Gene Expression Based Fertilization Strategies

Gene expression data can accurately reflect the growth and metabolic status of plants, with which we can predict and monitor the nutritional requirements of plants and then derive accurate fertilization strategies. In this study, Zhang et al. verified the feasibility and workability of gene information-based fertilization strategies and depicted the specific nutritional requirements of grapevine in terms of gene expression levels. The results showed that grapevine needs more P at the flowering stage, more N at the first berry expansion stage, less nutrients at the seed stone hardening stage, and more P and K at the second berry expansion stage and the veraison stage. ■

Constructing a Hierarchical OGR Map

Different levels of orthologous genomic regions (OGRs) play an important role in addressing various biological problems such as detecting both large-scale and small-scale genomic changes. Minkin et al. reported that a multiple-level map of OGRs could be more comprehensive than the single-level map. However, only a few studies exist concerning such integrated maps of OGRs. Based on different types of conserved genomic markers, we developed a method to construct a hierarchical map of OGRs between two closely related genomes. Using two cucumber genomes as a case study, the results indicated that at each level of OGRs many genomic changes were detected, although their divergence time is very short. The map of OGRs as well as genomic changes would be a useful resource for studying cucumber diversity of genomes and phenotypes. ■

Predicting Phenotypes in Forage Grasses

Genomic prediction allows the prediction of performances of families and individuals based on their genotypes. Fè et al. investigated the accuracy of predictions in forage perennial ryegrass. So far, genomic prediction has been tested mainly in crops farmed as homogeneous varieties (all plants have the same genotype), while forage grasses are grown in heterogeneous families in which single plants have different genotypes and the control of the genetic variation is far more complex. Different traits were predicted in different kinds of breeding material. Accuracies of the predictions were high for all traits both between and across different breeding materials.

That will allow the implementation of such prediction technique into the breeding program, likely leading to significant genetic gains in a shorter period of time. ■

Advancing Diploid Potato through Selfing

Most diploid potato plants are self-incompatible and will not set fruit on selfing, making the development of inbred lines difficult or impossible. Peterson et al. found self-fertile plants segregating within an F1 potato population then used a whole genome scan to observe the approach to homozygosity after three generations of selfing. Many unfruitful and weak plants had to be discarded in each generation resulting in more heterozygosity in the surviving population than expected based on predicted gene segregation. Pollen tube growth was observed in styles of both fertile and nonfertile plants ruling out the usual mechanism of self-incompatibility where pollen tube growth is arrested in styles of nonfertile plants. Inbred line development in diploid potato is limited to rare self-fertile genotypes that tolerate substantial inbreeding depression. ■

Unravelling Durum Leaf Rust Resistance

Leaf rust is increasingly impacting durum wheat production with the recent appearance of *P. triticina* races with virulence to widely grown cultivars in many durum producing areas worldwide. Aoun et al. report the identification of all-stage and adult-plant resistance in durum wheat accessions to several *P. triticina* races from the United States and Mexico. Thirty-seven significant genomic loci were associated with leaf rust response using the association mapping approach. Fifteen loci were previously unknown for wheat leaf rust resistance. Thus, this study provides information toward the development of tightly linked markers for marker-assisted selection of leaf rust resistance in breeding programs and to broaden the relatively narrow leaf rust resistance base in durum wheat germplasm. ■

Autopolyploid Relationship Matrices with AGHmatrix

The improvement rate in autopolyploid species breeding has been limited compared with their diploid counterparts, mainly because of a lack of software and methods for the prediction and selection of autopolyploids. Amadeu et al. developed an R package to construct the relationship derived from pedigree information, taking the genetic particularities of autopolyploids into account. Using this new package, we estimated the level and effect of double reduction in an autotetraploid blueberry breeding population. We found that for all the traits, the models that account for autopolyploidy create a better fit than a diploid inheritance model. This freely available package is unique, as it can create genetic relationship matrices for

different levels of ploidy, which can in turn be used by breeders to fit mixed models in the context of breeding value prediction. ■

Agronomic Performance Traits Mapped in Common Bean

Multiple traits, such as days to flowering and maturity, plant architecture, and seed weight, contribute to higher yield in common bean. Dissecting the genetic architecture of these traits can accelerate the breeding process for yield. Moghaddam et al. used a genome-wide association study to discover multiple genomic regions and candidate genes associated with six critical agronomic traits that contribute to yield. In particular, we discovered regions that account for 21 to 33% of the variation in plant architecture traits. These discoveries provide a starting point to confirm the genes that control important features of common bean and will facilitate the breeding of improved bean varieties. ■

AlphaSim: Simulation Software

Simulation is a rapid and cost effective way to develop and test breeding program designs. Faux et al. report a newly developed software package for the simulation of breeding programs. AlphaSim can simulate sequence, genotypic, phenotypic, and pedigree data in a wide range of population types (e.g., animal breeding, plant breeding, human genetics, natural populations). AlphaSim emphasizes flexibility, computational efficiency, and ease of use. Populations can have almost any pedigree structure, almost any type of selection, a wide range of genotyping platforms, and multiple traits with a wide range of alternatives for genetic architecture. Additionally, AlphaSim also includes features for genome editing, manipulating the recombination rate and its genetic architecture, performing optimal contribution selection, and other "tricks." ■

Forage Grass Transcriptomes Sequenced

Understanding the behavior of genomes in interspecific hybrids, such as Festulolium (grass hybrid *Festuca x Lolium*), requires distinguishing parental alleles in subsequent generations of hybrid progeny. Stočes et al. report the reconstruction and annotation of transcribed genes in two forage grass species: meadow fescue (*F. pratensis* Huds.) and Italian ryegrass (*L. multiflorum* Lam.). Single-nucleotide polymorphisms (SNPs) that distinguish both genomes were identified in thousands of genes. With these SNPs, the genomic constitution in hybrid progeny derived from *Festuca x Lolium* crosses can now be studied with high resolution. Furthermore, they can be used to study allele-specific gene expression dynamics in hybrid genomes, which can play a key role in breeding of elite Festulolium cultivars with improved agronomic performance. ■

Improving Genetic Gain in Potato

Potato breeders consider a large number of traits during cultivar development and progress in conventional breeding can be slow. Slater et al. investigate opportunities for the application of genomic selection to potato, including novel breeding program designs. They consider the autotetraploid and heterozygous genetic nature of potato, the rate of decay of linkage disequilibrium, the number of required markers, the design of a reference population, and trait heritability. They calculate the expected accuracy of genomic selection for four key traits of varying heritability and propose that it will be reasonably accurate. They then compare the expected genetic gain from genomic selection with the expected gain from phenotypic and pedigree selection, and find that genetic gain can be substantially improved by using genomic selection. This finding will accelerate breeding and the improvement of this important crop. ■

Genomic Prediction of Kernel Regression Models

In genomic selection, genotype × environment interaction (G × E) can be modeled using linear genomic information (linear kernel) or nonlinear genomic information (Gaussian kernel). Cuevas et al. predict unobserved individuals in environments by using genomic G × E models with linear and nonlinear kernels and compare their prediction accuracy in wheat and maize data sets. For the wheat data, the genomic nonlinear kernel model had accuracies up to 17% higher than that of genomic linear kernel, whereas for the maize data set, the genomic nonlinear kernel model had accuracies up to 5 to 6% higher than the genomic linear kernel model. The superiority of the nonlinear kernel coupled with the G × E model is due to its more flexible structure that allows accounting for small, more complex marker main effects and marker-specific interaction effects. ■

Assembly Scaffolding with RNA-Seq Data

Short second-generation sequencing reads make assembly difficult, leading to fragmented genomes and gene annotations. Song et al. report a new highly efficient tool, Rascaf, that leverages the long-range contiguity information from intron spanning RNA-seq read pairs to detect new contig connections. Rascaf simultaneously improves an assembly and its gene annotations, producing longer scaffolds, more accurate scaffolds, and more complete gene models. The new method is highly precise and finds thousands of new verifiable connections in several draft Rosaceae genomes. Lightweight and practical, it can be incorporated into genome sequencing pipelines to improve an assembly and its gene annotations. ■

Identification, Characterization of QTL for Shattering in *Japonica* Rice Landrace Jiucaiqing

Easy shattering reduces yield from grain loss during rice harvest. Cheng et al. characterized a nonshattering *japonica* rice landrace Jiucaiqing from Taihu Lake valley in China. Four putative QTL for shattering were detected in Jiucaiqing, and the $qSH1^{JCQ}$ was fine mapped to a 98.4-kb region. The QTL $qSH1^{JCQ}$ can decrease shattering by inhibiting expression of shattering related genes (*qSH1*, *OsCPL1*, *Sh4*, *SH5*, and *SHAT1*). The elite allele identified in this study could be useful for rice breeding. ■

Sclerotinia sclerotiorum Resistance in Sunflower

Basal stalk rot (BSR) caused by *S. sclerotiorum* is a devastating disease of sunflower in the cool temperate areas of the world. Talukder et al. dissected BSR resistance segregating in a sunflower mapping population using currently available genomic tools. Both ubiquitous and environment-specific quantitative trait loci (QTL)

were identified across different positions in the sunflower genome, each of which explained moderate to high phenotypic variations for BSR resistance. Markers tightly flanking the important QTL were released for use in marker-assisted selection breeding in the development of BSR resistant sunflower hybrids. ∎

Plant CRISPR Hits and Misses

Compared with the common chemical and radiation mediated mutagenesis methods used in plant breeding programs, editing the plant genome using CRISPR-Cas9 technology offers a more precise and effective alternative for generating novel plant traits. Wolt et al. review current understanding of how CRISPR designs affect both efficiency of obtaining intended edits as well as the potential for off-target edits. As new technology with important implications for crop improvement, regulators need assurances that unanticipated downstream effects originating from off-target edits can be effectively minimized using CRISPRs that are designed and targeted with a high degree of specificity. Improved design tools that better discriminate target and potential off-target sites in plant genomes, that incorporate consideration of the designed nuclease fidelity and selectivity, and that are validated will help to increase confidence on the part of scientists, regulators, and the public of the safety and benefits of plant genome editing for crop improvement. ∎

Novel Leaf Rust Resistance Loci

The short-lived nature of leaf rust resistance (*Lr*) genes necessitates a continuous search for novel sources of resistance in wheat. Li et al. performed a genome-wide association study on a panel of 1596 wheat accessions and identified 14 quantitative trait loci (QTL) for leaf rust resistance at a false discovery rate (FDR) of 0.01. Of these, six are novel loci in bread wheat and are valuable additions to the leaf rust resistance gene pool. In addition, another 31 QTL were significantly associated with leaf rust resistance at a FDR of 0.05, and some of them are also useful sources of resistance for wheat breeding. ∎

Genomics Accelerate Peanut Breeding

In the breeding process, rapid and accurate genome-wide genotyping technologies are required to carry out selections based on genome data. However, in peanut, time-consuming methods had been used for analyzing large numbers of DNA markers across many samples. Shirasawa et al. performed a whole-genome resequencing analysis on the breeding lines to identify genome-wide DNA markers and developed the target amplicon sequencing technique to genotype the markers, which cover the entire peanut genome. Using the genome information and the techniques, genome-wide genotypes of the breeding populations were easily and rapidly determined. This strategy made it possible to achieve genomics-based breeding in peanut. ∎