Environmental Engineering and Management Journal

October 2012, Vol.11, No. 10, 1753-1761
http://omicron.ch.tuiasi.ro/EEMJ/

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ACCLIMATION OF A MICROBIAL COMMUNITY TO DEGRADE A COMBINATION OF ORGANOCHLORINE HERBICIDES IN A BIOFILM REACTOR

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Abstract

When microbial communities are exposed to a changing or stressing environment, they adjust their metabolic activity; usually, the changes result in acclimated communities that are more able to survive and function under repeated applications of the stressing condition. In this work, the variation of the biodegradation kinetics during the acclimation of a microbial community fixed in a packed-bed biofilm reactor that mimics an aerobic biobarrier, was followed at several operational conditions along four thousand hours. The presence of eight genes involved in the biodegradation of four herbicides was also examined during acclimation of the microbial community. Those genes were *atzA*, *atzB*, *atzC*, and *atzD* encoding enzymes of the catabolic pathway of atrazine and simazine; the *tfdA, tfdC and tfdD* genes that encode enzymes of the catabolic pathway of 2,4-dichlorophenoxyacetic acid, and the *puhB* gene encoding the first enzyme of the degradation of diuron.
The acclimation of the microbial consortium was manifested by changes in its metabolic activity, evaluated through quantitative parameters. By using the volumetric removal rates of COD and TOC $R_{V,COD}$ and $R_{V,TOC}$, and the values of cell concentration, the variation in the specific removal rates $R_{X,COD}$ and $R_{X,TOC}$ was estimated along the bioprocess. The change in these values, joined to the gradual improvement of the specific removal rates R_X of the four herbicides, indicate the long-term acclimation of the microbial consortium.

Key words: acclimation, biodegradation, biofilm reactor, herbicides, microbial consortium

Received: April, 2012; Revised final: September, 2012; Accepted: October, 2012

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