

Studying the function of non-coding RNAs

Background: The Arabidopsis genome has been completely sequenced, and large numbers of large numbers of RNAs that do not encode proteins have been identified. Many of these transcripts have been shown to serve regulatory functions, indicating that there may be a hitherto unsuspected layer of gene regulation in eukaryotes. The availability of the Arabidopsis genomic sequence coupled with the availability of large numbers of transposon-tagged mutant lines and the many other tools for studying Arabidopsis allows their functional significance to be systematically evaluated.

Experimental: We will collaborate with the Deng lab at Yale University, who will provide the sequences of numerous non-coding RNAs identified by high-throughput sequencing. We will search the SIGnAL (<http://signal.salk.edu/>) and AtEnsembl (<http://atensembl.arabidopsis.info/index.html>) databases for lines with DNA insertions in the sequences encoding these RNAs, and order lines containing insertions in the sequence itself or within 200 bp 5' to the start. Location of the insertion will be confirmed by PCR and sequencing, then homozygous lines will be obtained and grown under various conditions to attempt identifying phenotypic consequences. Complementation tests will be performed to confirm that the phenotype is due to the mutant ncRNA. We will then attempt to determine the function of the ncRNAs. We will compare their phenotypes to those of known mutants for clues as to processes they may be involved in. We will search for mRNA or other RNA targets that they may bind; we will test whether the loci that they come from or other DNA sequences that they might bind are differentially methylated in mutant and wild-type, and we will check whether the ncRNA are processed into smaller RNAs that may perform other functions. This is an opportunity to do some genuine cutting-edge research in bioinformatics in collaboration with one of the best labs in the world.