Improved Soybean Seed Phosphorus Partitioning

Soybean seeds have an effective deficiency of the critical nutrient phosphorus, as well as certain critical micronutrients, due to the presence of the antinutritional compound phytic acid. Phytic acid can account for as much as 72% of total phosphorous in typical soybean seed, which is all but indigestible by nonruminant animals. Gillman et al. report on genetic analysis of mutant alleles from two independent sources, which when combined resulted in almost complete elimination of antinutritional phytic acid. The atomic composition of modified seeds was found to be unaltered as compared to typical seeds. As a result, the potential bioavailable phosphorus, and certain critical micronutrients, is dramatically enhanced and should allow for improved human and animal nutrition from soybean derived foods and feed.

MaizeCyc: A Network of Maize Metabolic Genes and Pathways

MaizeCyc, the maize metabolic gene network and the free online database, provides information on about 391 metabolic and transport pathways, 8899 genes acting as enzymes and transporters, and 1450 compounds. Monaco et al. provide insights on the development of the metabolic network for maize, a tutorial on how to use the database, and an analysis of the maize genes expressed in leaf, root, anther, embryo, and endosperm with reference to the reported metabolic pathways in the database. In the comparative analysis of samples we found that 1062 differentially expressed metabolic genes mapped to 524 unique enzymatic reactions associated with 310 pathways. The article also provides insights on the expression of genes mapped to the chlorophyll, phenylpropanoid (lignin), anthocyanin, and beta-carotene biosynthesis pathways.

Genomewide Markers Control Background Noise

Association mapping relies on finding clear signals of marker-trait relationship amidst a sea of background noise. Such background noise is due to other genes found elsewhere in the genome. Previous approaches have relied on global, across-genome corrections for background noise. Bernardo proposes two models that make background-noise corrections specific to each chromosome being tested. From simulation experiments, he found that these two new models are superior to previous models that have been routinely used for association mapping in plants.

Accuracy of Genomewide Selection

Instead of evaluating potential new varieties in expensive field trials, large numbers of generic DNA markers can be used to predict the performance of experimental lines for different traits. Combs and Bernardo report on how the accuracy of DNA-based predictions varies according to three key factors: number of lines in the training population used to calibrate the prediction model, importance of genetic versus environmental effects on the expression of the trait, and number of chromosome segments underlying the trait. Combs and Bernardo discovered that even if all these factors are kept constant, the accuracy of DNA-based predictions varies among different traits. Yield traits had the lowest prediction accuracy in maize, barley, and wheat. Nevertheless, the predictions were accurate enough to enable screening of large numbers of experimental lines.

Genomic Selection Accuracy in Wheat

The marker-assisted selection theory has recently shifted from the use of a few markers targeted in quantitative trait locus (QTL) to the use of many more markers covering the whole genome. To be useful for breeding purposes, the accuracy of this genome estimate of breeding value (GEBV) should not be worse than the estimation based on phenotype. Storlie and Charmet designed cross-validation methods (CRV) to simulate genomic selection (GS) for yield in a wheat breeding program with data of 318 genotypes grown over an 11-yr period at six locations in France. Four cross-validation methods were designed: CVSW (cross-validation-specific without location as factor), CVSWO (cross-validation-specific without location as factor) and CVRWO (cross-validation-random without location as factor) and CVRW (cross-validation-random with location as factor). Results suggest the accuracy of the CRV methods using specifically selected genotypes (RM = 0.20) based on years grown were significantly less than methods using randomly selected genotypes (RM = 0.40–0.50). These results imply wheat yield is more difficult to predict for unknown, futuristic years than standard CRV methods suggest.
The Role of Genotype Validated Pedigrees

Individuals who differ from their designed mating scheme can be problematic for a breeding program. When undetected, such rogues may confound attempts of marker-assisted selection. Lucas et al. demonstrate genotype validated pedigrees are an immediate and significant benefit provided by molecular markers. Genotypes from several accessions and populations of biparental design suggest rogues are more common than expected. Mistakes can often be traced to human error or outcrossing events and are shown to affect the development of genetic maps and marker-trait associations.