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LEVEL OF ENVIRONMENTAL POLLUTION TRIGGERS COLONIZING *Miscanthus sinensis* BY ENDOBACTERIA POSSESSING GENES CODING FOR 2,3-DIOXYGENASE

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Abstract

Internal tissues of higher plants are often colonized by endobacteria, which interact with a host plant in different ways and may induce physiological changes in every level of their biological organization. Bacterial endophytes can support plant growth for example by production of phytohormones, N₂ fixation. Besides endophytic bacteria are able to degrade aromatic organic compounds and chelating heavy metals taken up by plants from an environment. The main group of bacterial enzymes that catalyze degradation of aromatic compounds are dioxygenases.

The aim of this study was to check whether endobacteria colonise plants of Chinese silvergrass (*Miscanthus sinensis*) and if so, whether there are differences in endobacteria profile in regard to level of environmental pollutions focusing especially on genes involved in degradation of xenobiotics and chelation of heavy metals.

Bacteria species identification was carry out using molecular methods with sequence of 16S rDNA gene. Total DNA was isolated from surface-sterilized leaves tissues. In PCR reactions catechol 2,3-dioxygenase and 16S rDNA sequences were amplified.

Results showed that endobacteria were present in plants growing both at clean, medium and heavy polluted sites. However, only plants collected from heavy and medium polluted sites were colonized by endobacteria possessing catechol 2,3-dioxygenase gene. Most of the identified bacteria belong to genus *Bacillus* sp.
