# MICROBIAL SOURCE TRACKING (MST) IN SOUTH CAROLINA: LESSONS LEARNED AND FUTURE DIRECTIONS

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## ABSTRACT

Microbial Source Tracking (MST) involves using different types of scientific analyses to distinguish origins of non-point fecal contamination in environmental samples by identifying host-specific characteristics of microorganisms. Because fecal microorganisms indicate the potential presence of enteric pathogens (bacteria, parasites, viruses), which pose a high risk to human health, it is essential to determine the origin(s) of contamination so natural resource managers and public health officials can safeguard waters used for recreation, public water supplies, and growth of fish and shellfish. Sources of fecal contamination must be identified prior to any intervention, remediation, or establishment of total maximum daily load (TMDL) requirements for contaminated watersheds.

Source tracking methods are divided into two broad categories: library dependent and library independent. Library dependent methods include carbon source utilization profiles, multiple antibiotic resistance methods (MAR, ARA, and ARP), REP-, ERIC and BOX PCR, whole genome restriction fragment length polymorphism (RFLP) methods such as pulsed field gel electrophoresis (PFGE) and ribotyping. Library independent methods include host-specific traditional and real-time PCR, and F+ RNA coliphage typing. Chemical methods include caffeine, optical brighteners, fragrances, and fecal sterols. The NOAA, CCEHBR Laboratory has used several of the above methods for MST studies, and recently has developed new molecular methods for pathogen detection. These newer methods will allow rapid diagnosis of microbial threats to human health along recreational beaches and in shellfish. Results from environmental studies, successes and failures with various MST techniques, along with advantages and disadvantages of the more widely used MST methods will be presented.

## KEYWORDS

Microbial source tracking, fecal coliform bacteria, human health, analysis