

## **Bacterial Source Tracking in Texas: Status and Future Directions**

George D. Di Giovanni, PhD

Texas AgriLife Research, Texas A&M University System

The premise behind bacterial source tracking (BST) is that laboratory tests can identify fecal bacterial strains that are host specific so that sources of fecal contamination can be identified. While many different fecal organisms have been used for source tracking, the fecal bacterium *E. coli* has several advantages as a BST target. These advantages include positive correlation with the presence of fecal contamination, its use in determining human health risk assessments, and water quality regulatory significance. However, a disadvantage of most *E. coli* BST methods is that genetic fingerprint reference libraries of *E. coli* isolated from known sources (*e.g.*, domestic sewage, livestock, and wildlife) are needed to identify the sources of *E. coli* obtained from water samples. The development of an identification library can be a time consuming and expensive component of a BST study. Ideally, a local watershed library should be developed using a large variety of potential fecal sources collected from the watershed at the same time water samples are collected. Unfortunately, time and resources infrequently allow for the development of such comprehensive local watershed libraries for each study. Because of the limitations of small libraries, including identification accuracy and bias, small local libraries should not be considered as stand-alone libraries. One solution to this dilemma appears to be the development of a statewide library by combining smaller collections of known source isolates.

Our current research focuses on the development of a Texas bacterial source tracking library of *E. coli* ERIC-PCR and RiboPrint (ERIC-RP) fingerprints obtained in several previous BST studies. A preliminary refinement of the library was performed by removing cosmopolitan *E. coli* strains that confounded accurate source identification. Challenge of the Texas library using known source *E. coli* obtained from different watersheds demonstrated that the developing statewide library identified the challenge isolates about equally well as small local watershed libraries, although neither provided acceptable identification accuracy. After further refinement, the Texas library revealed a 76% average rate of correct classification (ARCC) using a seven-way split of sources and an 87% ARCC using a three-way split of sources. Therefore, it appears that good progress is being made towards the development of a statewide library, although additional refinement and challenges need to be performed.

In accordance with the strategy outlined in the Texas Bacterial TMDL Task Force Report, library independent BST methodology is also being investigated. Progress has been made in the development and evaluation of *Bacteroidales* qualitative and quantitative PCR methodology, including a method to detect feral hog fecal pollution. Together, these efforts should help meet the future BST needs of state agencies in a cost-effective and timely manner.

## Biographical Sketch – Di Giovanni

Dr. Di Giovanni is Professor and Faculty Fellow of Environmental Microbiology with the Texas AgriLife Research Center at El Paso, Texas A&M University System. He received his Ph.D. from the University of Arizona and did postdoctoral work as a National Research Council Associate with the USEPA. Prior to joining Texas AgriLife Research, he was Senior Environmental Scientist for the American Water Works Company. His research program focuses on the detection and molecular analysis of waterborne pathogens, including *Cryptosporidium*, *Giardia* and viruses; and microbial source tracking to determine the human and animal sources of fecal pollution of water supplies. He and his research team were recently honored with a Texas Environmental Excellence Award.