

Status of Microbial Source Tracking in the North America

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In the United States and Canada, microbial source tracking is being investigated and used to identify source(s) of fecal pollution of water. Several events of the last year highlighted the advantages and present limitations of this field of research. Of importance to our state are the results and observations obtained during the first national investigation of present-day MST methods and target organisms. This study, conducted by the Southern California Coastal Water Research Project Authority, cataloged and compared the list of methods under consideration, compared similarities and differences between phenotypic and genotypic procedures, discussed the value of library vs. non-library based methods, evaluated different microbial targets (fecal coliforms, *Escherichia coli*, *Enterococcus* sp., *Bacteroides*, human, animal and bacterial viruses), and conducted a blind sample investigation in research laboratories in the United States. A United States Geological Survey investigation of the reliability of library-based source tracking results with *Escherichia coli* as the reference organism, was conducted by a team of researchers led by Don Stoeckel of the USGS, Ohio District. Investigators created a library of isolates from 9 different animals and compared blind and replicate sample isolates to this library. Data was examined for reproducibility, accuracy and robustness. Data was also examined to assist in the identify of methods that could be used in a specific location, to examine the method in a defined setting, or to understand how the method(s) would address a local issue(s). In the summer of 2003, a series of MST presentations at the biannual meeting of the US EPA Gulf of Mexico Program summarized the state of the art of MST research in the southeastern states. These presentations focused on new methods and approaches to MST and included discussions on the use of fluorescent whiting agents as targets of source tracking, the reliability of microbial source assignment using rep-PCR methods, targeted sampling using enterococci, commercial applications of MST, the implication of *E. coli* diversity for MST success and future prospects for MST research. This presentation will summarize these recent collaborations and discuss/suggest new or modified approaches in the search for reliable and valid methods of microbial source tracking.

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Oral Presentation requested

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