

IN SILICO RECONSTRUCTION OF THE CELL CYCLE PATHWAY IN PHYTOPATHOGENIC FUNGUS *MONILIOPHTHORA PERNICIOSA*

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We report here probable cell cycle pathway in *Moniliophthora perniciosa* (formerly *Crinipellis perniciosa*), causal agent of witches' broom disease of cocoa (*Theobroma cacao*), based on sequence homology studies with known *Saccharomyces cerevisiae* proteins, using bioinformatic tools. This information could lead to a better understanding on the biology of *M. perniciosa* and its interactions with the host. "Basic Local Alignment Search Tool" – BLAST was used to assess protein similarity in *M. perniciosa*. Protein sequences from the cell cycle pathway of *S. cerevisiae* obtained from KEGG (<http://www.genome.jp/kegg/>) were searched against the structural database of the *C. perniciosa* Genome Project (<http://www.lge.ibi.unicamp.br/vassoura>). We studied 108 proteins and their e-values ranged from 1e-95 to 7.9. Using an e-value threshold of e-15, we were able to identify homologs for 42% of the proteins (45 out of 108 studied), and using a slightly less conservative approach (e-value threshold of e-06) we identified homologs for as high as 62% of the proteins (67 out of 108 studied). Sequences from *M. perniciosa* showed greatest similarity with *Schizosaccharomyces pombe*, followed by *Neurospora crassa*. Based on these results we were able to reconstruct a probable cell cycle pathway on *M. perniciosa*.

Keywords: bioinformatics, cell cycle, comparative genomics, *Crinipellis*, *Moniliophthora perniciosa*.