PROTEIN PROFILE OF DORMENTS SPORES OF THE FUNGUS

Moniliophthora roreri

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The frosty pod rot is a disease on Theobroma cacao caused by Moniliophthora roreri, which has caused devastation in the cacao cultures of northwestern Latin America. This disease not has been found in Brazil but biogeographic studies reveal possibility of spread of thrush for the cacao plantations in the country. The main infectious propagules of the disease are the meiospores, these are very resistant and produced in large quantities in every infection. This infectious structure is not well studied molecularly. Here, the objective of this study was to perform proteomic analysis of spores of the fungus M. roreri during the dormant stage. The protein of dormants spores were extracted by Mares et al. (2011) method and were subjected to separation by 2D SDS / PAGE. The protein spots are being digested with trypsin and the peptides will be fractionated using UPLC nanoACQUITY chromatography coupled to the orthogonal QTOFmicro spectrometer (Waters, USA). Mass spectra and peptide sequences obtained by ms/ms will be used to identify the protein by searching databases in SWISSPROT, and NCBI genome of the fungus. 184 proteins were identified from the proteomic analysis of the dormant spores according to corresponding spots in the gel. The proteins can be viewed in all pH range and molecular weight, being more abundant those proteins with molecular weight between 30 and 60 kDa and with pH value between 3 and 5. The protein profile observed in dormant spore Moniliophthora roreri was similar to the profile observed in the hemibiotrofic fungus Moniliophthora perniciosa These results showed that the method protein extraction was efficient and resulted in the first protein map of dormant spores of the fungus Moniliophthora roreri.

Key-Works: Frosty Pod Rot, Spores Proteins, 2D-PAGE.