

# Microbial Water Quality and Sources of Indicator Microorganisms in Goose Creek

C. UNLU, L. M. GLOSE, B. A. PUKLIN, C. PARK, M. DURAN<sup>1</sup>

<sup>1</sup> Villanova University, Civil and Environmental Engineering Department, Villanova, PA 19085, USA

## Abstract

This study focused on microbial water quality and sources of indicator microorganisms in Goose Creek located in West Chester, PA. Microbial water quality of Goose Creek was monitored via cultivating and enumerating two indicator microorganisms, Fecal Coliform (FC) and *Enterococcus*. In addition, source of fecal pollution was predicted using a technology called fatty acid methyl profiling (FAME).

Indicator microorganisms are widely used to determine levels of fecal pollution and possible presence of pathogen in water environments. However, the presence and levels of fecal indicator bacteria (FIB) are not enough to determine the source of fecal pollution. Microbial source tracking (MST) or bacterial source tracking (BST) methods are employed to predict the sources of fecal contamination and their proportions (e.g. sewage, livestock and wildlife) in environmental samples.

136 *Enterococcus* and 138 FC isolates were cultured from a total of 30 Goose Creek water samples collected from characteristically 6 different locations. The FAME profiles of total 274 isolates were constructed and then compared with the FAME profiles in two known-source libraries containing 1,134 *Enterococcus* and FC isolates. The known libraries were initially constructed by Haznedaroglu et al. (2005) and Yurtsever et al. (2007) from 9 possible source of fecal pollution (sewage, chicken, cow, deer, geese, horse, sheep, swine and dog) and enlarged during this study in order to predict source of these indicator microorganisms (Duran et al., 2006; Haznedaroglu et al., 2007).

Enumeration of Goose Creek water samples for both FC and *Enterococcus* showed that 96% of the colony forming unit (CFU) counts were higher than EPA's acceptable limit of body contact recreational water. Eleven per cent of the samples were not clean enough to support EPA domestic water supply standards based on FC density. The site, downstream of a domestic wastewater treatment plant, that showed 21% relative human source, was one of the major sources of fecal matter. Horse fecal contamination was found as the most significant contributor for the other site in *Enterococcus* isolates as expected since there are two horse farms next to the sample collection location. More than 20% relative sewage contribution was found for two residential sampling locations. The lowest relative sewage contribution was obtained for the site located close to the Ridley State Park as expected since the obvious fecal pollution sources at that particular site were farm animals, pets and wildlife.

## **REFERENCES**

- Duran, M., Haznedaroglu, B. Z., Zitomer, D. H. (2006). "Microbial source tracking using host specific FAME profiles of fecal coliforms." *Water Res.*, **40**, 67–74.
- Haznedaroglu, B. Z. (2005). "Fatty Acid Methyl Ester Profiling of Indicator Organisms for Microbial Source Tracking." MS Thesis, Villanova University, PA.
- Haznedaroglu, B.Z., Zitomer, D.H., Hughes-Strange, G.B., Duran, M. (2005). "Whole-cell Fatty Acid Composition of Total Coliforms to Predict Sources of Fecal Contamination." *J. Environ. Eng.*, **131**(10), 1426-1432.
- Haznedaroglu, B.Z., Yurtsever, D., Lefkowitz, R.J., Duran, M. (2007). "Phenotypic characterization of *Escherichia coli* through whole-cell fatty acid profiling to investigate host specificity." *Water Research*, **41**, 803-809.
- Yurtsever, D. (2007). "Fatty Acid Methyl Ester Profiling of *Enterococcus* and *Escherichia coli* for Microbial Source tracking." MS Thesis, Villanova University, PA.