



Expression analysis of transcription factors from the interaction between cacao and *Moniliophthora perniciosa* (Tricholomataceae)

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Genet. Mol. Res. 9 (3): 1279-1297 (2010)

Received March 18, 2010

Accepted May 10, 2010

Published July 6, 2010

DOI 10.4238/vol9-3gmr825

ABSTRACT. Cacao (*Theobroma cacao*) is one of the most important tropical crops; however, production is threatened by numerous pathogens, including the hemibiotrophic fungus *Moniliophthora perniciosa*, which causes witches' broom disease. To understand the mechanisms that lead to the development of this disease in cacao, we focused our attention on cacao transcription factors (TFs), which act as master regulators of cellular processes and are important for the fine-tuning of plant defense responses. We developed a macroarray with 88 TF cDNA from previously obtained cacao-*M. perniciosa* interaction libraries. Seventy-two TFs were found differentially expressed between the susceptible (Catongo) and resistant (TSH1188) genotypes and/or during the disease time course - from 24 h to 30 days after infection. Most of the differentially expressed TFs belonged to the bZIP, MYB

and WRKY families and presented opposite expression patterns in susceptible and resistant cacao-*M. perniciosa* interactions (i.e., up-regulated in Catongo and down-regulated in TSH1188). The results of the macroarray were confirmed for bZIP and WRKY TFs by real-time PCR. These differentially expressed TFs are good candidates for subsequent functional analysis as well as for plant engineering. Some of these TFs could also be localized on the cacao reference map related to witches' broom resistance, facilitating the breeding and selection of resistant cacao trees.

Key words: Macroarrays; RT-qPCR; Gene regulation; *Theobroma cacao*; Witches' broom disease