



## USDA-CSREES 2006 National Water Quality Conference

### Use of Protein Biomarkers to Differentiate *Escherichia coli* Strains Isolated from Human and Animal Sources

Non-point source (NPS) microbial contamination is well recognized as a major threat to the safety of watersheds utilized for recreation and as sources of drinking water. The ability to identify the source of microbial pollution, Microbial source tracking (MST), is essential to any efforts directed toward eliminating NPS pollution. Although Coliform bacteria are commonly recognized indicators of fecal contamination of surface drinking water sources, it is very difficult to distinguish between contamination from human versus animal sources. Presently used methods of microbial source tracking (MST) such as antibiotic resistance, phenotype number ratios, DNA sequencing and ribotyping all have certain limitations such as cost, speed, accuracy and precision. We propose to develop a method using electrospray ionization-liquid chromatography/mass spectrometry (ESI-LC/MS) to identify the sources of microbial contamination based on peptide biomarkers. By comparing the mass spectra of proteins and peptides extracted from different *E. coli* strains isolated from the intestines of humans, and various wild and domestic animals we hope to develop a method capable of accurately linking coliforms recovered from suspected contaminated water sources to their animal source of origin.

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