

Bacterial communities inhabiting toxic industrial wastewater generated during nitrocellulose production

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Abstract

© 2016 Institute of Molecular Biology, Slovak Academy of Sciences. Investigating the microbial community structure and composition of toxic industrial wastes contaminated with nitrocellulose and various by-products is crucial for understanding the fate of these pollutants in the environment and for the development and application of effective bioremediation processes. In this study, we investigated the chemical properties and toxic potential of wastewater generated during nitrocellulose production. The analyzed wastewater from settling pond contained nitrocellulose powder particles as well as increased ammonium (570-760 mg/L), sulfate (1625-2045 mg/L) and sulfite (864-1014 mg/L) concentrations. The toxicity test results demonstrated that the wastewater samples present acute toxicity for *Paramecium caudatum* and *Daphnia magna*. Furthermore, bacterial community structure in the samples was characterized by pyrosequencing of 16S rRNA genes. Phylogenetic analysis of bacterial sequences indicated that Proteobacteria, Bacteroidetes and Firmicutes were the main phyla in the sample near inlet, whereas various phylotypes of the phyla Proteobacteria, Chlorobi, Bacteroidetes and Gemmatimonadetes dominated in the sample near outlet. Some bacterial members observed in the current work can be considered as agents capable of performing biodegradation of various hazardous contaminants, indicating that the described bacterial communities have a high potential for the development of effective bioremediation strategies.

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Keywords

bacterial communities, Nitrocellulose, pyrosequencing, toxicity, wastewater