

Meeting report

Crops in all shapes and sizes

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A recent conference of plant biologists held in Mexico brought together scientists working on a wide range of species, from the model organism *Arabidopsis thaliana* to crops such as maize, tomato and rice. Appropriately for the locale, research relevant to major Central and South American crops was conspicuous. A few of the highlights in the areas of maize and tomato genetics and plant computational biology are reported here.

Maize genomics, genetics and epigenetics

Maize (corn, *Zea mays* L.) was domesticated from a species of wild teosinte, the common name for a group of annual and perennial species of *Zea* native to Mexico and Central America. Phylogenetic evidence suggests that maize arose from a single domestication event that occurred in Mexico about 9,000 years ago and which gave rise to a group of ancient landrace varieties. As the main center of origin and domestication, Mexico has the largest diversity of maize genetic resources. John Jones (Washington State University, Pullman, USA) presented evidence from fossilized pollen suggesting that the ancient farmers of San Andrés Tabasco in southern Mexico were cultivating an early form of maize about 7,300 years ago, 1,200 years before any previous archeological evidence of maize cultivation. He suggested that, in addition to serving as an ancestral food source, maize may have played a role as a driver of cultural development.

Despite the importance of selection-dependent bottleneck effects that drastically reduced genetic diversity, most maize

genes have retained high levels of nucleotide diversity compared with other cereals. Erik Vollbrecht (Iowa State University, Ames, USA) presented work on the *ramosa1* locus (*ra1*) showing that during the domestication of maize from teosinte, this locus experienced positive selection, as indicated by low *ra1* nucleotide variability in both maize landraces and modern inbreds. *ra1* encodes a putative C2H2-type zinc finger transcription factor that is unique to the Andropogoneae (the large grass tribe that includes maize and sorghum), and Vollbrecht suggested that the gene originated coincidentally with the evolution of a specialized short-branched spikelet pair distinctive of maize and its close relatives.

Maize is an ideal model plant in which to study the epigenetic basis of phenotypic variation. Paramutation is an epigenetic phenomenon that results in the establishment of meiotically heritable expression that depends on the ability of specific DNA sequences to communicate *in trans*. Vicki Chandler (University of Arizona, Tucson, USA) reported that paramutation at the maize *b1* locus is mediated by seven unique 853 bp non-coding tandem repeats that are necessary for this *trans* communication. Transcription of these repeats into small interfering RNAs (siRNAs) depends on *mediator of paramutation 1 (mop1)*, a gene encoding an RNA-dependent RNA polymerase most similar to *RDR2* in *Arabidopsis*. Chandler has strikingly found that the presence of siRNAs corresponding to tandem repeats in non-paramutagenic individuals indicates that the siRNAs are involved in, but not sufficient for, paramutation, opening up the possibility of new discoveries about the basis of large-scale genomic information.

Palomero Toluqueño is an ancestral popcorn landrace with one of the smallest genomes among Mexican maize. One of us (J-P V-C) described progress in sequencing this genome,

undertaken to explore landrace genomic diversity and to complement the sequencing of the inbred maize line B73 by the Maize Genome Sequencing Consortium. The total Palomero Toluqueño sequence generated represents coverage of approximately 3x the full genome and 20x the gene-enriched regions. Structural and functional analysis reveals a large number of hitherto unreported genes, suggesting that the ancient landraces contain a large pool of unexplored genetic diversity. This diversity should be potentially useful for generating new crops as well as for the study of the evolution and domestication of maize and other cereals.

Molecular mechanisms of tomato fruit morphology

Edible fruits are markedly diverse in size and shape. Breeding and mutation analysis in tomato have resulted in a diverse collection of germplasm, which provides a rich resource for studies on fruit morphology. Fruit morphological changes occur during ovary formation and/or during fruit formation, and so tomato varieties with different-shaped fruits can give insights into these developmental processes. Esther Van Der Knaap (Ohio State University, Columbus, USA) described the work of herself and colleagues on the mechanisms underlying tomato shape, and reported the identification of the gene *SUN*, one of the major genes controlling the elongation of tomato fruit. *SUN* was positionally cloned and found to encode a member of the IQ67 domain family. Van Der Knaap reported that the *sun* mutation responsible for the elongated shape of some tomatoes is the result of an interchromosomal duplication mediated by a retrotransposon - an unusual 24.7-kb gene duplication event mediated by the long-terminal repeat retrotransposon *Rider*. This event resulted in a new genomic context that increased *SUN* expression relative to that of the ancestral copy, culminating in an elongated fruit shape. This discovery shows that retrotransposons may be a major driving force in genome evolution and gene duplication, resulting in phenotypic changes in plants.

Despite the fact that the tomato genome sequence is not yet complete, the release of partial information by the Tomato Genome Consortium [<http://www.sgn.cornell.edu>], together with extensive genetic data and new tools for functional genomics, has allowed significant advances in this model crop. Fernando Carrari (Instituto Nacional de Tecnología Agrícola, Buenos Aires, Argentina) and his colleagues combine genetic, genomic and metabolomic tools to dissect genetic determinants of quantitative trait loci affecting the chemical composition of tomato fruit. Carrari reported work using metabolic profiling and phenotyping of a collection of interspecific introgression lines to identify quantitative metabolic loci (QML) distributed across the tomato genome. The physical mapping of the QMLs is being addressed by using genome sequence information, an integrated analysis of metabolite and transcript levels during fruit development. Carrari reported that five genomic regions have been

screened in detail and 127 candidate genes for regulation of metabolism during fruit ripening have been found. Candidate genes are being evaluated by a combination of virus-induced gene silencing and transgenesis. An integrated view of tomato fruit metabolism will help to uncover traits and targets with potential for improving fruit composition.

Computational challenges for the plant sciences

In the post-genomic era, data integration, analysis and interpretation are major factors limiting advances in biological research. Fortunately, a new generation of scientists well versed in both computational and experimental aspects of plant biology is rising to the challenge. Seung Rhee (Carnegie Institution, Stanford, USA) presented a new bioinformatics approach based on gene function correlation networks, developed in collaboration with Insuk Lee, to identifying genes that code for enzymes catalyzing the 'missing' steps in known metabolic pathways. On the basis of these predictions, her group chose 18 genes for experimental validation, and, in collaboration with other laboratories in the plant metabolomics consortium NSF2010 Metabolomics [<http://www.plantmetabolomics.org>], determined the metabolomic profiles of 18 *Arabidopsis* lines carrying homozygous knockout mutations in these genes. The different mutants showed distinct alterations in their metabolomic profiles, and mapping the altered compounds in each mutant line back to the relevant metabolic pathway enabled the bioinformatics-derived predictions to be validated.

Computational modeling has also been applied to the mechanisms underlying the characteristic grain pattern of wood, which is determined by the orientation of cells in the vascular cambium. Grain pattern remains approximately constant for a tree's life, but can reorient in response to injury. This reorientation response is critical to the health of the tree as the grain direction determines the movement of water and assimilates in the stem. There are two competing hypotheses to explain wood-grain patterning: one proposes that the orienting signal is mechanical strain in the cambium; the other that it is a concentration gradient of the plant hormone auxin in the plane of the cambium. Eric Kramer (Bard College at Simon's Rock, Great Barrington, USA) described a computer model developed by his group that supported the second hypothesis by providing quantitative predictions of auxin concentrations and their correlation with grain pattern in *Populus* after injury. Their model was validated by experimental measurements of auxin concentrations around an injury site in *Populus*.

One of us (RAG) presented the new software platform VirtualPlant [<http://www.virtualplant.org>], designed in collaboration with researchers at New York University. VirtualPlant enables the visualization, integration, and analysis of genomic data from a systems-biology perspective and simplifies the use of mathematical and statistical

methods to help summarize and quantify the data. As proof of principle, VirtualPlant was used to predict the key transcription factors that regulate *Arabidopsis* gene networks in response to organic nitrogen (for example, glutamic acid). One predicted network was validated, showing that regulation of the expression of the master clock-control gene *CCA1* by glutamine or a glutamine-derived metabolite directly regulates the expression of the key nitrogen-assimilatory genes. This work also discovered unexpected connections between nitrogen metabolism and the circadian clock in *Arabidopsis*. Regulation of *CCA1* by organic nitrogen signals may represent a novel input mechanism for nitrogen nutrients to affect plant circadian clock function.

In the age of genomics, collaboration is key to successfully addressing outstanding questions in plant biology. The new iPlant Collaborative project [<http://www.iplantcollaborative.org>] presented by Rich Jorgensen (University of Arizona, Tucson, USA) is likely to play a key role in advancing plant sciences in the years to come. This 5-year \$50-million program funded by the US National Science Foundation aims to develop an international cybercommunity of plant biologists, computational specialists and other disciplines to enable new conceptual advances in plant science. iPlant will initially provide services through a small, committed centralized core, and will gradually become distributed throughout the community. Jorgensen stressed that iPlant is “by, for and of the community”, and the problems addressed through it must be driven by specific, compelling, and tractable ‘grand challenges’ that serve the entire breadth of the plant sciences. Plant researchers around the world are encouraged to put forward proposals and participate in the project.

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