

IN SILICO CHARACTERIZATION OF THE STEROIDS PATHWAY OF PHYTOPATHOGENIC FUNGUS *MONILIOPHTHORA PERNICIOSA*

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In this study, we identified genes related to the steroids biosynthesis pathway in *Moniliophthora perniciosa* (formerly *Crinipellis perniciosa*), causal agent of witches' broom disease of cocoa (*Theobroma cacao*), using bioinformatic tools. Steroids pathway includes enzymes that are targets for fungicides, especially those involved in ergosterol biosynthesis, and its characterization on *M. perniciosa* could lead to more efficient control and better understanding of the biology of this organism. Data mining was performed on the structural database of the Genome Project of *C. perniciosa* (<http://www.lge.ibi.unicamp.br/vassoura/>), and sequences retrieved from NCBI, SwissProt and KEGG were searched against the *Crinipellis* database using BLAST. We studied 49 proteins, and their e-values ranged from e-162 to 2.5; using an e-value threshold of e-06, we identified homologs for 69% of the proteins (34 out of 49 studied). On a more conservative approach (e-value threshold of e-15), 57% of the proteins were found (28 out of 49 studied). Sequences from *M. perniciosa* showed greatest similarity with *Coprinopsis cinerea* and *Cryptococcus neoformans*. Within the ergosterol pathway, C-8-sterol isomerase (5e-47), lanosterol-14- α -demethylase (7e-96) and sterol-C-14-reductase (3e-71) were found to be present in the fungus. This information will guide cloning and expression studies of potential targets that should be useful for the development of more potent fungicides.

Keywords: bioinformatics; *Crinipellis*; *Moniliophthora perniciosa*; steroids