of ten agronomic traits. These results will help to understand associations between phenotype and genotype and also will be used for validation of the candidate genes or quantitative trait loci previously identified in pepper.

### 309-TH. IDENTIFYING NOVEL SMALL PEPTIDES IN TOMATO USING RIBOSOME PROFILING

**Hsu P.Y.**[1], Calviello L.[2], Wu H.L.[3], Li F.W.[1,4], Rothfels C.[4], Ohler U.[2], Benfey P.N.[1,5]
*[1]Duke University, Durham, NC, USA; [2]Max Delbrück Center, Berlin, Germany; [3]North Carolina State University, Raleigh, NC, USA; [4]University of California, Berkeley, Berkeley, CA, USA; [5]Howard Hughes Medical Institute, Durham, NC, USA*
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Small peptides play important roles in short and long distance signaling in plants. They regulate plant growth and development, interactions between plants and the environment, as well as interactions

# Genome wide association studies correcting population stratification in pepper core collection

**Hea-Young Lee[1], Koeun Han[1], On-Sook Hur[2], Ho-Cheol Go[2], Jin-Kyung Kwon[1], Jung-Sook Sung[2] and Byoung-Cheorl Kang[1]***

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## ABSTRACT

Genome-wide association study (GWAS) is an effective approach for identifying genetic variants associated to useful agronomic traits. GWAS has emerged as a powerful approach for identifying genes underlying complex diseases or morphological traits at an unprecedented rate. In such studies, it is very important to correct for population stratification, which refers to allele frequency differences between cases and controls due to systematic ancestry differences. Population stratification can cause false positive findings if not adjusted properly. As we are performing GWAS for various agronomic traits in pepper, a genotyping-by-sequencing (GBS) approach was used to provide dense genome-wide marker coverage (>33,000 SNPs) for a 250 pepper core collection. Using GBS platform, high density haplotype map was constructed and various stratification methods, including distance based phylogenetic methods, principal component analysis (PCA), and bayesian phylogenetic methods (STRUCTURE) were performed to show the genetic diversity and population stratification. As a result, MLM using Q values combined with k-medoids clustering estimated from stratification methods were used to identify quantitative trait loci controlling the variation of ten agronomic traits. These results will help to understand associations between phenotype and genotype and also use for validate the candidate genes or quantitative trait loci previously identified in pepper.

## OBJECTIVES

- **Detection of genome-wide SNPs among pepper GWAS population using genotyping-by-sequencing (GBS) approach**
- **Construction of high density haplotype map**
- **Population structure analysis using various stratification methods**
- **Detection of candidate QTLs associated with interested phenotypes**

## MATERIALS & METHODS

### Plant material

A pepper GWAS population including 9 species, consisting of 351 accessions was constructed by combining three different collections. *Capsicum* species included in this population are shown in figure 1.

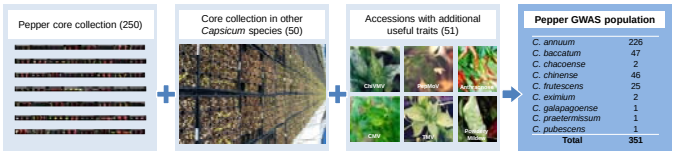


**Figure 1. Pepper GWAS population using in this study.** A total of 351 accessions were placed in this population constructed by combining three different pepper collections.

### Genotyping-by-sequencing (GBS)

DNA of germplasm was extracted by CTAB method. Two restriction enzymes (*PstI*-*MseI*), and a compatible set of 96 barcode were used to prepare the GBS library. Single end sequencing was performed on four lanes of an Illumina HiSeq 2000 at the Macrogen Inc (Seoul, Korea).

### SNP observation and haplotype map construction

The CLC Genomics Workbench was used to check sequencing quality (QC) and trim the sequence reads. Two software tools, BWA and GATK were used for the processing of Illumina sequence read trimmed data. Haplotype map was constructed using FILLIN in TASSEL 5 (Figure 2).

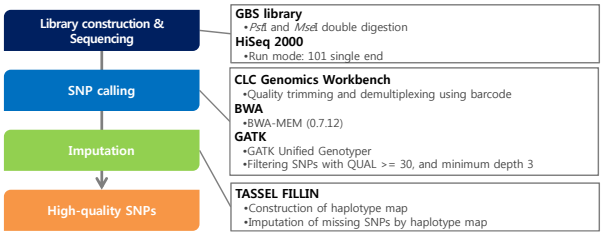


**Figure 2. Workflow of SNP calling and haplotype map construction.**

### Population structure and genetic diversity analysis

To better understand the genetic diversity of germplasm, phylogenetic analysis and PCA were performed by DARwin 6.0.9 (Perrier and Jacquemoud-Collet, 2006). Population structure was identified using STRUCUTRE 2.3.4 software.

## REFERENCE

1. Elshire RJ, Glaubitz JC, Sun Q, Poland JA, Kawamoto K, Buckler ES, et al. A robust, simple genotyping-by-sequencing (GBS) approach for high diversity species. PLoS One. 2011;6(5):1–10.
2. Liu L, Zhang D, Liu H, Arendt C. Robust methods for population stratification in genome wide association studies. BMC Bioinformatics. 2013;14(1):132.
3. Pritchard JK, Stephens M, Donnelly P. Inference of population structure using multilocus genotype data. Genetics. 2000;155(2):945–59.
4. Han K, Jeong H-J, Yang H-B, Kang S-M, Kwon J-K, Kim S, et al. An ultra-high-density bin map facilitates high-throughput QTL mapping of horticultural traits in pepper (Capsicum annuum). DNA Res. 2016;23(2):81–91.

## ACKNOWLEDGEMENT

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## RESULTS

### SNP observation in high density haplotype map

Overall 3,000,000 SNPs were detected among pepper 351 Capsicum GWAS population using PstI-MseI double digest enzyme set (average SNP depth: 86). SNPs with > 50% missing data and monomorphic SNPs were dropped from the data set. After strong SNP filtering, 33,843 SNPs were remained with call rates > 0.5 (Figure 3).

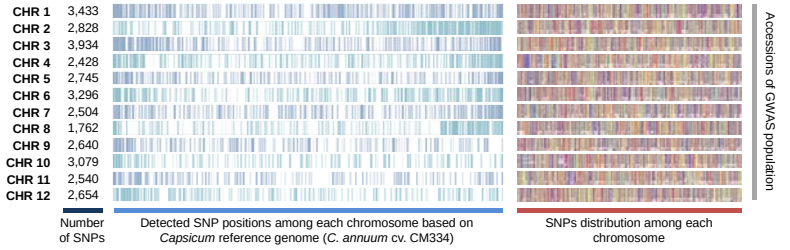


**Figure 3. SNP distribution among 12 pepper chromosomes.** Over 33,843 SNPs were used for construct the high density haplotype map.

### Genomic structure of pepper GWAS population

Based on the Bayesian phylogenetic methods, whole population showed two subpopulations as *C. annuum* and the other species. The first subpopulation which contains the other species was also divided in two subgroups as *C. baccatum* and the other species. The second subpopulation which contains all the *C. annuum* was tend to separate by fruit shape as hot pepper type and bell pepper type (Figure 4).

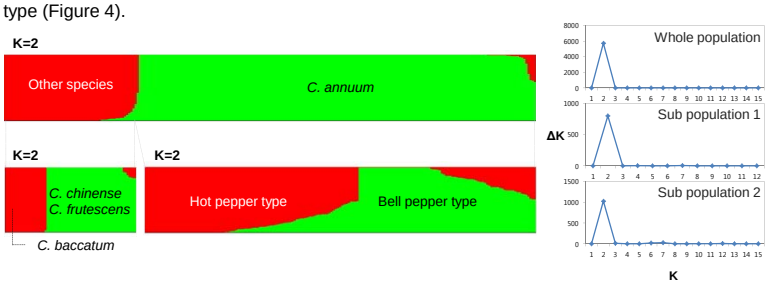


**Figure 4. Population structure of the *Capsicum* core collection (CC250) using GBS data.** ΔK reached its maximum value when K=2 following the *ed-hoc* method. Subpopulations were grouping by Q. Each subpopulation was separated in to two subgroups.

### GWAS on Capsicum GWAS population of various interested agronomic traits

Using MLM (K+Q), a total of 56 candidate QTLs associated with 12 various agronomic traits was detected among 12 Capsicum chromosome.

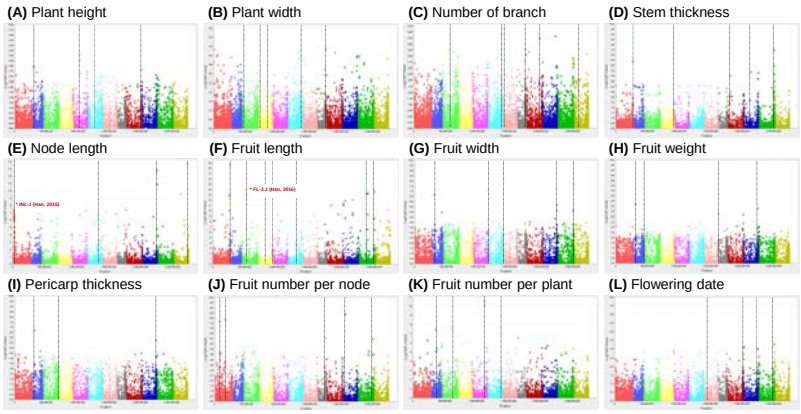


**Figure 5. Manhattan plots of association p-values over the 12 pepper chromosome.** MLM (K+Q) model was used to screen for association between genotype and (A) Plant height, (B) Plant width, (C) Number of branch, (D) Stem thickness, (E) Node length, (F) Fruit length, (G) Fruit width, (H) Fruit weight, (I) Pericarp thickness, (J) Fruit number per node, (K) Fruit number per plant, and (L) Flowering date.