

Proteomic profile of the fungus *Moniliophthora perniciosa* in response to PR10 from *Theobroma cacao*

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Witches' broom disease is caused by the hemibiotrophic basidiomycete *Moniliophthora perniciosa*. This pathogen is the main cause of the decline in cocoa production, and consequently of social, economic and environmental problems. The transcriptomic program of cacao allowed the identification of a pathogenesis-related 10 protein. The corresponding recombinant protein expressed in *Escherichia coli* BL21 showed a strong antifungal activity *in vitro* against *M. perniciosa*. Here, we developed a proteomic analysis of *M. perniciosa* proteins expressed in the presence of recombinant TcPR10. *M. perniciosa* was grown in CPD 2% agar medium; after 15 days, the fungal hyphae were broken and were brought together with 3 µg/mL of TcPR10 for 1h. After this time, the total proteins of the hyphae were extracted using the ADP method, followed by a simple cleaning using the method of SDS-dense and phenol. The quantification was made using a 2-D quantification kit. The proteins were extracted in triplicate and separated using a 12% bi-dimensional SDS-PAGE gel. The 2D map analysis showed approximately 300 "spots" per gel (control and one hour treatment) with differential protein expression pattern. The analysis using a mass spectrometry (naniESI-Q-TOF) was made for the identification of the spots. We identified several proteins involved in fungal metabolism, carbohydrates/proteins metabolism, related proteins to growth and phytotoxics proteins. More spots have been identified to better understand the mechanism of fungi response to protein PR10.

Word Keys: Bi-dimensional SDS-PAGE, mass spectrometry, fungal disease, Protein related-pathogenesis PR10

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