019025

TRANSCRIPTOME ANALYSIS IN THE WHEAT CULTIVAR TOROPI IN RESPONSE TO INFECTION WITH PUCCINIA TRITICINA, THE CAUSAL PATHOGEN OF LEAF RUST

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Leaf rust, caused by the fungal pathogen *Puccinia triticina* (*Ptr*), is a major constraint to wheat production worldwide. A *Ptr* infection time-course analysis was performed to explore the resistance mechanisms in the cv. Toropi, which confers a unique, durable adult plant resistance to leaf rust. RNA-Seq was undertaken at four time-points (0, 6, 12 and 24 hai) after inoculation with *Ptr* race MDT- Differential gene expression analysis was performed, comparing *Ptr* inoculated with mock inoculated (mineral oil without *Ptr*) taken at the same time-point. Reads were initially aligned against the wheat Chinese Spring TGAC and IWGSC RefSeq transcriptomes. Alignment results using the IWGSC reference (87.8%) yielded higher percentage alignments compared to the TGAC reference (78.2%). Unmapped reads were aligned against the *Ptr* transcriptome (Ensembl release 35). However, a low percentage of unmapped reads aligned against the *Ptr* transcriptome, primarily because the fungus is still in its initial stages of infection and fungal biomass levels are low. Salmon (alignment-base mode) was used to estimate the number of reads and edgeR to test for cross-conditional differently expressed genes (mock vs inoculated) at each time-point. Hierarchical clustering was performed across the time-course using K means (with Euclidean distance metric) in MeV. The total numbers of wheat genes differentially expressed in response to inoculation with *Ptr* were 1504, 2457 and 2776 at 6, 12 and 24 hai, respectively. Of these 71 and 386 genes were up- and down-regulated respectively at all three time points. The functional roles of the wheat differentially expressed genes were analyzed using gene ontology enrichment analysis. Many metabolic routes were altered during infection, gene involved in biological process such as oxidation–reduction, photosynthesis, electron transport chain and cellular metabolic process were, in general, down-regulated, while defence response-related genes were up-regulated. Toropi's defence mechanisms appear to shut down the photosynthetic and central metabolic pathways, rerouting the plant's energy to defence responses. Toropi's resistance against *Ptr* occurs at an early stage in the infection process, being primarily pre-haustorial. QTL for leaf rust resistance have been identified in Toropi on chromosomes 1BL, 3BS, 4BL, 5AL and 5DS (*Lr78*). Differentially expressed genes related with defense responses and close linked to these Toropi's QTL have been selected for further gene expression profiling analysis by RT-qPCR.