



Analysis of Common Transcription Factors in SnRK2 Gene Family in Rice

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Abstract: Cold, heat and water limitation impose osmotic stress in plant. Various signaling proteins which are induced under osmotic conditions and the stress hormone abscisic acid (ABA) such as several protein kinase families involved in stress responses. Among them the sucrose non-fermenting 1-related protein kinase 2 (*SnRK2*) is a member of the SNF1-related PKinase family plays a key role in signaling pathways that regulate plant responses to abiotic stresses. *Cis*-acting elements in promoters regions involved in the transcriptional regulation of abiotic stress responsive genes. Understanding the regulatory gene in stress response requires effective functional analysis of *cis*-acting elements and corresponding transcription factors (TFs). In this study, in order to find out the effective TFs of family members of SnRK2 in rice which contains 10 members (*SAPK1* to *SAPK10*), we investigate the common TFs among these genes, which act as a common module in response to the osmotic stress. Therefore, SnRK2 gene family promoters were examined using the Genomatix software (<http://www.genomatix.de/>). Also, FrameWork analysis was performed to determine which of them act in a common modules in response to osmotic stress. Our result indicate that, there are 11 transcription factors HEAT, NACF, MADS, MIIG, L1BX, DOFF, CCAF, MYBL, GTBX, AHBP and MYBS with a minimum promoter matches of 87%. We also identified two modules MYCL_MIIG_01 and GTBX_MYCL_01 and three modules CCAF_CCAF_01, CCAF_CCAF_02 and ABRE_CCAF_01 and a module HEAT_HEAT_HEAT_01 that function in response to dehydration, cold and heat, respectively. The existence of these modules demonstrates the important role of this gene family in osmotic stress response processes.

Keywords: osmotic stress; SnRK2 gene family; *cis*-acting elements; common TF

References

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