

WHEAT TRANSCRIPTOME ANALYSIS TARGETING LEAF RUST RESISTANCE-RELATED GENES

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Leaf rust is an important disease affecting wheat production in Brazil, due to both production losses and increased management costs. Plant pathogen fungicide resistance demands discovery of new disease management control strategies, and improved genetic breeding is one such effective approach. Toropi is a Brazilian wheat cultivar that shows an important characteristic for Brazilian wheat breeding; adult plant resistance (APR) to leaf rust. In order to better understand the leaf rust APR in Toropi we compared RNA-Seq from Toropi, at different time points after inoculation (0, 6, 12, 24 hai) with *Puccinia triticina*, to the available Chinese Spring (CS42) transcriptome, identifying putative genes unique to Toropi. Reads from Toropi libraries were mapped to the CS42 transcriptome, as well as a bulk of the Toropi libraries being used to build a reference transcriptome via *de novo* assembly. Contigs from the Toropi *de novo* assembly were submitted for similarity analysis using Blast against the CS42 transcriptome to identify contigs unique to Toropi. Differential expression (DE) analyses were performed using RSEM and EdgeR. Around 58-59% of Toropi reads were mapped to the CS42 transcriptome, while around 66K contigs presented no homology. Among the 10,181 DE contigs, 9,156 were present in both Toropi and CS42, while 1,025 contigs which were differentially expressed in Toropi in the presence of the fungus had no hits in CS42. These Toropi-specific sequences could represent new resistance candidate genes to be used in wheat breeding and need further study to determine their role in plant defense.

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