S2-1

Glucose sensing and Signaling in the Cyanobacterium *Synechocystis* sp. PCC 6803

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The photosynthetic cyanobacterium *Synechocystis* sp. PCC6803 is chosen as a model organi sm for identifying general mechanisms and principles for glucose sensing and signaling. We have screened Transposon (Tn) 5 mutant strains provided from SMCC (*Synehcosystis* Tn Mutant Culture Collection) with respect to dysfunction in glucose sensing/signali ng by growth analysis, in vivo Chlorophyll fluorometry, in vivo far-red light spectroscopy and proteomics approaches. Among 1,935 Tn mutants screened, we selected 136 mutants with abnormal response to glucose and identified 37 genes/promoters by inverse-P C R. Currently, functional studies for 14 out of 37genes identified are under the way using knock-outs/GFP-reporter mutants. In addition to the random approaches, we selected 56 genes by transcriptomics as well as bioinformatics.

S2-2

Rice Histone Deacetylase: a Global Regulator in Gene Expression

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Histone deacetylases (HDACs) modulate chromatin structure and transcription. We isolated the rice *OsHD AC1, 2,* and *3* genes, which are related to the RPD3 family of histone deacetylases. Genomic structures and Southern blot analyses revealed that *OsHDAC1, 2,* and *3* contained 7, 6, and 7 exons, respectively, and constituted a class I-type family in the rice genome. *OsHDAC1* was expressed at similar levels in the leaves, roots, and callus cells, whereas *OsHDAC2* and *3* were expressed in the roots and callus cells, but not in the lea ves, exhibiting distinct tissue specificity. To explore the role of histone deacetylases in transgenic plants, we inserted the *OsHDAC1* cDNA fragment into the expression vector *Ai::OsHDAC1* under the control of the ABA-inducible promoter *Ai,* and transformed the construct into rice. Levels of mRNA, protein, and HDAC activity were significantly increased in *Ai::OsHDAC1* callus cells. The amount of tetra-acetylated H4 in the transgenic cells was greatly reduced, and the reduction was abolished upon treatment with trichostatin A. These results demonstrate that *OsHDAC1* overexpression in transgenic cells both yields enzymatically active HDAC complexes and induces changes in histone acetylation in vivo. The overexpression leads to a range of novel phenotypes, involving increased growth rate and altered plant architecture, suggesting that *OsHDAC1* functions in the genome-wide programming of gene expression. Microarray results from 60K oligomer chip on OsHDAC1 overexpressor will be discussed.