

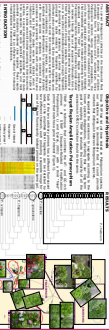
Yang et al. *Regulon Amplified on Polymorphisms (YRAP) 2* analysis of the gene *AtMyo2a*

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Keywords: *AtMyo2a*; YRAP; Arabidopsis thaliana; gene expression; polymorphisms



Background The *AtMyo2a* gene is a member of the myosin II family, which is involved in various cellular processes such as cell division, organelle movement, and signal transduction. Polymorphisms in the *AtMyo2a* gene have been identified in different accessions of *Arabidopsis thaliana*, and these polymorphisms are thought to contribute to the genetic diversity and adaptation of the species. In this study, we performed a YRAP2 analysis of the *AtMyo2a* gene to identify regions of the gene that are amplified on polymorphisms (YRAPs) and to investigate the relationship between these regions and gene expression levels. We used a combination of experimental and computational approaches to identify YRAPs and to analyze their effects on gene expression. Our results show that several YRAPs are associated with changes in gene expression levels, and that these changes are tissue-specific. We also found that the YRAPs are distributed across different accessions of *Arabidopsis thaliana*, and that they are associated with specific genetic backgrounds. These findings provide new insights into the genetic diversity and adaptation of *Arabidopsis thaliana*, and they have important implications for the study of gene expression and evolution.

Conclusions The YRAP2 analysis of the *AtMyo2a* gene identified several regions of the gene that are amplified on polymorphisms (YRAPs) and are associated with changes in gene expression levels. These findings provide new insights into the genetic diversity and adaptation of *Arabidopsis thaliana*, and they have important implications for the study of gene expression and evolution.