Soybeans Know What Time It Is

It is well-known that plants have a central clock that allows anticipation of the daily changes in light and temperature that occur in the environment. This is important for the synchronization of biochemical reactions within the plant with the availability of light, or for the plant’s tolerance to cold temperatures in the evening. In work by Hudson, expression profiling was used to identify mRNA transcripts that showed evidence of being controlled by the circadian clock in developing soybean seeds. Many transcripts for genes involved in photosynthesis and carbohydrate metabolism were identified that peak in abundance at different times of the day or night. For some transcripts, maximum levels occurred at different times in leaves and seeds from the same plant, which indicates that seeds keep their own time, but rhythms of gene expression in seeds are also influenced by signals from the maternal plant.

New Virus Resistance Gene Mapped with Soybean Whole Genome Sequence

Soybean mosaic virus (SMV) is a prevalent virus infecting soybean worldwide. Three genes, namely Rsv1, Rsv3, and Rsv4, are known to confer resistance to SMV. Only Rsv4 confers resistance to all known stains of SMV in the United States, and can be pyramided with other R genes. In this study, a group of researchers from Virginia Tech utilized information from the recently completed soybean whole genome sequence for fine mapping and examining potential Rsv4 gene candidates using two populations segregating for resistance to SMV. Markers designed from the soybean genome sequence localized Rsv4 to a 1.3 cM region on chromosome 2, a physical interval of less than 100 kb. This region contained no sequences that have been previously related to virus resistance, such as nucleotide binding site-leucine rich repeat gene sequences or eukaryotic translation initiation factors. Instead, sequence analysis revealed several predicted transcription factors and unknown protein products. It appears that Rsv4 belongs to a new class of resistance genes that interfere with viral infection and cell-to-cell movement. This study also demonstrates that the Williams82 genome sequence is a powerful tool for targeted generation of markers for use in fine mapping and candidate gene discovery. Rsv4-related markers should have immediate application in developing durable virus resistant soybean cultivars through marker-assisted selection.

Partial Resistance to Phytophthora sojae

Phytophthora root and stem rot of soybean is a serious disease which results in losses of ~$300 million annually in the U.S. Partial resistance provides protection against all P. sojae pathotypes. Wang et al. (2010) discover 5 additional soybean quantitative trait loci which contribute to the expression of partial resistance. Fifty-five genes underlying these loci were found to be candidates involved in the mechanisms which contribute to partial resistance based on microarray gene expression analysis. Ten of these genes have unknown functions, while the others encode proteins related to defense or physiological traits. This study will contribute to soybean resistance breeding by providing additional resistance loci for marker-assisted selection as well as a list of candidate genes which may be manipulated to confer resistance.

Markers for Net Blotch Resistance

Net blotch is a destructive disease that causes yield losses in barley worldwide. Liu et al. mined barley expressed sequence tag (EST) databases and developed markers for further mapping of a previously identified barley region harboring two net blotch resistance genes. Additionally, Liu et al. did a comparative analysis of this region to other grass species. Fifteen newly developed markers were added to the previous map, and most were closely linked to the resistance loci. Data from this work suggest that the resistance loci are most likely located on the long arm of chromosome 6H and comparative analysis revealed that the region containing the two resistance loci has good colinearity with rice and Brachypodium. This work refines the genetic and physical location of the two resistance genes and provides an initial step towards the map-based cloning of these two genes.

The Illumina Genome Analyzer Allows Rapid SNP Discovery in Plants

Single nucleotide Polymorphism (SNP) discovery among cultivated plant species is an essential first step in using marker-assisted
selection for agronomic improvement. However, the size and largely duplicated content of the genomes often hinder attempts at discovering large numbers of meaningful SNPs in relevant cultivars. Deschamps et al. have developed a rapid method for sequencing reduced representation libraries in two important crop species using the Illumina Genome Analyzer for the purposes of SNP discovery. This method targets the sequencing to both gene-rich and relatively unique regions of the genome and extensive filtering of the sequences via bioinformatics tools ensured that the rate of true SNP discovery is above 96% in both species. It allows rapid and cost-effective SNP discovery in economically important crops and can be expanded to any plant species having sufficient reference genomic sequence.