Bacteria Source Tracking To Improve TMDL Development in Bacteria-Impaired Streams

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Problem Statement
Surface water impairment by fecal coliform bacteria is a water quality issue of national scope and significance. In Virginia alone, more than 775 streams segments are on the Commonwealth’s 303(d) list of impaired waters because of fecal coliform bacteria. One of the major obstacles to improving stream water quality is that the potential sources of fecal coliform bacteria are numerous and the dominant sources are generally unknown. This study demonstrates the emerging technology of bacteria source tracking (BST) and its cooperative effort between the USGS, the Department of Environmental Quality, the Department of Conservation and Recreation, and Fairfax County.

Watershed Modeling (HSFP)

1) Fecal Coliform Modeling Process
2) Accotink Creek: Fecal Coliform Simulation
3) Recalibrate Model to BST Data
4) Current Fecal Coliform Conditions

Bacteria Source Tracking Results

What can be done to reduce bacterial contamination and improve water quality?

1) Cattle: Daily direct access to streams
2) Poultry: Extend waste composting period
3) Dogs and Cats: Clean-up after your dog and properly dispose of litter box contents
4) Human: Locate sewage contributions

Future Directions
The USGS is developing a human wastewater study in Accotink Creek. The system was found to be impacted by bacteria of human origin. To identify the distribution and physical sources of the human waste in Accotink Creek, we will initiate a comprehensive, multi-phase investigation of the streams, tributaries, and flowing storm drains in the watershed.

Potential human sources: failing septic systems, leaking and broken sewer lines, environmental pipes, straight pipes, sewer line overflows

Indicator tracers: fecal coliform, e. coli, phosphorus, nitrogen, conductivity, temperature, turbidity

Confirmatory tracers: naphthalene, pH, naphthalene, ortho-phenylphenol, tetrachloroethylene, total suspended solids, organic compounds (caffeine, cotinine)

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Site Descriptions
Three watersheds with diverse land uses and potential bacteria sources were studied.

Methods
The field samples were collected during both low-flow and storm-flow periods, processed in the field (membrane filtration), incubated for 24 hours, and enumerated for fecal coliform concentrations.

E. coli were isolated from the fecal coliform bacteria and analyzed by genetic fingerprinting (ribotyping). The ribotyping analysis characterized the E. coli for each strain isolated from the source and the dominant sources were identified.