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Differential expression and identification of new adult plant resistance genes to leaf rust in Brazilian wheat cultivar Toropi

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Wheat leaf rust, caused by *Puccinia triticina*, endemic of South America, it is an important wheat disease. The Brazilian wheat cultivar Toropi has proven, durable adult plant resistance (APR) to leaf rust and prehaustorial resistance phenotype. The objective of this study was to identify, characterize and to understand the interaction between *P. triticina* and Toropi by quantitatively evaluating the temporal transcription genes related to infection and defense in wheat. RNA-Seq libraries from the Toropi here produced at 0, 6, 12, 24 hours after inoculation with *P. triticina*. Three replicates of each inoculated and control libraries were sequenced for each time point. A comparison to the Chinese Spring (CS42) transcriptome was performed aiming to identify putative genes unique to Toropi. A total of 58 million bp per library were produced: 10,181 contigs of which 9,156 were common to CS42 and 1,025 were unique to Toropi expressed only in the inoculated libraries. The expression profiles of 15 selected genes varied over time. Classical defense genes, including peroxidases, b-1,3-glucanases and an endochitinase were expressed (pre and post haustorial) over 72 hours infection time course, while induction of transcription of other infection related genes with a potential role in defense, although variable was maintained throughout. These genes had a role in plant lignification, oxidative stress, the regulation of energy supply, water and lipid transport and cell cycle regulation. These Toropi specific sequences could represent new resistance candidate genes to be used in wheat breeding and to guide further functional studies on APR to leaf rust.

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Identification of maize grain Fe and Zn homeostasis-associated QTL in two mapping populations

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Iron (Fe) and zinc (Zn) are essential for plant, animal and human nutrition. Low Fe and Zn in crops and livestock results in their reduced health, which when consumed over prolonged periods can in turn negatively impact the nutrition of human populations. Maize is grown worldwide as a staple crop for some and a valuable commodity for others and has the potential to be a useful tool for targeting the dietary Fe and Zn deficiency among the undernourished poor. Maize's remarkable global spread is largely due to the degree of genetic and phenotypic diversity that can be harnessed into adaptation to local conditions. This study was performed on the Goodman Diversity Panel (GDP) with corresponding analysis of the nested association mapping (NAM) population, to take advantage of greater statistical power and resolution and to perform joint linkage (JL) and genome-wide association (GWAS) analyses of quantitative genetic loci (QTL) across 3 temperate and 2 tropical locations. Previous studies that have used a candidate-gene knockout approach have yielded narrower successes in identifying genetic determinants of ionic homeostasis, whereas the NAM JL-GWAS approach, in this study, has borne significant QTL identification. Currently 227 JL ionic-QTLs have been identified with successive rounds and accompanying GWAS data we anticipate discovery of good QTL for twenty different elements including those for Fe and Zn homeostasis. A web interface for browsing the maize co-expression network has been developed for querying individual genes or large regions of the genome that will shortly become available for public use.

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