A high resolution map of the Arabidopsis thaliana developmental transcriptome based on RNA-seq profiling

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Abstract

© 2016 The Authors The Plant Journal © 2016 John Wiley & Sons LtdArabidopsis thaliana is a long established model species for plant molecular biology, genetics and genomics, and studies of A. thaliana gene function provide the basis for formulating hypotheses and designing experiments involving other plants, including economically important species. A comprehensive understanding of the A. thaliana genome and a detailed and accurate understanding of the expression of its associated genes is therefore of great importance for both fundamental research and practical applications. Such goal is reliant on the development of new genetic and genomic resources, involving new methods of data acquisition and analysis. We present here the genome-wide analysis of A. thaliana gene expression profiles across different organs and developmental stages using high-throughput transcriptome sequencing. The expression of 25 706 protein-coding genes, as well as their stability and their spatiotemporal specificity, was assessed in 79 organs and developmental stages. A search for alternative splicing events identified 37 873 previously unreported splice junctions, approximately 30% of them occurred in intergenic regions. These potentially represent novel spliced genes that are not included in the TAIR10 database. These data are housed in an open-access web-based database, TraVA (Transcriptome Variation Analysis, http://travadb.org/), which allows visualization and analysis of gene expression profiles and differential gene expression between organs and developmental stages.

Keywords

alternative splicing, Arabidopsis thaliana, differentially expressed genes, gene expression analysis, RNA-seq, transcription factor