



ABSTRACT

“RNA processing mutants meet whole-genome tiling arrays - Uncovering the hidden layer of the *Arabidopsis* transcriptome”

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Many recent publications report about the pervasive transcription of almost the entire genome of several different model organisms. In the model plant *Arabidopsis thaliana*, 32,000 protein-coding genes, pseudogenes and non-coding RNAs are annotated and this number is still expected to rise. But what is the best method to gain a comprehensive view in the transcriptional activity of the *Arabidopsis* genome? We utilized whole genome tiling arrays and found more than 1,000 ‘intergenic’ regions that are actively transcribed during the life cycle of wild-type plants as well as novel transcripts that occur only under certain stress conditions such as salt, heat or cold stress. However, we still might have missed many transcripts, especially those that are processed very rapidly such as primary microRNA transcripts. Indeed, whole genome tiling array analyses of *Arabidopsis* mutants impaired in miRNA processing, splicing, or mRNA quality control reveal the existence of many transcript that are undetectable in wild-type plants. These RNAs might constitute unstable, but important regulatory molecules of the *Arabidopsis* transcriptome or RNA processing intermediates that are eliminated during RNA maturation. Taken together, our results highlight the potential of identifying novel RNAs and RNA maturation pathways by in depth transcriptome analyses of RNA processing mutants.