

Classification and Expression Profiling of Putative R2R3 MYB Genes in Rice

Kim Bong Gyu, Ko Jae Hyung, Min Shin Young, and Ahn Joong-Hoon
Department of Molecular Biotechnology, Bio/Molecular Informatics Center,
Konkuk University, Seoul, Korea;
TEL : +82-2-450-3764, FAX +82-2-446-9001

Abstract

MYB genes, comprising group of related genes found in animal, plant, and fungal genomes, encode common DNA-binding domains composed of one to four repeat motifs. MYB genes containing two repeats (R2R3) constitute largest MYB gene family in plants. R2R3 MYB genes play important roles in regulation of secondary metabolism, control of cell shape, disease resistance, and hormone response. Eight-four R2R3 MYB genes were retrieved from rice genome for functional characterization of MYB genes. Analysis of MYB domains revealed each MYB domain contains three α -helices with regularly spaced tryptophan residues. R2R3 MYB genes were divided into four subfamilies based on phylogenic analysis result. Real-time PCR analysis of 34 MYB genes revealed 12 MYB genes were highly expressed in seeds than in leaves, whereas 4 genes were highly expressed in leaves.

References

1. Cubas, P., Vincent, C., and Coen, E. (1999) An epigenetic mutation responsible for natural variation in floral symmetry. *Nature* **401**, 157-161.
2. Arthur, W, (2002) The emerging conceptual framework of evolutionary developmental biology. *Nature* **415**, 757-764.
3. Jiang, C., Cu, X., and Perteson, T. (2004) Identification of conserved structures and carboxy-terminal motifs in the Myb gene family of *Arabidopsis* and *Oryza sativa* L. ssp. Indica. *Genome Biology* **5**, R46.1-R46.11.