

Regulatory Networks during *Arabidopsis thaliana* Development

Rebecca S. Lamb
Plant Cellular and Molecular Biology
Ohio State University
Columbus, OH 43210
lamb.129@osu.edu

During plant development, regulation of gene expression is essential. Gene regulatory pathways often converge at the level of gene transcription, where interactions among regulators and target genes result in the establishment of spatio-temporal patterns of gene expression. The identification of direct target genes for transcription factors is increasing at a very fast rate, both through traditional and high-throughput experimental approaches. This will allow the elucidation of regulatory networks at the genome level. Toward this end, we have developed the *AGRIS* (*Arabidopsis Gene Regulatory Information Server*) database. *AGRIS* consists of three linked databases and contains all *Arabidopsis thaliana* promoter sequences for annotated genes, transcription factors, and their target genes and functions. *AGRIS* can be accessed at <http://arabidopsis.med.ohio-state.edu>. In parallel to this effort, we are using high-throughput methods including ChIP-Chip to identify direct targets for a set of selected transcription factors involved in *Arabidopsis* developmental pathways, including epidermal development and flower development. The data generated will be deposited into the *AGRIS* database and used to build regulatory modules. In addition, direct target gene promoters will then be used to test bioinformatic methods for identifying transcription factor binding sites in plants. Progress on all three parts of the progress will be presented.