



"Gheorghe Asachi" Technical University of Iasi, Romania



Session 1
**ADVANCES IN BIODEGRADATION OF ORGANICS AND INORGANICS,
PHYTOREMEDIATION AND MYCOREMEDIATION**

Keynote lecture

**BACTERIA WITH AN UNUSUAL APPETITE FOR THE FUEL
OXYGENATE METHYL TERT-BUTYL ETHER (MTBE)**

Max M. Häggblom

*Dept. of Biochemistry and Microbiology, School of Environmental and Biological Sciences, Rutgers University, 76 Lipman Drive,
New Brunswick, NJ 08901, USA*

Abstract

Over the last 30 years methyl tert-butyl ether (MTBE) has become a widespread and persistent pollutant of water resources from its use as a fuel oxygenate in gasoline. As a new anthropogenic pollutant with no natural sources, we are only slowly observing the evolution/selection of bacteria with the ability to degrade MTBE. Degradation rates are slow and MTBE will continue to be a problematic groundwater contaminant for decades to come. Anaerobic MTBE degradation can occur under different anoxic conditions, and may be an important process in anoxic environments and a potential means for remediation of contaminated aquifers. Anaerobic MTBE degradation results in extensive carbon and hydrogen fractionation. Compound-specific stable isotope analysis has thus emerged as a useful tool to demonstrate active in situ MTBE biodegradation and will contribute to the development of appropriate remediation measures. Although complete anaerobic mineralization of MTBE has been demonstrated, MTBE is typically transformed to tert-butyl alcohol. Utilization of the methyl group can ultimately be coupled to either sulfidogenesis or methanogenesis. Aryl O-methyl ethers, such as syringic acid, that are O-demethylated by acetogenic bacteria, can increase the rate of anaerobic MTBE-degradation and these co-substrates offer a potentially useful method of stimulating MTBE-degradation rates in situ. Nonetheless, we still know very little about the anaerobic MTBE degradation process and the responsible organisms have not yet been identified or isolated. To enrich for and characterize the bacteria that degrade MTBE we have maintained sediment enrichment cultures supplemented with MTBE as the sole carbon source for over a decade. Terminal restriction fragment length polymorphism (T-RFLP) analysis in combination with clone analysis was used to identify the phylotypes enriched on MTBE. Three dominant phylotypes that clustered within the Deltaproteobacteria, Chloroflexi and Firmicutes were enriched, with one or more of these mediating the initial attack on MTBE and using the methyl group as a carbon source. The identification of microorganisms mediating anaerobic MTBE degradation is being further pursued by stable isotope probing experiments. The goal is to identify bioindicators for use in combination with compound-specific stable isotope analysis to monitor natural or enhanced in situ biodegradation in polluted environments. This work is important for gaining an understanding of different microbial processes and how these processes, and thus bioremediation, are affected by different amendments and other engineering approaches.
