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DIVERSITY OF CULTIVABLE FUNGAL ENDOPHYTES ASSOCIATED WITH SHOOTS OF BT AND NON-BT MAIZE PLANTS

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Interactions between endophytes and host plants could be affected by various factors such as the genetic modification of plants. In the present study, impact of genetic modification (*Bacillus thuringiensis* (Bt) cry proteins) of maize plants on the diversity of fungal endophytes was investigated. This was carried out by assessing diversity of fungal endophytes associated with a Bt-maize (MON810) and its isogenic, non-transgenic parental line at pre-flowering (50 days) and post-flowering (90 days) developmental stages. Fungal communities inhabiting the phyllosphere of Bt-maize and its isogenic parental line were isolated and identified. Twenty-one isolates were obtained from the shoots of Bt-maize and 27 from its isogenic parental line, representing 14 genera and 19 OTUs. The most frequently isolated groups were *Fusarium* from tassels as well as *Epicoccum* and *Alternaria* from leaves. In both cultivars, the leaves had the highest fungal diversity. Results obtained in the study indicate that there was no significant difference between isolates from Bt-maize and its parental line, which means the genetic modification did not affect the diversity of cultivable fungi associated with the Bt-maize genotype. This study further highlights the diversity of fungal endophytes that may benefit their hosts through nutrient cycling and biological control of diseases.

BIOGRAPHY

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