

## AN ABSTRACT OF A THESIS

### THE USE OF OLIGONUCLEOTIDE PROBES FOR THE DETECTION OF

The Use of Oligonucleotide Probes for the Detection of Sulfate Reducing  
Bacteria in a Constructed Wetlands Treatment System

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Traditional methods for the identification and quantification of contributing microbial populations in an ecosystem have relied on methods such as selective enrichments, pure culture isolations, most probable number estimates, and phenotypic characterizations. Typically these methods result in the isolation of fast-growing "weeds" rather than detection of all microorganisms that contribute to the complex, inter-related food webs that are the rule in natural ecosystems. Nucleic-acid based techniques (molecular biology techniques) are now being developed and used to address these limitations. Over the two decades, hundreds of oligonucleotide probes have been designed and used to identify and quantify populations in a variety of environments.

In this study, molecular biology techniques have been employed to determine if bacteria belonging to the domain Eubacteria, and families *Desulfovibroionaceae* and *Desulfobacteriaceae* were present in one of the treatment cells at the subsurface flow constructed wetlands treatment system at the Baxter, TN, wastewater treatment plant. Based on this work, it was concluded that Cell B at the subsurface flow constructed wetlands treatment system at the Baxter, TN, wastewater treatment plant contains bacteria belonging to the domain Eubacteria, and bacteria belonging to the family *Desulfobacteriaceae*. The sample from the wetland hybridized to all four probes tested: the universal probe, the eubacterial probe, the *Desulfovibrio* probe, and the *Desulfobacter* probe. The presence of bacteria belonging to the family *Desulfovibrionaceae* is supported by the results, but definitive proof for this conclusion is lacking given that the *Desulfovibrio* probe hybridized to the *E. coli* sample.

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