Marcelo Pomeranz[1,2], Shin Gene Kang[1,2], John E. Price[1,2], Pei-Chi Lin[2,3], J. Finer[1,2] and J C Jang[1,2,3]

[12]Department of Horticulture and Crop Science, [2]Plant Biotech Center and [3]Department of Plant Cellular and Molecular Biology
The Ohio State University, Columbus, OH 43210 USA

In plants, one common signaling mechanism is the interaction between DNA elements and DNA-binding transcription factors (TFs). Despite the fact that at least 10% of all plant genes are sugar responsive, very few regulatory circuits are known to be associated with sugar signaling. We hypothesize that sugar-responsive TFs play central roles in tying sugar signals to an interconnected gene regulatory network. Based on the results of our microarray analyses, a highly sensitive sugar-responsive bZIP1 TF has been chosen as a model to test this hypothesis. Phenotypic analyses show clear differences of growth patterns in both knockout, and over-expression mutants from that of the wild-type plants suggesting that bZIP1 is likely involved in sugar signaling and may control other downstream sugar-responsive genes. It is known, that bZIP factors activate gene expression by forming hetero and homo-dimers and our protein-protein interaction analyses have shown bZIP1 interaction with 4 other bZIP factors. Since the DNA-binding specificity and affinity is determined by the bZIP pair combination, it is imperative to determine specific target genes activated by each bZIP pair and how these combinatorial effects impact sugar response. To accomplish this goal, a research plan including the following experiments will be presented:

1) Expression analyses to determine the temporal and spatial expression pattern of each bZIP in the interacting network.
2) Develop a high throughput system to decipher the downstream genes targeted by each bZIP pair.
3) Functional analyses using knockouts or over-expression of each bZIP pair.

Reference:

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