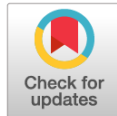


Characteristics of root endophytic fungi communities associated with genetically modified plants



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Root endophytic fungi (EF) spend at least parts of their life cycle inside plant tissues without apparent harm to the host. There is a hypothesis that the endophytic lifestyle is a common strategy for most fungi and they have endophytic ancestors [1]. By receiving habitat and nutrients EF can increase the solubility of nutrients in the plant rhizosphere, stimulate plant growth, and activate the plant's systemic resistance to stress. One of the alternatives to the use of pesticides is the use of resistant transgenic plants, but the potential effects of crop modifications on their associated microorganisms are poorly studied.

The EF communities of transgenic lines of cotton, sugar cane, and maize containing the expressed Cry1 protein from *Bacillus thuringiensis* were compared with communities of non-transgenic plants. There were no significant differences in the composition of the EF community [2, 3]. The introduction of phosphinothricin-N-acetyltransferase and imazapyr herbicide resistance genes for corn and sugar cane also did not affect on EF communities but did affect the bacterial community [3, 4]. The similar effect was observed for transgenic maple plants [5]. The stage of plant development had a more significant effect on EF community than the fact of transformation itself [1].

We believe that the fungal community is more conservative and the introduction of herbicide resistance or toxin synthesis genes into the plant genome has a significantly lesser effect on EF community than on the bacterial one.

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