

295c Dynamic Transcriptional Profiling Analysis of *Arabidopsis Thaliana* under CO₂ and NaCl Stress

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In systems biology conventional systems engineering approaches are used to solve biological problems. Systems engineering requires the system to be perturbed in multiple systematic ways to study the response of the perturbation and hence to elucidate the relationship between different system variables. Simultaneous measurement of the system variables in a dynamic way is essential to get a comprehensive understanding of the functionality and interrelationship of the variables.

In this context we present a high throughput transcriptional profiling analysis of *Arabidopsis thaliana* liquid culture system subjected to multiple perturbations. This is a first effort, to the best of our knowledge, where multiple perturbations were applied to a eukaryotic system in a systematic way and the dynamic response was studied at the transcriptional level using full genome DNA microarray. Specifically, *A. thaliana* liquid cultures grown for 12 days under constant light and temperature were subjected to (1) step input in CO₂ level in their growth environment (2) Osmotic stress through addition of NaCl in growth media, applied individually or in combination. Liquid cultures were harvested over a period of 30 hours after initiation of the treatment to monitor the dynamic short-term response of the stresses. The obtained measurements was used to (a) develop and validate hypothesis testing and other analytical techniques for the time series gene expression data (b) study the effect of individual as well as combined perturbations (c) compare the effect of combined perturbation with that of the individual perturbations using statistical testing methods like two-factor ANOVA (d) develop methodologies to upgrade the information content of the gene expression data by using additional constraints based on previous biological knowledge and (e) get valuable insight about gene regulation. The results were validated in the context of the known *A. thaliana* physiology. Apart from providing information about the response of the of the *A. thaliana* system to perturbations, this analysis is expected to greatly contribute in enhancing the currently available experimental database and in advancing the systems biology computational and experimental toolbox.