

## Stress Response in Strawberry

Plant Genome 12–23

Strawberry is an important crop that belongs to the Rosaceae family, which includes other agronomically important plants including other berries, several fruit trees, and ornamental species. Unfavorable environmental conditions such as extreme temperatures, soil salinity, and drought can devastate strawberry crops. In an advance toward understanding the plant's response to these stresses, the authors report an extensive description of the global gene expression of strawberry plants exposed different stress conditions to which strawberry crops are often exposed. The substantial number of expressed sequence tags (EST) generated allowed the identification of several expressed genes that had not been observed before in any Rosaceae species, including six genes homologous to stress-related genes from other species. The large amount of data provided by this work represents a useful resource to advance our understanding of the stress-response mechanisms in strawberry and, potentially, in valuable tree crops in the Rosaceae family. ■

## Association Mapping in Alfalfa

Plant Genome 24–35

Marker-assisted selection could enhance the efficiency of selection for yield. The authors identified markers related to biomass yield and cell wall composition in a tetraploid alfalfa breeding population by association mapping. Using simple sequence repeat DNA markers, they detected 15 alleles that showed a strong association with yield in at least one of five environments; most alleles were associated with yield in multiple environments spanning Iowa, New York, and Quebec. Only one allele showed strong association with acid detergent fiber and one allele with acid detergent lignin. Alleles associated with traits could be directly applied to a breeding program using marker-assisted selection. ■

Published in The Plant Genome 3:iv–v. Published 18 Dec. 2010.

doi: 10.3835/plantgenome2010.10.0002rh

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## RNA-seq of the Melon Fruit

Plant Genome 36–46

The melon fruit is an important crop and model system for the genomic study of both fleshy fruit development and the Cucurbitaceae. Portnoy et al., report on a method to obtain high quality RNA for RNA-seq using 454-pyrosequencing methodology. The global digital expression data was validated indicating that high-quality, non-biased cDNA for next-generation sequencing can be prepared from mature, fleshy fruit, which are notorious for difficulties in RNA preparation. ■

## Minor Impact of Plant Density on Gene Expression in Barley and Maize Seedlings

Plant Genome 47–54

The ability of crop plants to tolerate high planting density results in overall yield increases. Thus, plant breeders have been selecting for more density tolerant plants to increase plant density and grain yield. However, little is known regarding gene expression changes resulting from the stress of high planting density. St. Pierre and colleagues examined barley and maize seedlings and showed that high planting density results in morphological changes; however, only minor changes in gene expression were detected. These results indicate that plant density stress likely alters gene expression in a subtle and tissue- and developmentally-specific manner. ■

## Rsv3 Locus Complexity Demonstrated by Soybean Genome Sequence

Plant Genome 55–64

Soybean mosaic virus (SMV) disease is one of the most devastating viral diseases in soybean production worldwide. There is an increasing need for soybean germplasm with multigenic resistance to SMV because of the rapid evolution of strains that overcome single gene resistance. Suh et al. (2011) used populations to examine *Rsv3*, as it confers resistance to SMV strains that overcome *Rsv1* and to additional strains when pyramided with *Rsv1*. Examination of the soybean genome sequence delimited the *Rsv3* locus to a 154 kbp interval on chromosome 14. Mapping of numerous new markers confirmed parallel alignment between the genetic and sequence maps in the *Rsv3*-containing region and its flanking regions. The *Rsv3* region contains 11 genes, five of which are members of a well-characterized superfamily of CC-NB-LRR resistance genes. However, the genes associated with *Rsv3* belong to a subclade different from that of the previously characterized soybean R genes. These results are useful in elucidating *Rsv3* molecular structure and function and interaction with SMV, and provide tools for breeding durable SMV-resistant soybean cultivars. ■

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## Genomic Selection found Accurate in a Wheat Breeding Program

Plant Genome 65–75

Genomic selection uses phenotypic and genome-wide DNA marker data from previous breeding cycles to predict the value of new breeding lines on the basis of marker data alone. These predictions enable breeders to increase selection intensity and accelerate breeding cycles by reducing time consuming, expensive phenotyping in early selection stages. Heffner et al. investigated genomic selection prediction accuracy for 13 agronomic traits in a wheat breeding program and discovered that the average accuracy of genomic selection was comparable to phenotypic selection and was more accurate than conventional marker-assisted selection. Averaged over several multi-trait selection indices, genomic selection was more accurate than phenotypic selection alone. The results from this study suggest that the use of genomic selection in plant breeding could significantly increase the genetic gain per unit time and cost. ■

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## Hot News from Cold Barley

Plant Genome 76–91

Barley is a versatile crop in terms of its end uses and an excellent model system for identifying genes necessary for addressing the effects of climate change. VonZitzewitz et al. used genome wide association mapping to locate genes determining low temperature tolerance in barley. This information will allow breeders to efficiently develop barley varieties adapted to environments where low temperature stresses may occur. These varieties will provide farmers with a cereal crop alternative and end-users with new sources of supply. ■

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## SNP Development in the Grain Amaranths

Plant Genome 92–101

The grain amaranths (*Amaranthus* sp.) are important pseudo-cereals native to the New World. During the last decade they have garnered increased international attention for their nutritional quality, tolerance to abiotic stress and their potential as an alternative crop uniquely suited for subsistence agriculture. Unfortunately, only a few molecular investigations have been reported for the grain amaranths and even fewer molecular tools, needed for advanced genomic studies, have been developed. Maughan et al. report the development of the first single nucleotide polymorphism (SNP) assays for amaranth as well as the first complete genetic linkage map in the genus. The SNP assays were developed on the KBioscience KASPar genotyping chemistry using a Fluidigm IFC Access array. The utilization of this chemistry combined with the nano-fluidic Fluidigm chip reduced the overall data point cost to US\$0.05 per data point—an important feature considering that the implementation of marker-assisted breeding strategies often requires the generation of thousands of data points per population. The SNP markers and linkage map reported are essential steps toward the development of marker-assisted selection programs for recalcitrant traits of agronomic importance in amaranth. ■