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Comparative transcriptomics of the moss *Physcomitrella patens* under biotic stress

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Motivation and Aim: The moss *Physcomitrella patens* is a non-vascular, multicellular land plant. It used for studying cell biology and evolution processes. In contrast to the polyploid flowering plants, mosses have prevalent the haploid gametophytic stage in their life cycle. *P. patens* is an interesting model organism for exploring the mechanisms of adaptation in plants due to its evolutionary stage between green algae and flowering plants. Here we present research project related to complex analysis of high-throughput sequencing data from our study and publicly available transcriptomics data. This project provides information on the regulatory mechanisms that developed during land plant evolution.

Methods and Algorithms: Moss gametophores were cultivated on Knop's medium and inoculated with suspensions of *Pseudomonas syringae*, *Pseudomonas viridiflava* and *Xanthomonas arboricola* (OD 0.4). A five days post inoculation gametophores were grinded, mRNA was extracted, and cDNA libraries were constructed. Sequencing of cDNA libraries was performed on SOLiD platform. Sequence reads were mapped to the *P. patens* genome and transcriptome V3.3 using Bowtie and Tophat. For quantifying gene and isoform abundances RSEM was used. Additionally we have compiled a gene set database for pathway analysis in *P. patens*. For this purpose we have collected previously published transcriptome datasets of *P. patens* from Gene Expression Omnibus (GEO, www.ncbi.nlm.nih.gov/geo/) and ArrayExpress (www.ebi.ac.uk/arrayexpress/). Gene IDs from various sources were converted to Phytozome gene symbols. STAR, kallisto and RSEM were used for data analysis. Data visualization was performed with IGV Tools and Phantasus.

Results and Conclusion: About 84 M of 50 bp reads were obtained for each sample and nearly 68 % of reads were aligned to transcriptome. As a result, it was shown 33055 differentially expressed transcripts. The majority of genes up-regulated by *P. syringae* and *P. viridiflava* encode endocytosis, while down-regulated genes encode nitrogen metabolism, histidine metabolism and cyanoamino acid metabolism. As to *X. arboricola*, the majority of up-regulated genes encode ribosome biogenesis, RNA transport, photosynthesis, and flavonoid biosynthesis, whereas down-regulated genes encode alpha-Linolenic acid metabolism, glutathione metabolism, and nitrogen metabolism. 10 RNA-Seq datasets taken from GEO and ArrayExpress. KEGG database was used for analysis of signaling networks. Transcriptomic profiling of moss samples under different biotic and abiotic conditions has provided an opportunity for investigation of gene expression and molecular pathways.

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