

# Accepted Manuscript

Title: Genomic Survey and Expression Profiling of the *MYB* Gene Family in Watermelon

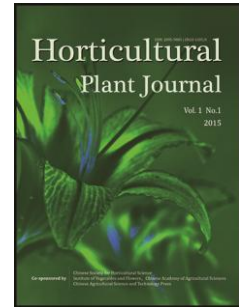
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PII: S2468-0141(17)30345-X

DOI: <https://doi.org/10.1016/j.hpj.2017.12.001>

Reference: HPJ 108

To appear in: *Horticultural Plant Journal*



Please cite this article as: Qing Xu, Jie He, Jianhui Dong, Xiaojin Hou, Xian Zhang, Genomic Survey and Expression Profiling of the *MYB* Gene Family in Watermelon, *Horticultural Plant Journal* (2017), <https://doi.org/10.1016/j.hpj.2017.12.001>.

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# Genomic Survey and Expression Profiling of the *MYB* Gene Family in Watermelon

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Received date; Received in revised form date; Accepted date

Available online date

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## Abstract

Myeloblastosis (MYB) proteins constitute one of the largest transcription factor (TF) families in plants. They are functionally diverse in regulating plant development, metabolism, and multiple stress responses. However, the function of watermelon MYB proteins remains elusive to date. Here, a genome-wide identification of watermelon MYB TFs was performed by bioinformatics analysis. A total of 162 *MYB* genes were identified from watermelon (*Clamyb*). A comprehensive overview of the *Clamyb* genes was undertaken, including the gene structures, chromosomal distribution, gene duplication, conserved protein motif, and phylogenetic relationship. According to the analyses, the watermelon *MYB* genes were categorized into three groups (*R1R2R3-MYB*, *R2R3-MYB*, and *MYB-related*). Amino acid alignments for all MYB motifs of *Clamyb*s demonstrated high conservation. Investigation of their chromosomal localization revealed that these *Clamyb* genes distributed across the 11 watermelon chromosomes. Gene duplication analyses showed that tandem duplication events contributed predominantly to the expansion of the *MYB* gene family in the watermelon genome. Phylogenetic comparison of the *Clamyb* proteins with *Arabidopsis* MYB proteins revealed that watermelon MYB proteins underwent a more diverse evolution after divergence from *Arabidopsis*. Some watermelon MYBs were found to cluster into the functional clades of *Arabidopsis* MYB proteins. Expression analysis under different stress conditions identified a group of watermelon MYB proteins implicated in the plant stress responses. The comprehensive investigation of watermelon *MYB* genes in this study provides a useful reference for future cloning and functional analysis of watermelon MYB

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