

5th Annual Joint Bioinformatics Workshop

July 19, 2005
2229 Seamans Center
University of Iowa

by

Rhonda DeCook
Iowa State University

Genetic control of gene regulation during shoot development in Arabidopsis

ABSTRACT

The genetic control of gene expression during shoot development in *Arabidopsis thaliana* was analyzed by combining quantitative trait loci (QTL) and microarray analysis. Using oligonucleotide array data from thirty recombinant inbred lines derived from a cross of Columbia and Landsberg erecta ecotypes, the *Arabidopsis* genome was scanned for marker-by-gene linkages or so-called eQTLs. Single feature polymorphisms (SFPs) associated with sequence disparities between ecotypes were purged from the data. SFPs may alter the hybridization efficiency between cDNAs from one ecotype with probes of another ecotype. In genome scans, five eQTL hot spots were found with significant marker-by-gene linkages. Two of the hot spots coincided with classical QTLs conditioning shoot regeneration suggesting that some of the heritable gene expression changes observed in this study are related to differences in shoot regeneration efficiency between ecotypes. Some of the most significant eQTLs, particularly those at the shoot regeneration QTL sites, tended to show cis-chromosomal linkages in that the target genes were located at or near markers to which their expression was linked. However, many linkages of lesser significance showed expected "trans-effects", whereby a marker affects the expression of a target gene located elsewhere on the genome. Some of these eQTLs were significantly linked to numerous genes throughout the genome suggesting the occurrence of large groups of coregulated genes controlled by single markers.