

GENE EXPRESSION ANALYSIS USING MICROARRAYS OF PRION POSITIVE AND NEGATIVE YEAST STRAINS. A. Watkins, S. Sarchet, S. Tyler, C. Erickson and I. Evans*, Department of Biological Sciences, aaw5261@rit.edu; imesbi@rit.edu

The model organism *Saccharomyces cerevisiae* is extremely advantageous in the study of gene expression in eukaryotes containing prion proteins (PrP). Human prion proteins can be infectious, disease-causing agents that convert the 'normal' form of a protein into a different prion conformation leading to neurodegenerative effects. In yeast prion proteins do not cause disease and may even be advantageous. Prion proteins are believed to have two or more different conformational forms as a result of different tertiary structures that are formed. We analyzed two genetically identical strains of yeast that differ only in the conformation of Sup35, a prion-like yeast protein. In the [PSI+] strain, Sup35 assumes a prion conformation while in the [psi-] strain, the Sup35 gene product in its non-prion conformation codes for a translation release factor protein. Whether or not the conformational differences of the Sup35 gene product effect gene expression is investigated using DNA microarrays which measure simultaneously transcription of all genes (6,400) in the yeast genome. Genes that are over and under-expressed in the prion-positive strain [PSI+] versus the prion-negative strain [psi-] are enumerated using a MAGIC software program to try to determine why prion proteins are conserved in many yeast strains.