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Co-expression analysis of DREB family transcription factors in rice

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In the course of evolution, plants have evolved specific defense mechanisms by expressing variety of genes to adapt and survive stressful events. There are many signaling networks in plants involved in abiotic and biotic responses. Moreover, these signaling pathways stimulate expression of specific sub-sets of genes that activate the overall stress defense responses. Among them, Dehydration Responsive Element-Binding (DREB) proteins are important Transcription Factor Family (TFF) which plays a critical role in developmental and abiotic stress (drought and temperature) mediated gene expression networks in plants.

This study investigated co-expression analysis of DREB family transcription factors in rice and the study comprised 14 genes which belong to DREB family in rice. The main objective of this study was to discover the functional roles of DREB family members using the co-expression genes. In addition, GC content of each gene in *DREB1* and *DREB2* family members were calculated. Furthermore, 27, 201 genes for each DREB TF family genes in rice were analyzed to investigate putative functions of those genes in both biotic and abiotic stresses by calculating weighed Pearson correlation coefficient (WPCC) and mutual rank (MR). Then genes with MR<10 were selected and GO enrichment analysis was carried out to identify the significant functions in *DREB* genes. Interestingly, co-expressed genes of both DREB1and DREB2 families were shown to be enriched with GO terms related to stress related functions such as protein ubiquitination, regulation of transcription, response to abscisic acid stimulus, response to deep water, abscisic acid catabolic process. The findings of this study will provide a platform for future studies on uncovering functional roles of *DREB* family genes in rice.