

SESSION I • DIVERSITY-TAXONOMY/CROP GERMPLASM DIVERSITY

CHAIRPERSON: ELLEN DEAN (UC DAVIS, USA)

CO-CHAIRPERSON: IRMA ORTIZ (UC RIVERSIDE, USA)

My graduate research is not related to diversity-taxonomy, and I appreciate the opportunity to have co-chaired this session. I learned a wide array of topics discussed in the first session of the Solanaceae conference at UC Davis. The big picture from this session is that there is vast diversification in Solanaceae.

The plenary speaker for the session, Dr. Sandra Knapp, from the British Museum, spoke about diversification in the Solanaceae and then focused on the genus *Solanum*. Evidence indicates that the most ancient members of the Solanaceae evolved in South America and dispersed outward from there. Dating of the branches on phylogenetic trees indicates that the family is too young to have been part of Gondwana. Analyses indicate that there may have been as many as 17 dispersal events out of South America, first to Africa and then onwards to Asia and the Pacific. Many of those dispersal events date to about 5-6 million years ago. More recently, humans have been very active in taking Solanaceae plants from the New World to the Old World and vice versa either on purpose or by accident. The Solanaceae consists of approximately 3000 species and half of these are in the genus *Solanum*. There is a misconception that the region of the world that has the greatest number of *Solanum* species (South America) has the highest rates of species diversification. Phylogenetic studies that estimate diversification rates indicate that the rate is highest in arid zones of Australia and Africa. Dr. Knapp discussed why this might be so – could it be due to pre-adaptation? She thinks that Solanaceae plants with the right traits happened to be in the right place at the right time with the right traits. According to Sandy, species are a hypothesis of variation observed at a specific time point.

Elizabeth McCarthy zoomed in to study diversification in *Nicotiana*. Dr. McCarthy's studies focus on the effects of allopolyploidy on floral evolution using *Nicotiana* as a model genus. Allopolyploids often have novel floral phenotypes that differ from either parent species. She works with *Nicotiana tabacum*, which is an allopolyploid derived from *N. sylvestris* and *N. tomentosa*. She showed photos of the floral pigments that we see with the human eye as well as the patterns seen by the pollinators. She showed the floral diversity among two accessions of *N. tabacum* that display different floral colors (magenta and pink) using pigment profiles and transcriptome data. Although the transcriptome data does not correlate with pigment changes, further transcriptome analyses will be done in the near future to understand the differences in the floral evolution in diploids and polyploids.

Gloria Barboza, and Carolina Carrizo focused on the the genus, *Capsicum*. Dr. Barboza first gave us an overview of the morphological variation within the genus including the calyx, corolla, fruits, and seeds. Drs. Barboza and Carrizo have done a phylogenetic reconstruction of 34 *Capsicum* taxa (49 accessions) collected from Mexico to Argentina. At least 35 species are distinguished today in the genus but the number may increase as they continue their studies.

Toni Granell's work analyzes the variability of fruit quality in the European tomato. The tomato was introduced to Europe during the colonization of America. As a result, a number of tomato varieties have been developed by European farmers. Dr. Granell studies the tomato phenotypic and genotypic variability in European farms and public repositories. He has studied 137 quantitative and qualitative traits in approximately 1500 tomato varieties. The variability in ripening behavior is observed by measuring parameters such as firmness, which is important to the plant's ability to grow and set fruit under limited water. His research has a project website that is publicly available at TRADITOM.EU.

Overall, the first session showed diversity and taxonomy research conducted in the American and European continents. The four research groups study the diversity in Solanaceae

from a biogeographical to a genomic scale. It was a pleasure to have co-chaired the first session of the 13th Solanaceae conference in UC Davis!

SESSION II • BARRIERS TO BREEDING

CHAIRPERSON: ROGER CHETELAT (UC DAVIS, USA)

CO-CHAIRPERSON: BENNY ORDONEZ (UC DAVIS, USA)

Elucidating mechanisms and dynamics of reproductive isolation in wild tomato species

by Pat Bedinger

Tomato is an ideal model for the study of Interspecific Reproductive Barriers (IRBs), due to a variety of barriers between cultivated tomato and its relatives. Unilateral incompatibility (UI) is a prezygotic barrier in which pollinations are incompatible in one direction: Self-incompatible (SI) plants reject pollen from Self-compatible (SC) ones, but the reciprocal cross is compatible. This suggests that SI factors occur in this type of UI. In the Solanaceae clade, SI depends on the interaction of S-locus pistil-expressed S-RNases and pollen-expressed S-locus F-box (SLF), as well as non-S-locus factors, such as pistil HT proteins. However, in tomato, pollen from the SC red-fruited species is also rejected by SC accessions of green-fruited species that lack S-RNase, a key protein expressed in pistils of SI *Solanum* species. The introduction of both S-RNase and HT genes into cultivated tomato is sufficient to establish a UI barrier to pollen of the red-fruited species.

A further exploration of mating systems transitions in *S. habrochaites* was analyzed using accessions from Peru and Ecuador. In the north, IRBs are weakened, and in some cases are lost altogether, due to accumulation of mutations in pistil and/or pollen SI factors. There was a loss of SI due to at least two independent events causing loss of S-RNase expression. In the south, an S-RNase allele encoding a low-activity protein is associated with the loss of SI and pistil IRBs seem to be unaffected. Moreover, they found prezygotic IRBs including pollen tube rejection, conspecific pollen precedence, and lack of ovule targeting. Also, postzygotic IRBs causing defective seed development were discovered in sympatric populations. The results have implications for mating system transitions. It's suggested that these transitions must occur in a specific sequence, and that the transition from SI to SC also affects interspecific compatibility.

Wild tomato: Populations structure and evidence of Natural *S. chilense* x *S. Peruvian* hybrid populations

by Ian Beddows

The aim of the research was to understand the ancestry of two widespread allogamous, self-incompatible (SI) sister species, *S. chilense* and *S. peruvianum*. An individual RNA sequencing on 36 individuals was performed from different populations of the species mentioned above. After the analysis of the population structure in both species using transcriptome data and test cross data, it was discovered that the northernmost populations of *S. chilense* (collected near Rio Acari in Peru) are in fact

S. chilense × *S. peruvianum* interspecific hybrids with transgressive phenotypes in several traits. The hybrid populations are stable through time and may therefore be an example of homoploid hybrid speciation. These populations present a new opportunity to study hybrid zones and crossing barriers.

The gamete eliminator as a mechanism of isolation in wild populations and a remnant of introgression in cultivated tomato

by David Francis

The Gamete eliminator gene (*Ge*) is comprised of at least three alleles Ge^P , Ge^C and Ge^N in cultivated varieties, and causes abortion of gametes due to allelic interaction as first reported in tomato by Rick (1966). Rick also mapped *Ge* to the centromeric region of chromosome 4 on the tomato classical map. Female and male gametes are affected to the same extent; elimination of gametes is dependent on the interaction of Ge^P and Ge^C in heterozygotes, and *Ge* behaves as if it were incompletely penetrant.

The aim of the research was to identify the gene underlying *Ge* using a combination of genetic mapping, analysis of haplotype and allele frequencies, and re-sequencing in a population derived of *S. lycopersicum* × *S. pimpinellifolium*. Clustering of candidate genes supports that there is a minimum of two divergent groups of processing tomato germplasm in the *Ge* region. Also, alleles from *S. lycopersicum* and *S. pimpinellifolium* of several candidates are identical (Ge^P and Ge^C). And, there are more than three alleles within the *Ge* candidate region. Finally, there is an effect in hybrids, where yield is greatly reduced in heterozygotes for the *Ge* region, consistent with *Ge*-caused seed abortion and reduced fruit size.

Lifting barriers in diploid hybrid potato breeding

by Pim Lindhout

Despite tremendous genetic variation between potato varieties, and the availability of genomic tools and knowledge of gene functions, there are still constraints to develop new and better potato varieties. A drawback of this genetically flexible species is a strong inbreeding depression, due to increased homozygosity at loci with deleterious or lethal alleles. As a consequence, breeders have favored tetraploid, highly heterozygous potato varieties, partly to avoid inbreeding.

Solynta is using a diploid breeding scheme as an alternative to traditional potato breeding by generating homozygous inbred lines. To initiate its diploid breeding program, Solynta took advantage of the *S-locus inhibitor (Sli)* gene, which inhibits self-incompatibility in diploid potatoes, and introduced it into elite diploid germplasm. They have used this self-compatibility system to produce inbred lines and are evaluating hybrids in the greenhouse and in the field. The preliminary results encouraged them to test the new hybrids in several locations in Europe. Moreover, advanced inbred lines are being used to introgress late blight resistance genes. Solynta's inbred lines are also used by several consortia in studies on plant development, efficiency of photosynthesis, heat tolerance, metabolism of tuber pigments and predicting breeding value

SESSION III • GENOMES AND GENOME TECHNOLOGIES

CHAIRPERSON: MASSIMO DELLEDONNE (UNIV. OF VERONA, ITALY)

CO-CHAIRPERSON: ARSENIO NDEVE (UC RIVERSIDE, USA)

I would like to thank the organizing committee of the 13th Solanaceae conference - 2016 for giving me the opportunity to participate in the event and learn about the current advances in Solanaceae research. Also, I should mention that it was my honor to be considered as co-chair of the Genomes and Genome Technologies session where I could learn particularly about the current advances in plant genome sequencing, sequencing technologies and the application of reference genomes in research to answer pertinent question otherwise not easy to solve utilizing merely plant based phenotype.

In this session, the research talk by Dr. Dario Cantu, from University of California Davis, was the opening plenary of the session. His talk provided an insight on the outcome of the interaction between grapevine and associated microbial communities and the utility of PacBio technology to generate diploid genomes. He sequenced the genomes of both grapevine and associated microbial communities utilizing single molecule real time sequencing technology which allowed to generate genome sequences of high quality through which he deciphered the outcome of this interaction using metatranscriptomic approach and the profile of expressed genes. He emphasized that sequencing of grapevine metatranscriptome allowed to understand the relationship between the diversity of microbial community in grapevine, their activity and gene expression. Also, through integrated “omics” analysis of the interaction between grape berries and biotrophic and necrotrophic grape pathogens he found that microbial activity can affect berry development and metabolism. In addition, Dr. Dario showed that with PacBio now it is possible to reconstruct chromosome homologs separately and make diploid genome.

The research story by Dr. Lidija Berke (Wageningen University) also gave emphasis on the application of genome resources, in particular the use of these resources to unravel trait evolutionary relationship between tomato and potato. Dr. Berke, on her research, investigated the basis of differences between both crop species at chromosomal, molecular and at phenotypic level. For this purpose, Dr. Berke considered *Solanum etuberosum* as an appropriate candidate related species of tomato and potato to conduct this study because it is an outgroup species, and generated and assembled genome sequences by combining illumina

and BioNano genomics for the optical maps which yielded high quality genome assembly, through which the genome sequence was annotated and the evolution of key genes of both crop species accounting for phenotypic expression determined. Phenotypic traits considered in this study included tuber formation, resistance to pathogens, flower color and glycoalkaloid biosynthesis. Dr. Berke considered that *S. etuberosum* genome is a good genomic resource to study and to understand the genus *Solanum*.

Another speaker from UC-Davis was Dr. Amanda Hulse-Kemp. One of the highlights of her talk is that advances in genome technologies are crucial to attain high quality genome sequencing resolution given the limitation of current genome sequencing technologies in handling complex genomes or large genomes such as of pepper. Dr. Hulse-Kemp mentioned that the use of third generation sequencing technology is promising not only for pepper genome sequencing, but also for other crop species, for it yields long range sequence information to improve the generation of high quality references using a smaller number of larger scaffolds than next generation sequencing technology which generate larger number of smaller scaffolds. In addition, Dr. Hulse-Kemp showed that using second generation sequencing technology, 10X Genomics Chromium, to produce synthetic reads allowed to improve the current pepper genome, and also perform de novo genome assembly in short time and at low cost. The other advantage of this technology is it performs phased assembly otherwise not achieved by other sequencing technologies. Dr. Hulse-Kemp findings indicate substantial improvement of the pepper short read genome assembly so far and according to her this genome sequencing technology will be released soon.

The last research story was by Dr. Nicolas Sierro, from Philip Morris International R&D, his talk emphasized the usefulness of sequencing genetic resources to generate genome resources which can be used to perform genome-based evolutionary studies, in particular for *Nicotiana* species. Dr. Nicolas believe that the current available draft genomes resources of *Nicotiana* species together with his new additional draft genomes of *Nicotiana* species will enhance our understanding of the diversity and in particular the impact of polyploidization event that have taken place through evolutionary process in the *Nicotiana* genus.

To sum up, all talks converged on the usefulness of high quality genome reference resources and novel genome technologies which undoubtedly amplify the value of plant reference genome on research. With no doubt, these talks have showed that genome technologies are now improving dramatically our ability to generate high quality genome reference assemblies and consequently our understanding of genome biology.

SESSION IV • HIGH-THROUGHPUT PHENOTYPING

CHAIRPERSON: ALLEN VAN DEYNZE (UC DAVIS, USA)

CO-CHAIRPERSON: LAV KUMAR YADAV (WEST VIRGINIA STATE UNIV., USA)

Topic 1: In-field high-throughput phenotyping for plant architecture and internal fruit quality in tomato.

Dr. David Slaughter

Dr. Slaughter talked about generating non-destructive 3D model of the plant, tree architecture and its blossom. To achieve this he talked about putting sensors all around the plants. Some of the sensors he talked about are GPS, Lidar, R-camera, Pattern strobe, L-camera and Vector navigation. Lidar works with detecting echoes of ultrasound. Lidar works on 2D+Depth principle. R-camera does the 3D phenotyping. Pattern strobe shines light on plants and gets the reflective image. X-arc cameras are used to get images of plants from each and every angle. 32 high resolution cameras are used with 16 stereo pairs. All the different pictures are put together into interprocessor to obtain a perfect 3D image. It is a process where you don't have to destroy the plant to get the data like height, leaf size, interception, biomass, etc. There are two modes: one for 2D+Depth mode and the other high throughput mode. In high-throughput mode 32 pictures are taken at once. GPS triggers the camera. In best view mode the quality of picture is 10x.

Internal quality of the fruits, bulbs are also accounted for. In this case a high beam light is passed through fruits or onions to see internal anatomy and condition. Soluble solids, flesh color and drymatter content can be measured. The measurement time for this is just 3 seconds.

Topic 2: Persistent homology: A tool to universally measure plant morphologies across organs and scales.

Dr. Mao Li

Persistent homology is a concept of mathematics that shows connectivity of components. It makes 3D structure of leaf shape, root architecture and leaf serration which can be used in genetic analysis. This technology tracks evolution of features across all scales. It basically puts picture outline in series of rings to get the contour and estimate density. It then used the

concentration of data points to get local and smooth view. It also gives the sideview of the leaf. In a plane you can move top to bottom and record connected components. Then plot contour plane depending on number of components of images. It gets us a persistence barcode. We can eventually get barcodes of different images and compare those using barcodes.

Elliptical fourier transformation gets the frequency of the different images. Higher the harmonic frequency more betters the picture. It shrinks the pink region of the picture and gradually increases it. It can also give us the root architecture which uses distance function. It moves from blue to red region i.e. to the core region to quantify the complex. It gives the hills as the data on contour lines higher the peak betters the resolution of the image. The readings that can be taken from this technology are: tomato introgression line, leaf shape quality, multidimensional scaling, and canonical variate analysis. It changes these data into curves showing characteristic box plot with medium value points.

This technology is robust to noise, invariant with respect to orientation and capable of application across diverse species.

Topic 3: Field platforms for high-throughput phenotyping in Arizona.

Dr. Padro Andrade-Sanchez

This talk talks about tractor based high throughput phenotyping. It uses field scanners placed on tractor to generate data. It is a tractor based approach and all the components of it are commercially available. It should have ample supply of DC power and pay load capacity. Tractor has adjustable height for clearance. It has frame in built with agricultural tooling parts with vertical horizontal and rotational adjustments. It can take plant canopy thermal response data. It has apogee of 51-121 inches, in cured radiometer 4-14 micrometer window, 38⁰ field view nadir and 30⁰ orientations. It measures plant height by sonar sensor. It measures plant canopy spectral response with 420 acute light sensors. It has horizontal and vertical GPS sensors giving accurate reading upto approximately 1cm horizontal and 2cm vertical.

Performance Parameters: Field capacity 0.91ha/hour, 676kb per event, 259 bytes per m², 2.1mb per hour and 4 events per day. Data processing is done by GIS plots layout. No imaging unit is present in this unit.

Field Phenomics

Arizona has Gantry based field phenotyping system. Its dimensions are 285m long and 28m width. It's like a large 3D scanner. It can also work at night. This machine generates point clouds. It has Lemra scanner with scanning area 22*206m². It has following systems in it like: imaging system, stereo RaB, laser, thermal, hyperspectral, fluorescence units.

In summary, High-throughput phenotyping interdisciplinary integrated approach. Tractor based approach is reliable and high quality data is generated. Gantry based approach though extract high quality and quantity data, it is an expensive unit to maintain.

SESSION V • GENE-EDITING AND NEW BREEDING TECHNOLOGIES

CHAIRPERSON: ANNE BRITT (UC DAVIS, USA)

CO-CHAIRPERSON: JULIE PEDRAZA (CSU, FRESNO, USA)

Introduction

University of California, Davis (UC, Davis) hosted the 13th Annual Solanaceae Conference on September 12 to 16, 2016. Over 360 research scientist and members from all around the world arrived at the conference to present their research in Solanaceae genomics and the advance technology applied to improve crop production. Session V, topic “*Gene-editing and new breeding technology*” was hosted by Dr. Anne Britt from UC, Davis and student co-chair Julie Pedraza from California State University, Fresno (CSU, Fresno). Research presenters were Dr. Joyce Van Eck, Dr. Angela Chaparro-Garcia, Dr. Sundaram Kuppu and Dr. Colby Starker.

Genetic Engineering and Genome Editing in the Solanaceae

Dr. Van Eck from the Boyce Thompson Institute, in Ithaca, New York

The use of CRISPR/Cas 9 technology in genetic sequencing has brought a precise and versatile method of manipulating genes by cutting out, adding or replacing segments of DNA sequences. The Cas 9 enzyme cuts specific sections of the DNA strand allowing for bands of DNA to be removed or added. In tomatoes species CRISPR/ Cas 9 technology was used to target the specific genes ARGONAUTE 7 and SIAGO7 that are connected the expression of phenotypical characteristics of wiry, needle like leaves. Previous research indicated four genes in tomatoes associated to the negative regulating of auxin responses in tomatoes in which the disruptions would cause wiry to occur in the leaves. The use of CRISPR/ Cas 9 technology, specifically with two of the genes ARGONAUTE 7 and SIAGO7 these two genes showed phenotypical results with 49% tomato plants expressing wiry where homozygous of 90bp was deleted. The success of CRISPR/ Cas9 technology in tomato mutations opens windows of opportunity to further test several genes and the effects they have on the architectural structure of tomatoes in a shorter time frame.

Susceptibility genes for resistance against *Phytophthora infestans*

Dr. Chaparro-Garcia from the Sainsbury Laboratory, Norwich Research Park, Norwich, United Kingdom

In potatoes, the pathogen *Phytophthora infestans* (late blight) is problematic and causes over 6 billion dollars in losses to tomatoes. Although the plant breeding industry is dominate by breeding through dominate wild types for resistance, the CRISPR/ Cas 9 technology could be used to mediate resistance by surface or intracellular receptors where the pathogen-associated molecular patterns are recognized by specific receptors to trigger immunity. Using susceptible genes as a resource to improve the resistance of plant diseases by means of protein effectors could lead the industry by better techniques against pathogens. The use of CMPG1 targeted by

AVR3a reduced late blight infections of potatoes. In tomatoes the S1CMPG1 locus was successful in induced indel introns causing partial resistance to the pathogen. Some samples had homozygous deletion and the remainder contained various mutations along the S1CMPG loci. The homozygous mutations were required to improve the resistance to late blight. The modification of genes through susceptible genes using CRISPR/ Cas 9 technology permits targeted editing for the developing of resistance crops with high turnover results in a short period of time, thus improving the method with little to not trade-offs.

Creating tomato haploid inducer through single amino acid substitutions in CENH3 histone fold protein

Dr. Kuppu from the Department of Plant Biology at UC, Davis in Davis, California

In the pollen of *Arabidopsis thaliana* (*Arabidopsis*) the CENH3 which is a histone 3 variant gene that manipulates the centromeres to produce haploids at the 3/32 fold. In vitro the GFP tail swap occurred in 30-40% of the plants tested. The EMS could possibly induce a mutation at certain points and was used to test 10 amino acids in *Arabidopsis* with those that induce trichomes or no trichomes. The EMS induced CENH3 mutations by 92%, resulting in fertile plants with a 3/41 haploid cross of wild types. The success of the EMS inducing the mutant CENH3 by centromere manipulations through isolated amino acids is a newly developed method that could be applied to other crop species and would be identified by TILLING.

Assessing the impact of gene replacement and gene modification methods in a crop species at the whole genome level

Dr. Starker from the Department of Genetics, cell biology and development and center for genome engineering at the University of Minnesota, Minneapolis, Minnesota

Genetic engineering of crops has added value to the agricultural community but not without regulatory concerns over the technology used to make propagated crops. CRISPR and TALEN technology for gene editing are the two tools used and could also help regulators make decisions regarding the impact of clonally propagated crops, by detecting off-target effects. The use of ALS1 which contains a mutation that causes herbicide resistance is used with two copies of EPSPS genes while using Cas 9 and GUIDE-seq to improve the variant and off target effects of the nucleases. The success of using DHMRH S% for transformation DNA was able to target specific trade-offs of the ALS1 modified herbicide resistance transgene with the use of CRISPR and TALEN.

Conclusion

Session V, speakers were professional presenters that delivered an organized and understandable research. The research by Dr. Chaparro-Garcia, was very interesting and a new approach to using susceptible genes for resistance. Her finding interested me and the research I do with *Candidatus Liberibacter solanaceum* bacteria and its effect on the biochemical defense compound pathways in potato plant. My current research of specific defense compounds induced upon infections could be applied through genetic markers that cause induction and could be correlated with her research of susceptibility genes that cause infection.

The Solanaceae conference was by far one of the best conferences I have had the honor of attending. I enjoyed meeting scientist from all around the world and establishing research

opportunity relationships with geneticist interested collaborating with my interest biochemical pathways in plants. I met Dr. Barbara Liedl from West Virginia and took her on as my mentor throughout the conference asking her questions about the presenters' research for understanding. I enjoyed the Keynote address by Dr. Robert Chetelat whom eloquently shared the life of Dr. Charley Rick and the Origins of the Tomato Genetics Resource Center as well as the research in Session XIII and XIV. Dr. Britt was a gracious host, kept me well informed and made me feel welcomed.

SESSION VI • EPIGENOMICS AND METHYLATION

CHAIRPERSON: LUCA COMAI (UC DAVIS, USA)

CO-CHAIRPERSON: RANDI JIMENEZ, UC DAVIS., USA)

THE FUNCTIONS OF DNA METHYLATION IN FLESHY FRUITS

Philippe Gallusci

It is known that in plants, methylation is controlled by complex machinery, but so is demethylation. By understanding the basic mechanisms of methylation, it can be altered and the repercussions observed. For instances, the functions of methylation in tomato fruit can be elucidated by inhibiting methylation, resulting in hypo-methylation, and recording the pleiotropic effects. Targeting which sites are altered in their methylation, and seeing the effects can not only help identify epigenetic influences of loci, but can also be used in research and breeding. Furthermore, plants with altered methylation can be used in crosses to develop hybrids with mosaic methylomes that may produce different, desirable traits. An example of altering methylation to change economically important traits is in tomato fruit. It has been shown that hyper-methylation in DML RNAi tomato plants causes altered fruit ripening as well as gene expression. Furthermore, the demethylation of DNA in ripening tomato fruit stimulates gene expression and halts the ripening process. Methylation plays a notable role in tomato fruit ripening. Similar processes may be occurring in wild tomato species, and current projects on grape berries are underway to see if this is true of other fleshy fruited species.

miR160 IS A KEY REGULATOR OF AUXIN MEDIATED DEVELOPMENTAL PROCESSES IN TOMATOz

Subha Damodharan

Several miRNA expression patterns affect flower development and other reproductive stages in tomato by regulating Auxin Response Factors (ARFs). sly-miR160, one such miRNA, represses several auxin response factors thereby regulating auxin regulated processes. Down regulation of sly-miR160 causes changes in tomato ovary shape very early in ovary development. Interestingly, down regulation and over expression of sly-miR160 cause opposite phenotypes in leaf shape due to differences in auxin mediated processes, which is suggestive of a common mechanism behind these auxin regulated processes, involving sly-miR160 guided cleavage of Corresponding targets. miR160 has several isoforms with different effects. CRISPR/Cas9 mutants revealed different alleles with novel phenotypes in tomato

reproductive morphology. The sly-miR160 mutants are and will continue to be important in the elucidation of the mechanisms regulating Auxin response factors.

AN ERF TRANSCRIPTION FACTOR ACTS AS A POSITIVE REGULATOR IN THE ANTIVIRAL RNA SILENCING IN PETUNIA

Cai-Zhong Jiang

Virus-induced RNA silencing and interrupting function in petunia of RNAi is a useful tool to understand its genetics and transcriptional regulation. Tobacco rattle virus based VIGS was used to study gene function in petunia. An ethylene-responsive element binding factor (PhERF2), a gene involved in the regulation of silencing, RNAi lines in petunia were produced. When color gene CHS was silenced in these petunia lines, mosaics and different responses based on variety resulted. This suggests that VIGS may be under some genetic control. Whether PhERF2 was silenced or over expressed also greatly impacted the expression of silencing-related genes. This was also true of Cucumber mosaic virus (CMV) resistance. When PhERF2 was silenced, there was a higher susceptibility to CMV, while plants overexpressing PhERF2 showed higher resistance. These results indicate that PhERF2 acts as a positive regulator in RNAi and is required for gene-silencing to occur.

SESSION VII • GENOMICS-ASSISTED BREEDING

CHAIRPERSON: JEANNE JACOBS (NEW ZEALAND INSTITUTE FOR PLANT AND FOOD RESEARCH)

CO-CHAIRPERSON: KIEU-NGA T. TRAN (LOUISIANA STATE UNIV., USA)

Introduction to Solanaceae species:

The Solanum family includes a number of economically important crops such as *Solanum lycopersicum* (tomato), *Solanum tuberosum* (potato), *Capsicum annuum* (chili pepper) and *Solanum melongena* (eggplants). Among these, tomato and potato are the two most studied species in the Solanaceae family. Members of the Solanaceae family are widespread throughout the world, but most originate and are widely distributed in Central and South America.

Why study and breed tomato and potato?

Tomato has been widely used not only as food, but also as scientific model plant. Researchers have been using tomato to study fruit development and ripening (Giovannoni 2004), fungus and viral infection etc. Because of its importance as food, tomato has been bred to improve productivity, nutritious dense fruit, protection from disease and insects, and resistance to biotic and abiotic stresses. Breeders can create new varieties of good crops by taking advantages of the great varieties of wild tomato species. A successful variety would need to meet the demand of growers for high yield, customers for taste (Brix; measure for sugar) and processors for extended field holding (easy for post harvesting service and deliver them to processing factory).

Potato is one of the world most important crops with nearly 400million tons produced worldwide every year. Even though the desirable traits are easy to find in wild relatives of potato, breeding

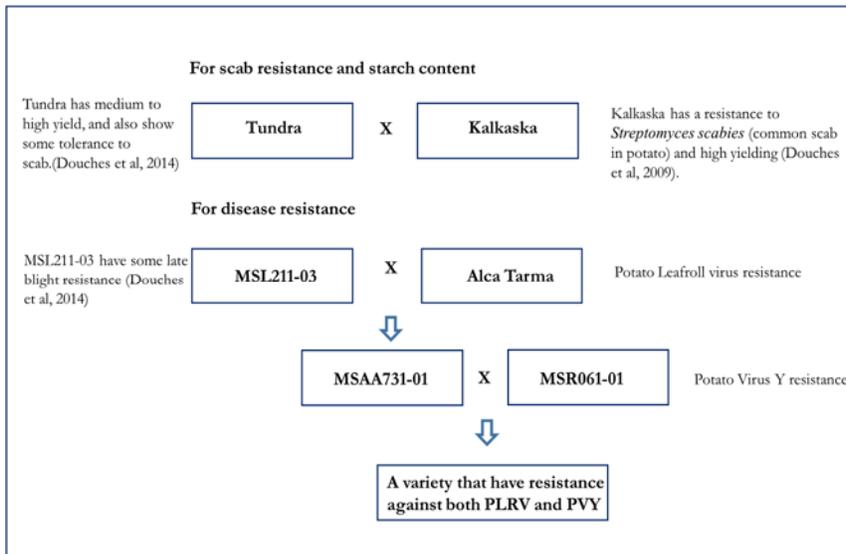
potato is prone to have more problems compared to other crop species due to its long breeding time (about 15 to 20 years using traditional breeding), high heterozygosity, and polyploidy. In fact, the popular cultivars have few traits from the wild potato germplasm due to their genetic complexity. (Hirsch et al, 2013; Douches et al, 2009)

Why is California suitable for growing crops like tomato?

California has a Mediterranean climate which is characterized by dry summer and mild, moist winters. Hence, it is not only easier to control the irrigation, but also help to reduce molding, and fungus and viral infections which directly affect the yield and quality of the fruits. California State produces 50 tons of tomato per acre and 265,000 acres as of 2016 are used to grow tomato. It also responsible for 35% of processing tomato world wide and 95% of US processing tomato. Processing tomatoes are needed for manufacturing of tomato sauces, juices, paste, ketchup etc. (HM Clause field trip)

Talk summaries:

Talk 1: Genomics Assisted Breeding in Potato by Dr. David Douches from Michigan State University.



Dr. Douches’ work focuses on potato breeding. He presented a new potato SNP chip for genetic analysis. He also presented an example of breeding for scab resistance. In addition, he also bred to obtain a variety that has high starch content, and also carries resistance genes to PVY (Potato Virus Y) and PLRV (Potato

Leafroll Virus).

Talk2: Empirical Evaluation of Genomic Selection for Resistance to Bacterial Spot of Tomato by Debora Liabeuf from The Ohio State University.

Liabeaf's research focuses on breeding to make a tomato variety that has resistance to *Xanthomonas* species that cause the bacterial spotted disease in tomato. To capture the genetic variation, she predicted genetic value of selection candidates based on GEBV (Genomic Estimated Breeding Value).

$$y = x\beta + \varepsilon$$

With y is the vector of phenotypic value. X is marker matrix. β marker effect. ε is a constant.

Talk3: GBS-assisted recovery of “lost” introgressions in advanced backcrosses of *Solanum incanum* to cultivated eggplant (*S. melongena*) by Pietro from Gramazio Universitat Politècnica de València, Spain

Pietro started by introducing his plant model, *Solanum incanum*, a herb or soft wooded shrub which has a lot of medicinal properties such as anti-oxidant, cardioprotective, anti-carcinogenic, anti-obesity, anti-diabetic, anti-inflammatory. Breeding of *S. incanum* and *S. melongena* produced F1 hybrid, followed by 5 backcrosses to *S. melongena* to produce introgression lines. With published genome available and completed genetic map, he identified 800 SNPs in the hybrid. The analysis of the introgression line population will help to improve the current lack of knowledge of complex traits in eggplant.

Talk4: Analyzing and Evaluating the usefulness of existing molecular markers for breeding of elite tetraploid potato by Ea Sundmark from Aalborg University, Denmark.

With 50 published markers and 16 markers developed in her lab, she was able to identify some known and new haplotypes at markers' loci. She then made prediction models based on the observed haplotypes for phenotyping correlation. Simple traits can be predicted from small populations with certain number of supported genetic markers.

Talk5: Genomics-assisted QTL mapping for agronomical traits in pepper by Koeun Han from college of information science and technology Daejeon, Republic of Korea

To identify QTLs controlling pepper traits including plant height, fruit color, weight, and pungency, we constructed high-density maps by re-sequencing 120 recombinant inbred lines (RILs) derived from an intraspecific cross (*C. annuum* 'Perennial' × *C. annuum* 'Dempsey') and by genotyping-by-sequencing (GBS) of 96 RILs from an interspecific cross (*C. annuum* 'TF68' × *C. chinense* 'Habanero'). Single nucleotide polymorphisms (SNPs) were detected. To improve efficiency of genetic map construction, adjacent SNPs were combined to bins using sliding window approach. Genotypes of the bins were determined based on the ratio of SNPs with different genotypes. From GBS, a total of 8,500 highly reliable SNPs were obtained for the interspecific population and used for a linkage map construction resulting in a map length of 1,186 cM.

It was my pleasure to attend and serve as co-chair at Solgenomics conference 2016. Even though I do not work directly on crops, I found majorities of the talks interesting. I was particularly interested in abiotic stress like genes or traits that can increase salt/drought tolerance in crops. In addition, studies that were done to improve crops ability to resist viral/bacterial/fungal infections were also nicely presented. Feeding a growing population of 7 billion people is undoubtedly a huge challenge that we are facing nowadays. Thus it emphasizes the importance of breeding and biotechnology to generate ideal crops that can give the best yield possible despite the unfavorable conditions due to climate changes.

SESSION VIII • SYSTEMS BIOLOGY AND NETWORKS

CHAIRPERSON: SIOBHAN BRADY (UC DAVIS, USA)

CO-CHAIRPERSON: SOPHIA JINATA (CSU SACRAMENTO, USA)

Keynote Speaker: Robert Last

Talk title: “The tip of the trichome: Specialized metabolic diversity in the Solanaceae”

Glandular secreting trichome molecules have exhibited synthesis of a wide variety of specialized secondary metabolites. Analysis of specialized metabolism in the trichome tip cells of tomatoes reveals species specific pathways. The acyl sugars produced in the trichome tip cells act as defensive molecules, protecting plants from consumption by larvae hatchlings. As they feed on the tomato plants, insects also ingest the acyl sugar molecules, which contains cyclized sugars with carboxylic acids and acyl chains in ester linkages. When the insects lay larvae on the tomato plants, the larvae are covered in carboxylic acids residues from the metabolized acyl sugars. The acid residues act as an attractant for other insects, such as ants, marking the larvae as a food source, thus, protecting the tomato plant from further predation.

The variation in acyl sugars between closely related species is seen in the acyl chains attached during biosynthesis. The trichome IPM synthase gene was modified to lack a regulatory domain, thus preventing feedback inhibition and allowing for constitutive synthesis of an acyl sugar precursor, leucine. Additionally, allelic differences in the modified IPM synthase gene have been found to influence the acyl chain phenotypes seen in *S. penellii*. Employing a phylogenetics approach to look at homologous ASAT2 enzymes has identified amino acid changes that alter donor-substrate specificity during acylation of the cyclized sugar. Further analysis of the ASAT gene alleles imply a gene duplication event in a common ancestor of the tomato species followed by independent neofunctionalization events, resulting in the species-specific pathways with altered ASAT activities seen in present-day tomatoes.

Prior to advancements in genomic sequencing, the steps in a biochemical pathway were discovered and evaluated through analysis of multiple generations of clones and bred offspring. To this day, prior knowledge of biochemical pathways influences current studies on the generation and utilization of organisms' metabolites. Incorporation of present knowledge on biochemical mechanisms with modern analyses on genetic variation in conjunction with evolutionarily plastic traits will assist in future efforts to decipher specialized metabolic pathways as well as deepening our understanding of interactions between specialized metabolites and other organisms.

Speaker 2: Yoshihito Shinozaki

Talk title: “A high-resolution spatiotemporal atlas of the tomato fruit transcriptome”

Although the pericarp tissue often gains most of the attention from researchers, other tissues affect the development of the tomato fruit. Laser microdissections have been utilized to obtain spatial resolution of the different tissue layers in the tomato fruit. The spatial information yielded can be used to analyze co-expression of genes across the tissue layers, leading to a much simpler network integrating both temporal and spatial gene specificity.

To perform such analyses, the Tomato Expression Atlas is being developed. This transcript and co-expression database gives a non-invasive model allowing visualization of the tomato fruit development at varying dimensions. The Expression Cube, an analysis platform in the Atlas, visualizes data output of tissue-specific gene expression at different stages of plant development. Case studies of the tomato genes RIN and CHS revealed that the data yielded by the Expression Cube are consistent with the co-expression data documented for each respective gene.

Speaker 3: Sharon Gray

*Talk title: “A Systems-level Study on the Effects of the Elevated Atmospheric CO₂ on *Solanum lycopersicum* and *Solanum pennellii*”*

Current patterns of energy consumption and increasing demands of plant supplies present higher levels of pressure to understand plant responses to varying aspects of climate change. Elevated atmospheric levels of CO₂ has been one of the issues at the forefront of the climate change debate, prioritizing the importance of evaluating plant responses under such conditions. Anticipated effects of elevated CO₂ include increased rates of photosynthesis, increased plant mass, reduced water usage, and higher levels of nitrogen fixation. Although not much is known about plant response to CO₂ in combination with other environmental stressors, genetic variation as well as root development can further current understanding of plant response to elevated CO₂ as a standalone stressor.

The model organisms *Solanum lycopersicum* and *Solanum pennellii*, both differing in root morphology and cellular anatomy as well as tolerance capabilities under drought and high salinity conditions, were grown in controlled environments and sampled at varying stages in the tomato plant development. RNA sequencing data revealed nineteen dominant expression patterns with lots of variation between root and shoot tissues, species and growth environment. Increased levels of protein expression, anticipating increased plant biomass and water, were seen in genes associated with increased amino acid profiles and larger xylem tissue diameters. Additionally, higher photosynthesis rates resulted in increased shoot and root biomass in both species. Both species exhibited consistent changes in response, however, the magnitude and timing of the response differed between the two, leaving no evidence for specific CO₂ by species interactions. Future studies may include studying CO₂ response in model organisms in conjunction with other environmental stressors such as drought or high salinity levels.

Speaker 4: Spela Baebler

Talk title: “Network analysis unravels crosstalk between ethylene and salicylic acid signaling pathways in virus-infected potato”

Phytohormones, such as salicylic acid and ethylene, have shown to be involved in plant immune system signaling (PIS) cascades. Data on the plant immune signaling cascades seen in *Arabidopsis* are spread between dispersed data sets and current signaling models with little redundancy between the two data pools. Combining the two pools into a large network allows for cross analysis, which has led to the generation of novel connections meant to improve the current PIS model in *Arabidopsis*. Connections between the EIN3 and NPR1 pathways involving different phytohormones have been identified through network analysis in *Arabidopsis*.

Orthological data was utilized to transfer *Arabidopsis* information to potato systems and a PIS model in *Solanum tuberosum* was developed through targeted and untargeted co-expression networks. Combining a large knowledge network with the co-expression networks generated an integrated network, allowing for identification of crosstalk between different pathways. Both ethylene and salicylic acid pathways have been shown to interact with expression of NPR1 in *Solanum tuberosum* infected with the Potato virus Y.

SESSION IX • ABIOTIC STRESSES

CHAIRPERSON: JULIN MALOOF (UC DAVIS, USA)

CO-CHAIRPERSON: LUMARIZ HERNANDEZ (UNIV. OF PUERTO RICO)

NEW TOMATO MUTANT COLLECTIONS FOR THE IDENTIFICATION OF KEY GENES INVOLVED IN TOLERANCE TO SALINITY AND DROUGHT

Flores F.B., Angosto T., Moreno V., Lozano R., Bolarín M.C.

Department of Stress Biology and Plant Pathology from the Spanish Research Council (CSIC), Spain

In this talk Dr. Flores presented previous and preliminary data from a collaborative study of four different mutants studied to identify genes involved in drought and salinity stress. In their previously studies, they described the *altered response to salt stress 1 (ars1)* mutant, in which the transcription factor R1-MYB is mutated. Wild-type plants close their stomata in response to salt, however in the *ars1* mutant stomata remain open under salinity stress, indicating that this gene regulates the stomatal aperture with salinity stress. *ars1* mutants also had higher sodium accumulation in the leaves and increased transpiration and sodium transport. Dr. Flores also presented data on *ARS1*-overexpression (OE) lines. These lines showed the opposite phenotypes of the *ars1* mutant, with reduced transpiration but increased tolerance to salt. Also, this study shows that the fruit yield and growth of these mutated plants was not affected when the plant was not in stress, giving an important role for future biotechnological approaches.

Another mutant that Dr. Flores described was the *restored cell structure by salinity (res)*, a mutant that strongly reduces root and shoot development. Surprisingly, when the salinity stress was applied to *res* plants their phenotype and cell structure were restored, suggesting that this *res* mutation needs salinity stress for normal root growth. This mutant lines were used to study jasmonic acid. This hormone helps the plant with biotic and abiotic stress. Their data suggest that the jasmonic acid is synthesized in the roots. In their study, plants that possess the *res* mutation without the stress applied showed an increase of genes associated with the jasmonic acid synthesis. Also, high levels of jasmonic acid found in roots was associated with an inhibition of roots growth, so it seems that the *res* phenotype is caused by excess jasmonic acid production in the roots under control conditions.

Recently, this group of researchers have been studying the mutations: *salt hypersensitive esculentum 1 (she1)* and *salt hypersensitive pennellii 1 (shp1)*. In plants with the *she1* mutation, when salinity stress is applied a rapid accumulation of sodium in plant leaves was observed in comparison with the control. Phenotypically the plant has leaf swelling and chlorosis. They observed a lower reduction of stomata closure and transpiration of those mutant plants. They suggest that the *she1* mutation is recessive and monogenetic.

In the case of the mutant *salt hypersensitive pennellii 1 (shp1)* with salinity stress phenotypically plants showed leaf chlorosis. When the plant is no longer in the salinity stress the chlorosis gets reversible returning to its normal stage. Similarly, as the *she1* mutation, the leaf accumulates sodium as well creating the leaf chlorosis. Sucrose was not detected in mutated plants with salinity stress conditions compared to non-stress mutated and non-mutated plants. They suggest that this absence of sucrose must be linked to the reduction of chlorophylls affecting process like photosynthesis.

GALAPAGOS TOMATOES AS A GENETIC SOURCE FOR SALINITY TOLERANCE

Pailles Y., Ho S., Lightfoot D., Pires I., Mitchell C., Negrão S., Schmoeckel S., Tester M.
Plant Science Program King Abdullah University of Science and Technology, Thuwal, Saudi Arabia

In this talk Ms. Pailles studied the salinity tolerance of two wild tomatoes from the Galapagos islands: *Solanum cheesmaniae* and *Solanum galapagens*. From these two species 68 accessions were cultivated from seeds using hydroponics. The salinity tolerance was studied adding NaCl gradually from 75mM to 200mM. Then, the plants were harvest and data was collected. From those 68 Galapagos accessions 6 of them show salinity tolerance. New seeds of those 6 samples were cultivated until it bloomed. After that, a transcriptomic analysis was made. One of the samples resulted in good yield performance.

GENETICS AND GENOMICS OF TRAITS ASSOCIATED WITH WATER STRESS TOLERANCE IN WILD TOMATO (*SOLANUM HABROCHAITES*)

St. Clair D.A.

Plant Sciences Department, University of California, Davis, CA

Dr. St.Clair presented her research study in water stress tolerance of *Solanum habrochaites* a wild tomato that possess tolerance to chilling temperature and water stress. Analyzing chromosome 9 of *Solanum habrochaites* and *Solanum lycopersicum* as reference she found differences in structure and more repeats in *S. habrochaites*. Since her experimental data suggest that chromosome 9 possess water stress tolerance they are trying to develop new probes for chromosome 9 to have better understanding of *S. habrochaites* water stress tolerance like sequencing genomic BACs and analyzing transcriptional regulation by mRNA-seq.

DISSECTING THE GENETIC BASIS OF POLLEN THERMOTOLERANCE IN TOMATO

Driedonks N., Wolters-Arts M., de Boer G.J., Vriezen W., Mariani C.1, Rieu I.

Department of Molecular Plant Physiology, Radboud University Nijmegen, The Netherlands

In Ms. Driedonks talk she presented what happened to pollen development in high temperature and if the pollen exhibits thermotolerance. They studied 61 accessions of 13 wild species of tomatoes and applied heat gradually to its pollen. They found high variation in pollen thermotolerance between individuals within accessions, but no general tolerance. Those that had high thermotolerance was used as interspecific and intraspecific bi-parental F2 mapping population. A transcriptomic difference study found genes involved in hormone signaling and chaperones as being differentially expressed, suggesting possible mechanisms for this tolerance. They believe there are a variety of genes involved in pollen viability.

SESSION X • RESISTANCE, PATHOGENS, PESTS AND MICROBIOMES

CHAIRPERSON: GITTA COAKER (UC DAVIS, USA)

CO-CHAIRPERSON: KEVIN BABILONIA (TEXAS A&M, USA)

PHYTOPHTHORA BLIGHT IN POTATO: TIPPING THE BALANCE BETWEEN RESISTANCE AND SUSCEPTILITY

Francine Govers

Phytophthora infestans is a plant pathogen affecting Solanaceous crops around the world. In order to be virulent, it can secrete effector proteins to suppress basal defense responses in the host. RXLR effectors in *P. infestans* are a big family of proteins that can manipulate the host machinery to cause disease. However, plants have evolved with resistance genes to protect themselves through a gene-for-gene interaction which leads to effector-triggered immunity. One example of a characterized resistance gene is R1 in potato which recognizes AVR1, a protein that targets an important component of the exocyst complex, thus affecting vesicle trafficking. In addition to resistance proteins, plant Pattern-Recognition Receptors (PRR) are involved in basal defense responses by perceiving microbes extracellularly. One type of PRRs are Receptor-Like Kinases (RLK), which can trigger downstream signaling upon recognition of a pathogen. Several members of a subfamily of RLKs, L-type lectin receptor

kinases (LerRKs), have been shown to be important in defense against *Phytophthora* and other pathogens. Using its *Arabidopsis* counterparts, several LerRK orthologs have been found in tomato and tobacco. The silencing of potential LerRK candidates in these species can attenuate the immune response against *P. infectans*, highlighting the importance of LerRKs in defense.

TOMATO RECEPTOR FLAGELLIN-SENSING 3 BINDS FLGII-28 AND ACTIVATES THE PLANT IMMUNE SYSTEM

Sarah Hind

Plants can perceive Pathogen-Associated Molecular Patterns (PAMP) through Pattern-Recognition receptors (PRRs) in the cell membrane to induce the expression of defense genes. One well-characterized PRR is FLS2 which can recognize a flagellin peptide termed flg22. Upon recognition of flg22, FLS2 interact with its co-receptor BAK1 to trigger a signaling cascade. It was previously shown that some Solanaceous species can recognize another epitope of flagellin, flgII-28, through a PRR different from FLS2. A screening of different tomato accessions using ROS production made possible the mapping of Flagellin-Sensing 3 (FLS3), a receptor-like kinase necessary for flgII-28 recognition. The recognition of flgII-28 by FLS3 is specific and independent of FLS2. Transiently expression of FLS3 in tobacco leaves demonstrated that it can induce MAP Kinase activation and ROS production, which are classic defense responses in PAMP-triggered immunity. Importantly, a photo-affinity labelling strategy demonstrated the binding of FLS3 to flgII-28, indicating that FLS3 is the receptor for flgII-28.

LOCAL SMRT RENSEQ ENABLES RAPID CLONING OF RPI-SMIRA1 AND R10 FROM POTATO CULTIVAR SARPO MIRA

Kamil Wytok

The identification of new resistance genes is necessary to understand and control crop diseases caused by pathogens. The potato cultivar Sarpo Mira is resistance to the devastating *P. infectans* and bioinformatics analysis of its genome can provide insights of potential resistance genes absent in other cultivars. Using a SMRT R-gene enrichment sequencing (RenSeq) approach, a novel resistance gene against *P. infectans*, Rpi-Amr3i, was mapped. Further SMRT RenSeq analysis identified more candidate genes in Sarpo Mira, including Rpi-Smira1 and R10 which can recognize the effectors AvrSmira1 and Avr10, respectively.

OPPORTUNITIES TO IMPROVE TOMATO FRUIT BY TARGETING EARLY DEVELOPMENT AND RIPENING PROCESSES CO-OPTED BY PATHOGENS

Ann L. Powell

Understanding the fruit-pathogen interaction during different fruit stages can provide useful information towards preserving food quality in the field. It is known that ripped tomatoes are more susceptible to pathogen infection, thus the transcriptional changes in ripped vs green tomato will impact the level of resistance. Major hormones are differentially expressed during the fruit development but its roles in defense are not clear. Reduction of salicylic acid in tomato make them more susceptible to infection during the early stages of the fruit, but more resistant when they ripen. This results suggest that the hormonal fluctuation is not only necessary for fruit ripening but will also determine the outcome of the fruit-pathogen interaction.

SESSION XI • TUBERS AND ROOT SYSTEMS

CHAIRPERSON: GLENN BRYAN (THE JAMES HUTTON INSTITUTE, UK)

CO-CHAIRPERSON: JUSTIN MEDINA (CAL POLY POMONA, USA)

Root and Tuber Summary

The entire session was rich in cutting edge research related to roots and tubers. The first speaker Salome Prat who works in Madrid Spain in the Plant Molecular Genetics Department at El Centro de Nacional de Biotecnologia-CSIC. Her talk focused on potato tuberization in *Tuberosum* species and the effect of short days. Mobile signals encoded by regulate the response to short days through a potato-FT constans factor called stCOL1. This signal is correlated to suppression of tuberization under long day conditions. Without stCOL1 the SP6A mobile signal became upregulated. This signal when over expressed and not inhibited by the SP5G gene result in high tuber yield.

The second speaker was Elena Craita Bita from the Cell and Molecular Sciences Group at James Hutton Institute, Dundee, United Kingdom. Her talk focused on potato cultivars and their characterization of acquired thermotolerance. She explained that temperatures above 22C can reduce tuber formation. Acquired thermotolerance has not historically been bred for in potato but research on thermotolerance in *Arabidopsis* is beginning to emerge. Acquired Thermotolerance is a plants ability to survive high temperatures through previous exposure to increased temperature. In potato what found most interesting was that acquired thermotolerance was affected by light conditions. Under dark conditions potatoes could not acquire thermotolerance. Multiple potato genotypes were tested for acquired thermotolerance using an electrolyte leakage test providing information on which genotypes currently have acquired thermotolerance.

The third speaker was Jonathen Nielson was from Agriculture and Agri-Food Canada Potato Research Centre and the title of his talk was “Biological Predictors For Tuber Sweetening During Long Term Cold Storage”. He explained that current storage conditions of potatoes at 4C led to sugar accumulation in the tuber. This accumulation of sugar causes brown color when fried and toxic compounds like acrylamide. Multiple cultivars were tested and each had a different response to cold storage in the form of sweetening. They sequenced the potato varieties before and after cold storage and are now in the process of confirming genes that are involved in post-translational regulation that is linked to sugar accumulation. These genes can then be used in industry to select for superior cultivars that store at 4C with less sugar accumulation then before.

The fourth and final speaker was Hui Duan who is an employee at Simplot Plant Sciences. His talk focused on improving potato cultivars through TALEN mediated targeted DNA insertion. He focused mainly on a new GMO potato that contained the Polyphenol oxidase2 gene. This potato was called the Innate potato and had reduced browning and bruising which are both desired traits for sales. The Polyphenol oxidase2 gene was inserted using *agrobacterium*. Hui went on to explain a more precise DNA insertion method that can place the target sequence into a region of the genome that has known expression levels. This would also allow for breeding selection to be easier since precise gene location is known. The method explained was TALEN (Transcription Activator-Like Effector Nucleases) which causes double strand breaks in the genome in a predetermined location in the genome.

SESSION XII • FLOWERS, SEEDS, AND FRUIT

CHAIRPERSON: JIM GIOVANNONI (USDA/BOYCE THOMPSON INSTITUTE, USA)

CO-CHAIRPERSON: KIMBERLY RODRIGUEZ (NEW MEXICO STATE UNIV., USA)

This session included several talks regarding tomato fruit ripening, ranging from hormonal signaling, to regulation of genes, to pathogen induced ripening. Additional talks consisted of flower color macroevolution in the Solanaceae family and the genetics of chile pepper fruit size. The individualized talks and studies are summarized below.

Mondher Bouzayen, from INRA in Toulouse, France, spoke about the hormones and developmental factors in tomato fruit ripening. The plant hormones ethylene and auxin are known to control fruit ripening in tomato. Ethylene promotes fruit ripening, while auxin, on the other hand, delays fruit ripening. In order to identify whether ethylene responses are impacted by other hormones and whether Auxin Response Factors (ARF) can bridge known components of the ripening pathway, Bouzayen and his team conducted a study to determine the interactions between ethylene and auxin and tomato fruit ripening. It was discovered that SIARF2, a member of the ARF gene family, plays an important role in ripening. Specifically, ARF2 is found to be a recently discovered component of the tomato ripening regulatory network that works with other ripening regulators. It is unclear how Ethylene Response Factors (ERFs) mediate tomato ripening, but sub-class E ERFs were found to be active during the process. Overall, both ethylene and auxin play a role in tomato ripening and ARF2 was found to be an important component of the ripening regulatory network.

ZhibiaoYe, from Huazhong Agricultural University, in Wuhan, China, told the group about the role of long non-coding RNA (lncRNA) in tomato ripening. In plants, the expression and origin of lncRNA are not well understood. By examining lncRNAs in the cultivated tomato Heinz1706 and the wild species LA1589, Ye was able to determine that lncRNAs are not abundant in the Solanaceae family. Less than 0.4% of the tomato and potato genomes contained lncRNAs. Ye also found a specific lncRNA called lncRNA-314 that likely evolved as a result of two important events. These two events were: an insertion of a retrotransposon into chromosome 10 of *S. pennellii* and a deletion that occurred in *S. lycopersicum*. Upon further analysis, lncRNA-314 was found to be present in the Heinz1706 tomato and silenced in the LA1589 fruit, contributing to the knowledge of the basis of origins of lncRNAs in plants.

Carmen Catalá, from Boyce Thompson Institute at Cornell University, spoke about using genetic diversity to understand fruit ripening regulation. Wild species tomatoes serve as a unique gene pool for a wide array of phenotypic variations. Although it is understood that much variation is a result of differences in gene expression, the genetic basis of this variation is unknown. Many gene expression differences in tomato are the result of differential *cis*-regulatory control. In order to distinguish the genes that show changes in gene expression due to *cis*- versus *trans*-regulation, Catalá and her team

conducted a study observing the F1 progeny of a cross between *S. lycopersicum* and *S. pimpinellifolium*. The fruit pericarp of the F1 hybrids was collected at various times throughout their development and analyzed by RNA-seq. With the data, *cis* and *trans*-regulatory gene variants were observed and sorted. By comparing the *cis*-regulatory effects to previous studies, Catalá and her team were able to identify *cis*-regulated variants in candidate genes that are related to secondary metabolite content and hormone biosynthesis among others. This study presented a foundation for expanded understanding of the gene regulatory effects underlying phenotypic variation displayed amongst tomato genotypes.

Barbara Blanco-Ulate, from UC Davis, shared information from her work about *Botrytis cinerea* interactions with unripe tomato fruit. As a tomato transitions from an unripe green to mature red, it has been noted that there is increased vulnerability in the fruit cell wall conferring necrotrophic pathogen susceptibility. *Botrytis cinerea* is one example of an opportunistic necrotrophic pathogen that attacks tomatoes during the ripening process when cell walls and associated structural changes are predominant. *B. cinerea* also displays a unique infection mechanism that hastens the ripening of the fruit. In the study, unripe tomatoes were infected with the pathogen and during the ripening process, the fruit wall composition was analyzed. It was found that during infection, the genes responsible for cell wall degradation were induced by the pathogen. The homogalacturonan pectins are a class of cell wall polysaccharides that are attacked by *B. cinerea* during the infection process. Overall, correlations were detected between the modification of the cell wall during infection of unripe fruit and the modification of the cell wall during the normal ripening process. The study provided confirmation and broader mechanistic insights pertaining to how microbes participate in the interaction between *B. cinerea* and its host.

Stacy Smith, from the University of Colorado, spoke about her work on macroevolution of flower color in Solanaceae. Comparing red and white flower genotypes, it has been noted that red flower varieties, which make up 1% of the Solanaceae family, show few functional mutations as they have evolved. On the other hand, it has been noted that white flower genotypes, the most common in the Solanaceae family, have suffered loss-of-function mutations as they have evolved, but have been able to regain pigmentation as well in some instances. Anthocyanin pigmentation is responsible for this red/purple flower color and altered flux through the pathway is responsible for the variation in anthocyanins and associated color. In other plant species, it has been determined that loss of R2R3-MYB gene function causes white flowers. Smith and her team conducted a study to determine if this was also the case in the Solanaceae. Indeed she confirmed that R3-MYB was the strongest candidate for floral phenotypes characterized by lack of anthocyanin production, while additional pathway mutations affected red to purple to pink color variation. This discovery demonstrates that understanding the underlying pathways and allelic variation can help explain the presence of rare and common traits including in this instance, flower color.

Theresa Hill, from UC Davis, spoke to the group about the genetics of pepper fruit size. Large fruit size in the Solanaceae is a result of plant selection through domestication. Six genes from tomato have been linked to fruit size. Previously, Hill and her team have tried identifying genes with similar roles in pepper. They discovered that many pepper QTL are distinct from the defined tomato genes contributing to this trait, and speculated that crop-specific mechanisms may contribute to fruit size variation. By looking at pepper lineages leading to large fruit, certain genomic regions were found to be conserved. Using biparental populations, QTL for both shape and size of fruit were found. Analyzing this information, loci for both fruit size and weight variation have been identified in pepper. As a result, new genes responsible for variation in pepper fruit size and shape are likely to be identified and genetically validated.

SESSION XIII • PLANT DEVELOPMENT AND REGULATION

CHAIRPERSON: NEELIMA SINHA (UC DAVIS, USA)

CO-CHAIRPERSON: TIM BATZ (CAL POLY POMONA, USA)

The 13th annual *Solanaceae* Conference gathered researchers and scientists from all over the world to discuss advances and applications related to this economically important plant family. Session XIII focused on plant development and regulation. The speakers explored topics ranging from domestication to inflorescence evolution and grafting vigor, each attempting to uncover hidden regulatory mechanisms and their developmental effects. The session opened with Dr. Jiménez-Goméz, whose work helped discover the effects of tomato domestication on circadian rhythms. A mutation in the EID1 gene aided tomato's survival to longer daylight hours as it shifted to regions far above the equator. Dr. Sheehan presented *Petunia* work in which the mutations in a single gene, MYB-FL, result in transitions in UV absorbance with larger effects in pollination syndromes.

Roots were another topic of developmental study. Dr. Kajala studied tomato root cell and tissue type specific gene expression in response to flooding and drought, revealing many genes which are differentially expressed in response to those stressors. Further studies may provide insights into genes conferring flood and drought adaptations present in tomato. The research of Dr. Frank investigated long distance RNA movement between rootstock and scion tissues, suggesting this exchange of nucleic acids has a role in the phenomenon of grafting-induced vigor. Dr. Lemmon analyzed transcriptional differences in developing tomato meristems to understand the evolution of inflorescence diversity in the *Solanaceae*. He helped uncover over 282 genes which may have large developmental and regulatory effects on reproductive morphology in the *Solanaceae*.

The invited speakers came from universities and institutions representing the global span of *Solanaceae* research. From a developmental and regulatory focus, the talks gave insights into how these dynamics compare and contrast in several areas of plant biology. As session co-chair, I believe the talks were representative of major plant systems including meristems, roots, and floral organs. The methods implemented in the investigations were both familiar and new to me. I was introduced to many new

technologies and concepts during my time as co-chair. The conference benefitted greatly from the discussion and interaction spurred by the authors and the insights of their presentations.

SESSION XIV • METABOLITES, FLAVOR AND QUALITY

CHAIRPERSON: CATHIE MARTIN (JOHN INNES CENTRE, UK)

CO-CHAIRPERSON: SASSOUM LO (UC RIVERSIDE, USA)

Speakers: Pr. Harry Klee, Drs. Gaurav Moghe, Alain Tissier, and Itay Gonda

Summary

Incorporating information on consumer preferences is important for developing new tomato cultivars, and fruit quality such as flavor is one of the target traits. However, breeding for good flavor is nearly impossible due to the genetic and biochemical complexity of this trait. Modern tomato varieties are deficient in volatile content and lack taste compared to old varieties. In order to restore good flavor in elite varieties, Pr. Klee and associates explored tomato germplasm to identify desirable alleles affecting flavor chemical composition.

In contrast, Dr Moghe and collaborators are investigating the evolution of acylsugar biosynthesis, which are specialized metabolites produced in the glandular heads of trichomes (hairs) in Solanaceous plants. The main objective of this research was to understand the biosynthesis pathway of acylsugar, and determine how this pathway evolved in the family Solanaceae. By characterizing the genes encoding the acyl transferase enzymes in several Solanaceae species they found that acylsugar biosynthesis has emerged via gene duplication events and specifically via whole genome triplication.

The third speaker in this session was Dr. Tissier, who discussed how glandular trichomes develop and differentiate, how they achieve their high metabolic productivity, and the importance of the flavonoid pathway in trichome development. Based on multi-omics approaches they identified two quantitative trait loci (QTL) as well as genes controlling trichome development. Additionally they found that genes for importation and degradation of sucrose are overexpressed in trichomes. They also proposed a metabolic model for tomato glandular trichomes.

In the last talk Dr. Gonda and associates investigated the production and accumulation of various metabolites affecting tomato fruit quality. Using a recombinant inbred line (RIL) population, they were able to map metabolic trait loci. Specifically, they identify 103 genes underlying acetate ester QTLs including a cluster of five carboxylesterases. They also found that lycopene biosynthesis is controlled by the *SIZISO* gene.