

## Putting DNA Sequencing to Work for Plant Breeding

Plant Genome 92–102

Rapid advances in DNA sequencing technology can now be put to work for plant breeding and genetics studies. Poland and Rife give perspective on the many different applications of a new genotyping approach called “Genotyping-by-sequencing” and how it can be used to address a range of research questions. The new genotyping approach capitalizes on the huge investment in technology needed to reach the “\$1000 human genome.” The authors conclude that many areas of research are becoming very tractable due to these new technologies and approaches. Continual increases in sequencing output will lead to additional opportunities for breeding improved crop varieties that are needed to address growing populations, decreasing farmland, and climate change. ■

## Predicting Wheat Yields using Next Generation Sequencing

Plant Genome 103–113

Rapid advances in “next-generation sequencing” can now be put to work to improve crop yields through genomic-assisted breeding. Poland et al. report the use of genotyping-by-sequencing for developing high-density DNA markers on wheat breeding lines. Several imputation methods including a newly developed algorithm for unmapped markers were compared and found to have little effect on genome-wide prediction accuracy, but there were differences with respect to prediction bias. The high-density markers were then used in genomic selection models to generate predictions for yield and important agronomic traits. When used for genomic predictions of yield, the model based on GBS markers had significantly higher accuracy than with the previous marker platform. The low-cost and flexibility of genotyping-by-sequencing make this an excellent marker platform for use in genomics-assisted breeding. ■

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## Single Nucleotide Polymorphisms Identification, Characterization, and Linkage Mapping in *Chenopodium quinoa*

Plant Genome 114–125

*Chenopodium*, commonly known as the goosefoot genus, includes a wide array of species native to all inhabited continents. Many *Chenopodium* species are adapted to arid and/or saline environments and are notorious as invasive weed species, including *C. album* (lambsquarters) and *C. berlandieri* (pigweed). At least four species in the genus were domesticated anciently, either as vegetable or seed crops. One of these, the Andean species *C. quinoa* has risen from a neglected subsistence crop of indigenous farmers to become an important export commodity of the Andean nations of Bolivia, Peru, and Chile. Notable is the 2011 declaration of the Food and Agriculture Organization that 2013 is the official International Year of Quinoa. Maughan et al. report the identification of 14,178 putative single nucleotide polymorphisms (SNPs) using a genomic reduction protocol, as well as the development of 511 functional SNP assays. Linkage mapping of the SNPs in two recombinant inbred line populations produced an integrated linkage map. The SNPs identified here represent important genomic tools needed in emerging plant breeding programs for advanced genetic analysis of agronomic traits in quinoa. ■

## Association Mapping Identifies Markers for Grain Quality

Plant Genome 126–135

Grain quality in sorghum is an important criterion determining the end-use value of the grains. Sukumaran et al. discovered eight single nucleotide polymorphisms associated with grain quality traits in sorghum. A diversity panel of 300 sorghum accessions was analyzed using 1536 single nucleotide polymorphism markers for ten grain quality traits. Genetic diversity and population structure analysis identified five subpopulations that closely followed the races (durra, kafir, caudatum, guinea-caudatum, and zerazera-caudatum) in this diversity panel. Among the traits kernel hardness and acid detergent fiber showed variations among the subpopulations and races. Markers were identified for kernel hardness, calcium content, phosphorous content, and starch content in the grains. These identified markers could be used for improving grain quality traits in sorghum and related cereals. ■

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## Genomic Prediction of Genetic Values for Resistance to Wheat Rusts

Plant Genome 136–148

Stem and yellow rusts continue to cause major economic losses in various parts of the world. New races have caused yield losses even in areas where the rusts have rarely been detected and are more threatening to wheat worldwide than older races. Regions with vulnerability to yellow rust include, among others, the United States, Asia, and Oceania. Stem rust has also become epidemic in Africa. Durable resistance to the rust diseases of wheat can be achieved by developing lines that have race-nonspecific adult plant resistance conferred by multiple minor slow-rusting genes. Genomic selection is a promising tool for accumulating favorable alleles of slow-rusting genes. Ornella et al. studied five CIMMYT wheat populations evaluated for resistance which were used to predict resistance to stem and yellow rusts using 1400 DArT molecular markers and several statistical models. Results show that prediction ability for yellow rust was lower than for stem rust, probably due to differences in the conditions of infection of both diseases. For stem rust the correlation between predicted and observed values was greater than 0.50 in most evaluations, whereas for yellow rust, correlations ranged from 0.0637 to 0.6253. Results confirmed reports about the additive nature of rust resistance and also indicate that genomic selection is a promising tool for breeding to rusts resistance in wheat that will allow increasing genetic gains in shorter period of time. ■

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## Characterizing Genomes with Junction Sequence Analysis

Plant Genome 149–163

The assessment of genetically modified (GM) crops for regulatory approval currently requires a detailed characterization of the DNA sequence and integrity of the transgene locus. In addition, molecular characterization is a critical component of event selection

and advancement during product development. Typically, molecular characterization has relied on Southern blot analysis; here Kovalic et al. describe the use of recently emerged sequencing technologies along with novel “junction sequence analysis” bioinformatics in a new method for achieving molecular characterization of a GM event without the need for Southern blot analysis. They examine both simple and complex GM lines and demonstrate that the new method provides molecular characterizations equivalent to the current Southern blot based method. The new method, which may be considered a digital equivalent to Southern blot analysis, offers multiple advantages over current approaches, most notably its simplicity, efficiency, and consistency, and provides a viable alternative for efficiently and robustly achieving molecular characterization of GM crops. ■

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## Mapping QTL Affecting Agronomically Important Traits in Oat

Plant Genome 164–175

Hizbai et al. investigated the seed oil content and fatty acid profile in a population of oat progeny derived from a cross between parents with high and low oil contents. A new genetic map was developed, and the authors estimated that there are at least eight map regions containing genes that affect oil or fatty acid components. It was notable that all QTL had a similar pattern of effects across different oil-related traits, differing mainly in magnitude of effect. These results suggest that each region may contain similar genes that affect oil synthesis or accumulation in similar ways. Possible biochemical mechanisms are discussed. In addition, nine map regions had effects on plant height, heading date, lodging, and protein content. ■