Understanding Resistance Genes to Combat Stem Rust

Plant Genome 109–120

Researchers from a wide range of locations (Washington, Florida, Scotland, Minnesota, Lativa, and Iran) have initiated a project to clone and characterize genes that provide resistance to rusts that attack many plant species but are particularly destructive on cereal crops. The group's work centers on work with the barley resistance gene Rpg1 as well as the rpg4/Rpg5 complex locus.

The Rpg1 gene encodes a unique protein kinase with dual kinase domains, an active kinase, and a pseudokinase. Function of both domains is essential to confer resistance. The rpg4 and Rpg5 genes are closely linked and function coordinately to confer resistance to several wheat stem rust races, including the race TTKSK (also called Ug99) that threatens the world's barley and wheat crops.

Stem rust can seriously damage the wheat and barley crop if not vigorously combated and these researchers believe that the best way to defend against stem rust is by deploying effective resistance genes. To deploy those genes, we need to understand how they work. ■

Comprehensive Association Studies May Be in Economic Reach

Plant Genome 121–133

This large group of researchers from Cornell, USDA, and Roche Applied Science state that if the discovery of maize single nucleotide polymorphism (SNP) markers on the order of millions is to be economically viable, the use of low cost, next-generation DNA sequencing technologies is required.

The researchers aimed to adapt hypo-methylated partial restriction gene-enrichment sequencing to a massively parallel pyrosequencing platform and to develop a read-to-reference based SNP calling pipeline for short reads that maximizes SNP detection power, while controlling the number of detected false-positive SNPs.

Despite various limitations, a considerable number of SNPs were discovered at an acceptably low false discovery rate to construct high-density multiplexed genotyping products, but sequencing of additional maize inbred lines is needed to construct an SNP dataset with low ascertainment bias that is appropriate for phylogenetics or population genetics studies. The SNPs identified in this study, however, are immediately applicable for fine mapping of complex traits in the Intermated B73 × Mo17 population.

The researchers estimate the cost of SNP discovery in this study at $0.38/SNP, yet note that several aspects of the molecular methods used here can be optimized for much higher sequencing yield and broader genome coverage. Optimization, combined with further advances in high-throughput sequencing yield, longer read-lengths, lower error rates, and cheaper run costs, can further reduce the cost of SNP discovery in diverse maize, such that several million gene-enriched SNPs needed for comprehensive association studies is an economic possibility. ■

Building an Integrated Resource for Barley Linkage Maps

Plant Genome 134–140

A large group of researchers from Oregon, Montana, California, Minnesota, and Scotland have integrated new single nucleotide polymorphism and diversity arrays technology loci in barley with morphological loci and representative simple sequence repeat; sequence tagged site; and restriction fragment length polymorphism markers to prior quantitative trait locus (QTL) information. Malting quality QTLs were chosen to model this approach, because of their economic and scientific importance. This is the first step toward developing a Barley QTL Community Curation workbook for all types of QTLs and maps, on the GrainGenes website. ■

Low-Allergen Markers Identified for Soybean Breeding

Plant Genome 141–148

Soybean is an important source of high protein meal that is incorporated into many foods and feeds. However, soybean seeds contain multiple proteins that are allergenic to humans. In addition, livestock have been shown to have sensitivity to soybean meal proteins. The dominant soybean allergen is commonly known as P34. Large scale screening of the USDA soybean germplasm collection led to identification of two soybean lines with reduced P34 content. The researchers in the present study wanted an understanding of the molecular genetic basis for this trait.

Molecular marker assays were developed that detected the P34 genotype based on the presence or absence of a four-basepair insertion at the start codon. The researchers indicate that the use of the P34 molecular markers for direct selection of the mutant P34 allele would allow rapid incorporation of the low-P34 trait into elite germplasm through use of backcross breeding and identification

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and selection of individuals with heterozygous P34 alleles. The low-allergen phenotype could be recovered at the desired generation after selection of segregating individuals containing homozygous mutant P34 alleles. ■

Resistance to White Mold in Soybean Determined by Microarray

Plant Genome 149–166

White mold, caused by Sclerotinia sclerotiorum, can be a serious disease of crops grown under cool, moist environments. In many plants, such as soybean, complete genetic resistance does not exist.

To identify possible genes involved in defense against this pathogen, and to determine possible physiological changes that occur during infection, a group of researchers from Illinois, used a microarray screen conducted using stem tissue to evaluate changes in gene expression between partially resistant and susceptible soybean genotypes.

Although white mold is a difficult disease system to analyze, the in-silico mapping of the candidate genes in the soybean 7x genome provided an accurate comparison to serve as a starting point to identify key genes for future studies. The results of the mapping provided additional support of the microarray analysis for several cDNAs mapping close to known markers, their putative role in defense is supported by the literature. The results suggest that two of the seven markers analyzed are markers for the same locus. The cDNA sequences located close to markers can also be used as new candidate genes for resistance and for marker development. ■

Generating Mapped Markers in Bread Wheat

Plant Genome 167–178

This group of researchers from Canada used two different methods to identify single-feature polymorphism (SFP) markers. They mapped 1035 and 875 SFPs in a segregating population of 64 doubled haploid lines from bread wheat.

Statistical associations between the SFP maps and the rice genome agreed with known cereal syntenic blocks, and the mapping data were corroborated by previously established physical locations for wheat expressed sequence tags. Since the bread wheat genome has not been sequenced and the researchers were unable to do a direct verification of their SFP ordering, using rice as a surrogate genome allowed the rapid identification of markers from the genic regions of the complex hexaploid wheat genome.

The researchers believe that genotyping with the Affymetrix Wheat GeneChip offers a valuable high-throughput platform to generate mapped markers from genic regions in species with large, complex genomes, such as hexaploid bread wheat. ■

Increasing Phosphate and Nutritional Value in Soybean

Plant Genome 170–190

Plant seeds accumulate phosphorus in the form of phytic acid. Phytic acid is found complexed with cationic mineral species in the form of phytate, which is not well digested or absorbed by monogastric species such as humans, poultry, and swine. As a result, soybean has an effective deficiency of phosphorus and other minerals, despite high levels of minerals and phosphorus in the seed.

These researchers developed high-throughput molecular marker assays to directly select for the alleles that control the soybean low phytic acid phenotype. The researchers identify a novel *lpa2-b* allele in M766, a line that, to their knowledge, has not been utilized in any soybean breeding project.

The results suggest the next step for soybean low-phytic acid breeding efforts may be in the combination the nonsense *lpa2-b* allele from M766 with the nonsense lpa1-a allele from CX1834. Such a combination may produce soybeans with even lower levels of phytic acid and increased available phosphate levels, yielding enhanced nutritional value for food and feed. ■

Developing Herbicide Tolerance in Soybean

Plant Genome 191–205

By taking advantage of microarray technology, a group of researchers from the University of Illinois and USDA-ARS, Soybean/Maize Germplasm, Pathology, and Genetics Research Unit in Urbana, Illinois, conducted a large-scale investigation of transcription levels of ~36,000 genes in soybean leaf tissue treated with atrazine or bentazon, to understand the effect caused by these photosystem-II-inhibiting herbicides. In soybeans, atrazine is lethal while bentazon is nonlethal, because it can be metabolized by the plant.

Results revealed that only a small number of genes (12%) were differentially expressed between atrazine- and bentazon-treated soybean plants. These genes, however, convey important information about how plants respond to different chemicals. Ribosomal components in bentazon-treated plants were more abundant than in atrazine-treated ones. Similarly, a few GST and cytochrome P450s increased in transcript levels due to bentazon treatment but decreased due to atrazine treatment. Meanwhile, they noticed that among the genes that were expressed in opposite direction between two treatments, most of these genes increased in response to bentazon.

The researchers speculate that the gene(s) responsible for bentzon metabolism was adequately expressed and functioning during the first four hours after treatment and that many of the differently expressed genes after that time would be involved in recovery. In atrazine treatment, the expression was still related to continual futile efforts to survive. ■