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BST

Bacterial Source Tracking

UTHealth | School of Public Health
The University of Texas Health Science Center at Houston

Soil Water TSSWCB

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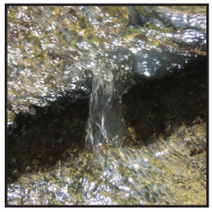
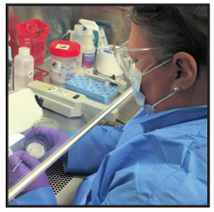
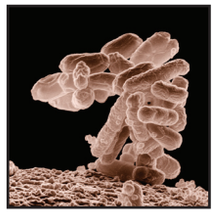
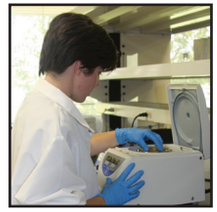
Developed by the Texas Water Resources Institute and funded through a State General Revenue nonpoint source grant from the Texas State Soil and Water Conservation Board

 EM-111

Learn why Bacterial Source Tracking is the foremost tool for identifying sources of fecal pollution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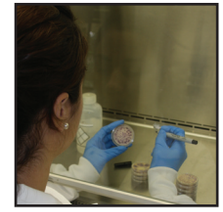

The Need

According to the 2010 Texas Integrated Report, there are 303 bacterially impaired waterbodies in Texas. Nonpoint sources (NPS) of pollution greatly affect water quality. Identifying and assessing sources of fecal pollution is a key component in effectively implementing a NPS pollution management program.

Proper evaluation of these sources is needed to properly assess risk in contact recreation, target best management practices, and develop effective watershed protection plans (WPPs) and bacterial total maximum daily loads (TMDLs).

The freshwater contact recreation use criterion used to determine impairment includes both a geometric mean for *Escherichia coli* (*E. coli*) of 126 colonies per 100 ml and. The saltwater contact recreation use criterion includes both a geometric mean for enterococci of 35 colonies per 100 ml. The oyster water use criterion includes a median fecal coliform concentration of 14 colonies per 100 ml and no more than 10% of samples may exceed 43 colonies per 100 ml.

BST Technologies

The premise behind BST is that genetic and phenotypic tests can identify bacterial strains that are host-specific so that the original host source of the fecal contamination can be identified.

Often *E. coli* or *Enterococcus* spp. are used as the bacteria targets in BST, as this provides a direct link with water quality standards which are usually based on one of these two indicators. The technologies used for BST have evolved greatly in the past few years.

Identification libraries consisting of thousands of isolates obtained from thousands of animal and human fecal samples collected in different geographical regions of Texas have already been established. In addition, several thousand more *E. coli* isolates from source samples have been archived and are available to researchers.

About the Texas *E. coli* BST Library

The Texas *E. coli* BST library currently contains 1,393 *E. coli* isolates obtained from 1,201 different domestic sewage, wildlife, livestock and pet fecal samples. Isolates were selected after screening several thousand isolates from nine different studies throughout Texas.

Library development is one of the most costly components of BST studies. Currently, Dr. George Di Giovanni, at the University of Texas School of Public Health – El Paso Regional Campus, and Dr. Terry Gentry, at the Texas A&M University Soil and Aquatic Microbiology Laboratory, are cross-validating the libraries generated in Texas BST studies in an attempt to explore issues of geographical and temporal stability of BST libraries, refine library isolate selection and determine accuracy of water isolate identification.

By selecting *E. coli* source isolates that are correctly identified from multiple watersheds, project partners hope to find more geographically stable and host-specific isolates, resulting in more accurate source tracking. Library-independent methods are also currently being explored, based on Texas Commission on Environmental Quality and Texas State Soil and Water Conservation Board Bacterial Total Maximum Daily Load Task Force recommendations.

Moving Forward

For future WPP and TMDL development projects, an assessment phase using a "toolbox" approach is recommended. The assessment phase should include targeted monitoring of suspected pollution sources, use of library-independent and dependent methods to identify the presence of domestic sewage pollution and screening of water isolates from the new watershed against the existing library to determine the need for collection of local source samples and expansion of the library.

Decision on which method to utilize can be assisted with the use of the matrix provide in Chapter 2 of the EPA Microbial Source Tracking Guide. It is critical to follow the same analytical protocols for comparability of BST data sets. The state BST laboratories (UTSPH – El Paso Regional Campus; Texas A&M Soil and Aquatic Microbiology Laboratory) can provide detailed BST protocols. In addition, the sharing of bacterial isolates and BST data between the state laboratories and others is welcomed.