

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

Water deficit is well known to reduce 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 drought and their over-expression can improve abiotic stress tolerance. Therefore, transcription factors (TFs), which may control various downstream genes, clearly play an important role controlling photosynthetic-related gene expression under water deficit. Given that little is known concerning the identity and function of these TFs, we plan to identify TFs that regulate this process, using the “yeast one-hybrid” system. Thereafter, functional analysis of the novel TFs will be performed using a mutant approach. These results will help to understand fundamental mechanisms of drought 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 water limited conditions.

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