

**Determining Sources of Fecal Pollution in the Blackwater River Watershed,  
Franklin County, Virginia**

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# **DETERMINING SOURCES OF FECAL POLLUTION IN THE BLACKWATER RIVER WATERSHED, FRANKLIN COUNTY, VIRGINIA**

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Crop and Soil Environmental Sciences

(ABSTRACT)

Antibiotic resistance analysis (ARA) was used to determine sources of fecal pollution in the Blackwater River in South-central Virginia. The Department of Environmental Quality designated six segments as impaired due to high fecal coliform concentrations with non-point source (NPS) agriculture the suspected source of impairment. The Blackwater River watershed encompasses 72,000 ha of dairy, beef, and intensive production agriculture, abundant wildlife populations and many homes with onsite septic systems. A library of antibiotic resistance profiles based on 30 concentrations of 9 antibiotics was developed for 1,451 enterococci isolates from human, cattle, chicken, horse, goat, sheep, deer, raccoon, muskrat, goose, duck, coyote, and wild turkey fecal samples. Each isolate was classified as human, wildlife or livestock. Correct classification rates were 82.3% for human, 86.2% for livestock and 87.4% for wildlife isolates when profiles were analyzed with discriminant analysis.

Profiles were also determined for 48 isolates from 128 stream samples collected periodically from August 1999 thru April 2001 and compared to the known sources using discriminate analysis. A human signature was found at each site at least once during the year, ranging from 0.0% to 85.0% of the sample isolates. The livestock signature varied from 2.3% to 100% over sites and months, and the wildlife signature varied from 0.0% to

79.5%. The results indicate that both humans and wildlife contribute to fecal pollution in addition to the suspected source, livestock, and reducing fecal pollution will require consideration of all three sources. The results from this research are being used to develop a total maximum daily load (TMDL) project allocations for fecal coliforms in the Blackwater River.

Isolates identified by ARA were also profiled using the Biolog™ metabolic identification system. A library of metabolic profiles was constructed from known source isolates. Stream isolates were identified by Biolog and the metabolic profile was compared to the Biolog library. Of ten stream isolates identified by ARA as human, the Biolog library identified one as human, four as livestock, and five as wildlife. Of ten isolates identified by ARA as livestock, the Biolog library identified seven as livestock and three as wildlife. Of ten isolates identified by ARA as wildlife, one was identified as human, three as livestock and six as wildlife. The overall correct classification of Blackwater isolates in the Biolog library was 14 of 30 isolates, or 47%. Although the Biolog library was constructed with some isolates from the Blackwater basin, there may not be enough isolates in the Biolog library to adequately represent the variability shown by the Blackwater isolates, resulting in lower than expected correct classifications. In spite of these results, Biolog remains promising as one of several tools with potential as a bacterial source tracking method.