

Identification and functional characterization of rice transcription factors that regulate photosynthesis-related genes under salt stress

Salt stress reduces photosynthetic efficiency, thus limiting plant growth and productivity. In rice, the transcription level of important genes associated with photosynthesis (*Rubisco Activase*, *Sedoheptulose-Bisphosphatase*, *Chloroplast ATP synthase* and *Oxygen evolving enhancer 2*) is down regulated under high salinity and their over-expression can improve abiotic stress tolerance. Transcription factors (TFs), which may control various downstream genes, clearly play an important role controlling photosynthetic-related gene expression under salt stress. However, little is known concerning the identity and function of these TFs. Using the “yeast one-hybrid” system, we aim to identify TFs that regulate this process. Functional analysis of the novel TFs will be performed using a transgenic and/or mutant approach. These results will help to understand fundamental mechanisms of salinity tolerance in rice especially regarding transcriptional regulation of the photosynthetic response. This understanding may eventually be used to improve photosynthetic capacity of crop plants and reduce productivity losses under stress environments.

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