Transcript Profiling Of Soybean Seed Development From Fertilization To Maturity

Dr. Sarah Jones*, Dr. Delkin Gonzalez, Dr. Lila Vodkin
University of Illinois

To understand gene expression networks leading to functional properties and compositional traits of the soybean seed, we have undertaken a detailed examination of soybean seed development from a few days post-fertilization to the mature seed using microarrays of up to 38,000 cDNAs. Genes involved with some storage proteins had their highest expression levels at the stage of largest fresh weight. Genes encoding many transcription factors and DNA binding proteins showed higher expression levels in the desiccating and dry seeds than in most of the green stages, perhaps indicating the preparation of pathways that will be needed later in the early stages of imbibition. To validate the results of the cDNA arrays, we selected 192 genes of interest for a highly repetitive oligo array in which each gene is represented by 40 spots per array, which are combined as replicates to yield data of high statistical value (Jones et al. 2010 BMC Genomics). We have also used high-throughput sequencing of RNAs from six stages of seed development to obtain over 25 million sequenced transcripts per stage. Transcripts have been identified against the gene models predicted from the recently sequenced soybean genome and correlated with the results of the microarray studies.

Poster Number: