



Uncovering Six New Rice MYB Orthologs Involved in Anthocyanin Pathways and Abiotic Stress-Responsive Regulatory Networks

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R2R3-MYB transcription factors (TFs) are key regulators of secondary metabolism and abiotic stress responses across plant species. However, limited information is available on the functional roles of R2R3-MYB TFs in rice in the context of sustainable agriculture. This study aimed to identify and functionally predict rice MYB transcription factors associated with anthocyanin biosynthesis and stress resilience using a comprehensive in-silico approach. Thirty-one MYB gene sequences linked to pigmentation and stress responses were retrieved from the Plant Transcription Factor Database. Conserved motif analysis confirmed the presence of the R2R3 domain and identified potential repressors. Phylogenetic analysis distinguished MYBs involved in anthocyanin biosynthesis, while the detection of EAR motifs in StMYB44 and PhMYB4 suggested repressor activity. Gene interaction network analysis revealed associations with stress-related pathways, including lignin biosynthesis, reactive oxygen species scavenging, stomatal regulation, and hormone signaling. Six novel rice orthologs, OsMYB52, OsMYB14, OsMYB26, OsMYB56, OsMYB64, and OsMYB80 were identified, showing close evolutionary relationships with functionally characterized MYBs from *Arabidopsis thaliana*, *Capsicum annuum*, *Zea mays*, *Triticum aestivum*, and *Vitis vinifera*. Cis-regulatory analysis revealed key promoter elements such as CAAT-box, TATA-box, ABRE, ARE, and G-box motifs, indicating responsiveness to environmental and hormonal cues. Experimental validation will be necessary to confirm the functional roles of the identified MYB candidates in stress resilience and anthocyanin accumulation.

Keywords: Abiotic stress resilience, Anthocyanin biosynthesis, MYB transcription factors, Phylogenetic analysis, Regulatory mechanisms