Title: EVALUATION OF THE SOIL FUNGAL COMMUNITY UNDER BT COTTON CULTIVATION

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Abstract:

Transgenic Bt cotton possess the gene *cry*, derived from the entomopathogenic bacterium *Bacillus thuringienses* Berliner, 1911, which encodes Cry 1Ac protein production. This crystal protein, when ingested by certain caterpillars, is solubilized by the alkaline pH (pH 9.5) in their intestinal tract and cleaved by intestinal proteases so that it is transformed into smaller peptides which bind to specific receptors on the epithelium and initiate a tissue lysis process, which ultimately leads to insect death. Transgenic Bt plants have provided economic and environmental benefits by reducing the use of insecticides, which explains their increased use. However, the introduction of transgenic plants in agricultural ecosystems raises questions of biological and environmental safety. The potential impact of Bt crops on non-target organisms of the soil must be considered, since the protein is expressed constitutively in all parts of the plant so that both the vegetable residues produced during plant development and remaining after harvest, as well as the exudates released by the roots of plants during growth, may contain the Bt toxin and be incorporated into the soil. Furthermore, studies show that the composition of the soil fungal community is strongly influenced by the plant root exudates. The aim of this study was to evaluate the effects of genetically modified cotton resistant to insects on the soil fungal community. The experiment was conducted in the agricultural area of the Universidade Federal da Grande Dourados, where two varieties of cotton (*Gossypium hirsutum* L.) were planted, one expressing a gene from *Bacillus thuringiensis* (Bt) and the other conventional, without the foreign gene. Data was collected monthly throughout the crop cycle, from December 2009 to May 2010. The quantity of fungi in the soil was obtained by the method of cultivation in Petri dishes, in triplicate, using Martin's culture medium and serial dilutions of soil. From the isolates the morphospecies were identified by amplification and sequencing of the Internal Transcribed Spacer (ITS) region of rDNA. The number of fungal colony-forming units in the soil was not directly influenced by the type of cotton grown or by the different growing phases. Soil planted with Bt cotton showed a higher fungal species richness and Shannon Diversity Index than soil cultivated with conventional cotton.

Keywords: Transgenic Cotton; Microbiota; Diversity; Ecology; Fungi.

Development agency: CNPQ