

Early and late transcriptional responses to the low concentration of salicylic acid in *Arabidopsis thaliana* L. root

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Motivation and Aim: Salicylic acid (SA) is a stress hormone in plants, also it was shown that SA regulates plant growth and development [1]. In majority of studies, the influence of high SA concentrations (> 100 µM), mainly on the aboveground part, and after a prolonged exposure to SA (~24 hours) has been studied. As a result, molecular-genetic mechanisms of low SA concentrations remain obscure, the same is true for the mechanisms of SA response in the root and early transcriptional response to SA. The goal of this study was to describe transcriptome response to low SA concentrations in early and late response in *A. thaliana* root.

Methods and Algorithms: We used RNA-Seq data, generated from roots of 3 dag seedlings of *A. thaliana* after SA-treatment (20 µM, 1h and 6h) and sequenced on Illumina-HiSeq4000 (BGI Tech, Hong Kong). RNA-Seq data analysis included quality control (FASTQC), preprocessing of the reads (Trimmomatic), mapping (STAR) and differential expression analysis (DESeq2, EdgeR). Functional annotation of differentially expressed genes (DEGs) was made with agriGO (<http://systemsbiology.cau.edu.cn/agriGOv2>) and DAVID (<https://david.ncifcrf.gov/>).

Results: We detected 1873 and 3662 DEGs in early and late response in *A. thaliana* root respectively. Low SA concentrations induced three times more genes than inhibits in both early and late response. Intriguingly, among the DEGs we found many genes providing for SA signaling under its high dosage. Consequently, functional enrichment analysis of DEGs showed many GO terms associated with defense and immune system even in the samples exposed to low-level SA for 1h only. After 6h-treatment was found a term «SA metabolism», that assumed activation of SA catabolism in late SA response.

Conclusion: Here we identified molecular targets of low SA concentrations in early and late response to low SA concentrations. Interesting that low level SA activates many defence reactions (through oxylipin, cytochrome, flavonoids, etc.). Next question is to compare the transcriptome response to low and high SA concentrations.

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References

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