

ARABIDOPSIS IS A WEED?: HETEROLOGOUS MICROARRAY USES IN WEED SCIENCE FOR NON-MODEL PLANTS. David P. Horvath, Research Plant Physiologist, USDA-ARS, Bioscience Research Lab, Red River Valley Agricultural Research Center, Fargo, ND, 58105.

Arabidopsis may not have weedy characteristics, but it certainly contains most of the same genes as weeds. Roughly 80% of the genes in Arabidopsis have recognizable counterparts in rice. Nearly half of these orthologous genes contain sufficiently long stretches of sequence similarity to allow gene probes from one species to hybridize to those of the other. Thus, it stands to reason that equivalent or greater number of genes would hybridize from species more closely related to Arabidopsis than rice. In addition to sequence conservation, there is substantial evidence that many signal transduction pathways regulating the expression of these similar genes are also well conserved. Interestingly, the most highly conserved genes are those involved in key steps in plant growth and development, photosynthesis, and stress responses. Consequently, the major differences in plant morphology and development are likely due to differences in expression or activity levels of a relatively small number of conserved regulatory genes.

We have taken advantage of these similarities to follow the expression of genes from leafy spurge and wild oats using Arabidopsis microarrays. We have also used tools developed for global expression analysis in Arabidopsis to infer information about the signal transduction pathways involved in growth and development of these two weeds. Our results have identified over 40 genes that are preferentially expressed in growing shoot apices of leafy spurge and seven that are preferentially expressed in the growing tiller of wild oat. Five of the seven genes preferentially expressed in wild oat tillers were also expressed in the growing shoots of leafy spurge. The expression of the putative orthologues of these genes in Arabidopsis suggest that several different regulatory pathways may be involved during growth and development of tillers and shoot apices in leafy spurge and Arabidopsis. There also appears to be some unexpected cross talk between cold-regulated and growth regulated signals transduction pathways.

Preliminary observations suggest that underground adventitious shoot buds of leafy spurge, often referred to as root buds in the literature, loose tight regulation of many growth responsive genes after three months of growth in the green house. Yet, the root buds of these plants do not develop into growing shoots unless the aerial portion of the plant is excised. These observations suggest an additional layer of growth regulation besides those of S-phase regulation previously shown to be imposed by the leaf derived signal. We have used Arabidopsis microarrays to identify 17 genes that are consistently preferentially expressed only in older dormant root buds, and one gene that is consistently preferentially expressed in the same buds upon growth induction. The results of these experiments will be discussed, although preliminary analysis appears to indicate that many of these genes are also responsive to light and oxidative stress.