MicroRNA Regulation of Abiotic Stress in Tomato

The 7B-1 mutant of tomato is a potential candidate for hybrid seed breeding and stress engineering. To identify small RNAs linked to stress tolerance of 7B-1, Omidvar et al. profiled small RNAs between the 7B-1 mutant and wild type in response to abscisic acid and mannitol-induced stresses. Using small RNA sequencing, we identified known and novel miRNAs, including miR159, miR166, miR472, miR482, miR#A, and miR#D that are likely to facilitate the blue-light-specific enhanced tolerance of 7B-1 to abiotic stress. Our data could be used as a benchmark for future work aiming at miRNA engineering of stress tolerance in transgenic crops, while these miRNAs could serve as diagnostic markers for stress conditions, as they can coordinate the regulation of multiple stress-signaling pathways as demonstrated in our study.

A Gene Controls Apple Acidity

A gene designated Ma1 was reported as a candidate controlling fruit acidity in apple. Ma et al. report that functional divergence has occurred between the Ma1 gene and its allele ma1. The Ma1 gene encodes a transport protein that resides in the tonoplast and can move organic acids into the vacuole. In contrast, the ma1 gene encodes a truncated protein because of a single nucleotide substitution of G with A in the last exon and plays no role in the transport of organic acids from the cytosol into the vacuole. The frequency of the Ma1/Ma1 genotype is very low in apple cultivars but is high in wild relatives, which suggests that apple domestication was accompanied by selection for the Ma1 gene. In addition, the Ma1 gene is not the only genetic determinant of fruit acidity in apple, as variations in the malic acid content of mature fruits were also observed between accessions with the same genotype in the Ma locus.

Mechanisms Underlying Broad Spectrum Resistance

Genome-wide interactions between Xanthomonas oryzae pv. oryzae (Xoo) and rice resulting from a broad-spectrum hypersensitive reaction (BSHR) mediated by a new rice R gene, Xa39, were investigated by comparative dynamic transcriptomic profiles in the incompatible and compatible interactions using three related rice lines and a highly virulent Xoo isolate, PXO99. Results indicated that the gene network consisted of 27 genes in four groups of distinct functions involving leading to BSHR of rice in the sequential events from the avrXa39 x Xa39 interaction → signal recognition and transduction → protein modification → programmed cell death. Combined evidence suggests LOC_Os11g37759, one of a two-member CC-NBS-LRR gene family on rice chromosome 11, as the most likely candidate for Xa39 in rice and two genes, XopN and XopX, involved in the type III secretion system of Xoo as the most likely candidate genes for the corresponding avrXa39 in Xoo.

Wheat Chromosome 5A: Physical Map

A physical map is a fundamental prerequisite to obtain high-quality sequences of complex genomes like that of bread wheat. Barbaschi et al. employed a variety of assembly strategies, genetic and genomic tools, and complementary anchoring approaches to produce a high-quality physical map for bread wheat chromosome 5A. It has an anchored physical coverage of 75% for short arm and 53% for long arm with high portions (64 and 48%, respectively) of contigs ordered along the chromosome. Moreover, a rich platform of 5A genomic resources, including about 9000 high-quality bacterial artificial chromosome end sequences and thousands of molecular markers, specific for chromosome 5A, were produced and are now available for the research community. Syntenic regions to reference genomes (rice, Brachypodium, and sorghum) were highlighted along the 5A physical map allowing a better definition of the conservation and breakages of syntenic relationships and inversions with respect to the genetic order. The 5A physical map provides an invaluable resource for the release of a reliable high quality genome sequence of bread wheat, as a background for the assessment of genes and other functional elements and as a fundamental step to gain insight into the evolutionary aspects of bread wheat.

Novel SNP Markers for Soybean N Traits

Symbiotic N2 fixation in soybean is highly sensitive to limited water availability, and breeding for reduced N2 fixation sensitivity to drought is considered an important objective. There is a paucity of data on genes or quantitative trait loci that contribute to prolonged N2 fixation under drought in soybean. Dhanapal et al. used a collection of 373 diverse soybean genotypes grown in four field environments (two years
and two locations) and characterized for N derived from atmosphere (Ndfa), N concentration ([N]), and C/N ratio. Genome-wide association analysis resulted in 17, 19, and 24 SNPs with significant association with Ndfa, [N], and C/N ratio, respectively, in at least two environments as well as with the average across all four environments. These markers may be useful for pyramiding favorable alleles and to identify genotypes for comparative physiological studies.

**Genomic Selection For Wheat Scab**

Fusarium head blight, also known as scab, is a destructive disease of wheat and other cereals. In epidemic conditions, the disease leads to mycotoxin contamination of the grains and significant yield reduction. Selecting for scab resistance is a difficult task because of the polygenic nature of resistance and its interaction with the environment. Arruda et al. report that scab resistance can be predicted with DNA information (single nucleotide polymorphisms [SNPs]) with moderate to high accuracy. Using a regression approach called genomic selection, the authors showed that the predictive ability increased with the number of SNPs, the number of wheat breeding lines used to train the model, and varied greatly among different statistical models. In addition, a striking advantage of SNPs over pedigree information was observed when predicting scab. The study supports genomic selection as a promising breeding strategy for improving the resistance levels of this important wheat disease.

**Soybean Collection Searched for Genes**

The USDA Soybean Collection contains many valuable genes that hold potential to improve the cultivated version of soybean. Finding these genes would be benefited by knowing more about the ancestry and diversity of the soybean collection as well as the association between genetic markers and valuable phenotypic traits. Using historical phenotypic data and dense genetic marker data on the entire USDA soybean collection, Bandillo et al. discovered how samples in the collection relate to one another and the importance of country of origin and maturity group in determining relatedness. Several strong associations between genetic markers and protein and oil were identified, which help narrow the search for genes controlling these important and genetically complex traits. The findings of Bandillo et al. (2015) will assist soybean researchers in their pursuit of genes that can be used to further improve soybean for agricultural production.

**Collard Landraces Harbor Genetic Diversity**

Landraces have the potential to provide a reservoir of genetic diversity for crop improvement to combat genetic erosion of the food supply. A landrace collection of the vitamin-rich specialty crop collard was genetically characterized to assess its potential for improving the diverse crop varieties of Brassica oleracea. Pelc et al. report that the collard landrace collection harbors substantial genetic variation. The landraces had twice the polymorphic markers and 10 times the unique alleles of any of the other crop varieties examined. In addition, a low level of population structure and sufficient marker coverage will allow for future genome-wide association studies of economically important traits in this collection.

**Comparative Genome Analysis Reveals Divergent Genome Size Evolution in a Carnivorous Plant Genus**

The nuclear genome size of eukaryotic organisms does not correlate with organismic complexity (C-value paradox). Vu et al. sequenced the genomes of two carnivorous plant species, Genlisea nigrocaulis and G. hispidula, with the aim to find reasons for and consequences of the 18-fold genome size difference. They suggest a common ancestor of intermediate genome size and a rapid genome size evolution in opposite directions with whole genome duplication (WGD) and retrotransposition in one clade and retroelement silencing and deletion-biased double-strand break repair in the other clade. Genome shrinkage and expansion took place under similar environmental conditions and independent of geographic distribution and life strategy. Shrinkage of small genomes was found to be counteracted by WGD. Thus it is argued that (i) large genome size variation can be selectively neutral; (ii) many of the repeats of the larger genome are dispensable, challenging their functionality; and (iii) long-term genome shrinkage is enabled by recurrent WGD.

**Wild Tomatoes Resist Emerging Pathogen**

Bacterial speck disease is a persistent problem on tomato, and current varieties do not have resistance to increasingly common race 1 strains of the causative pathogen. Bao et al. identified accessions of a wild relative of tomato that are resistant to a race 1 strain. Genetic analysis of one accession indicated that quantitative loci on chromosomes 2 and 8 contribute to the resistance. The region on chromosome 2 has a gene, qRph1, that is a good candidate for conferring resistance as it encodes a receptor-like protein kinase and is induced specifically by pathogen-associated molecules. In the future, the qRph1 gene might be useful for enhancing resistance to race 1 strains and its characterization could provide novel insights into the plant immune system.

**Genomics Push Barley Breeding**

Progress in barley genetics and genomics research has been continuously moving forward for the last decade. Silver et al. report on the genome zipper and population sequencing as valuable tools for barley research and breeding. The combination of both should allow users to effectively accomplish fine mapping schemes and physically delimit those genomic regions containing interesting traits, facilitating a directed use in barley breeding.

**Population Genetics and Structure of Foxtail Millet**

Foxtail millet is one among the most ancient crops of dryland agriculture, valued for its drought tolerance and short duration and for its nutritionally superior grain. Sequencing germplasm resources of foxtail millet enhances effective management and use of germplasm resources in breeding programs. Through a genotyping-by-sequencing approach, Upadhyaya et al. characterized foxtail millet germplasm accessions including core collection using 17,714 high-quality SNPs and revealed that foxtail millet germplasm accessions are highly diverse and structured along both on the basis of race and...
associations. This study and SNP data will provide a foundation for exploration of foxtail millet diversity and for mining novel alleles and mapping genes for economically important traits.

Accessions of race indica are highly differentiated from those of maxima and moharia. A genome-wide association study on plant pigmentation and days to 50% flowering using the high-quality SNPs resulted in identification of significant marker–trait associations.