

Brief Summary of BST Report by Dr. Mark Franna & Dr. Elichia Venso, Salisbury University, July 2009.

MDE has contracted with researchers at Salisbury University to conduct Bacteria Source Tracking (BST) for watersheds in Maryland impaired by bacteria. A final report was received in July 2009 from Salisbury University for eight watersheds in Anne Arundel County. These watersheds include: Furnace and Marley Creeks, Magothy River, Severn River, South River, Rhode & West Rivers, and the Anne Arundel County Coast along the Chesapeake Bay, near the mouth of the Severn River. MDE staff collected the samples and Salisbury University completed the laboratory and statistical analysis. Bacteria source tracking (BST) is used in the bacteria TMDL development process to identify the relative contributions of different sources of bacteria to in-stream water samples. BST monitoring is conducted in one or more stations in the watershed under study, where samples are collected at least once per month for one year. Sources are defined as domestic (pets and human associated animals), human (human waste), livestock (agricultural animals), and wildlife (mammals and waterfowl).

The methodology used was the Antibiotic Resistance Analysis (ARA), with *Enterococcus* spp. as the indicator organism. Samples are collected within the watershed from known fecal sources, and a BST technique known as ARA is used to identify the patterns of antibiotic resistance of these known sources. To identify probable sources, these antibiotic resistance patterns are then compared to isolates of unknown bacteria from ambient water samples. Previous BST publications have demonstrated the predictive value of using this particular technique and indicator organism. A variety of different host species can potentially contribute to the fecal contamination found in natural waters. In ARA, the premise is that bacteria isolated from different hosts can be categorized with a known probability based upon differences in the selective pressure of microbial populations found in the gastrointestinal tract of those hosts (humans, livestock, pets, wildlife). Microorganisms isolated from the fecal material of wildlife would be expected to have a much lower level of resistance to antibiotics than isolates collected from the fecal material of humans, livestock and pets. In addition, depending upon the specific antibiotics used in the analysis, isolates from humans, livestock and pets could be differentiated from each other. Finally, a statistical analysis is used to then predict the likely host source of the water isolates (unknowns).

The following tables show the results specific to Furnace and Marley Creeks, and include the species identified during field collection that are potential contributors to bacteria in these watersheds.

Furnace Creek: Source category, total number, number of unique patterns for the Furnace Creek known-source library.

Source Category	Potential Sources	Total Isolates	Unique Patterns
Human	human	185	133
Livestock	n/a	0	0
Pet	dog	173	105
Wildlife	deer, fox, rabbit, raccoon	207	72
Total		565	310

Furnace Creek: Predicted host source distribution of water samples/isolates.

Source	Distribution
Human	32.5%
Livestock	0
Pet	29.4%
Wildlife	38.1%
Total	100%

The results for Furnace Creek show that wildlife contributes the highest percentage of bacteria to the watershed, followed by human and dogs. No livestock was observed in the Furnace Creek watershed.

Marley Creek: Source category, total number, number of unique patterns for the Marley Creek known-source library.

Source Category	Potential Sources	Total Isolates	Unique Patterns
Human	human	166	126
Livestock	n/a	0	0
Pet	dog	155	81
Wildlife	beaver, deer, fox,	152	44
Total		473	251

Marley Creek: Predicted host source distribution of water samples/isolates.

Source	Distribution
Human	34.2%
Livestock	0
Pet	34.6%
Wildlife	31.2%
Total	100%

The results for Marley Creek are slightly different than Furnace Creek and show that the predominant source is dogs, closely followed by human and finally, wildlife. Again, there were no livestock.

MDE has discovered that in many of the more urban watersheds, dog waste can potentially be a significant source. Human sources were collected from the Patapsco WWTP that serves this area, but discharges to the Patapsco River.

Field Observations:

The following is a quote from field observations during the year-long scat collection for Furnace and Marley Creeks: "These watersheds drain Glen Burnie. Characterized by flat to gently sloping coastal plain sediments (often coarse tightly packed sands) in the Western Shore Uplands geologic region. This is densely populated suburban/ urban, middle to lower income working families mostly served by public sewer which discharges outside of the watersheds but has lots of infrastructure potential for failure/ overflow. There are few parks and public dog walking areas. Pet waste along the B&A trail is abundant. There is no livestock within these watersheds but there are horse

and hog farms adjacent. Wildlife is predominated by fox. Their abundance was surprising. There were almost no whitetail deer- something else I found surprising.”

The other watersheds included in the report had results showing wildlife or pet as the predominant source. Details are found in the full report. According to the results of the report the following is a summary of the sources in the six other watersheds:

Magothy River: Wildlife 28%; Pet 26%; Livestock 26%; Human 20%.

Severn River: Wildlife 28%; livestock 24%; Human 24%; Pet 23%

South River: Pet 33%; Livestock 24%; Wildlife 22%; Human 21%

West Chesapeake Bay: Pet 37%; Human 28%; Wildlife 19%; Livestock 15%

Rhode River: Wildlife 36%; Livestock 24%; Human 22%; Pet 18%

West River: Pet 37%; Human 28%; Wildlife 19%; livestock 15%