

4. Article Two, B.5- Water Quality Monitoring (“WQM”) Plan – Report on whether any of the semi-annual (or annual) WQM required under Article Two, B.5, was conducted during the quarter, and if so, in which sewer basins, and report the results of that monitoring (both BST and fecal coliform) for each such sewer basin.

The 2011 annual round of water quality monitoring was conducted on March 29, 2011. All 26 of the sewer basins were sampled (semi-annual and annual). Human source fecal bacteria were identified in one or more samples from four sewer basins. Results are presented below.

As part of a periodic re-evaluation of the Water Quality Monitoring Plan and of the methodologies used, the Virginia Tech laboratory that provides the Bacterial Source Tracking (BST) testing services has conducted a library-independent test for human *Bacteroides* gene on over 25% (15 of 51 samples) of the Polymerase Chain Reaction (PCR) tested samples, including all those that reported measurable human source percentages by PCR. These results are presented below.

A limited round of water quality samples from four stations in the Anacostia River watershed, was collected on June 14, 2011. Quarterly sampling from one station in each of four sewer basins is supplemental to the annual and semi-annual sampling program. Results will be reported in the Third Quarter of 2011.

Basins Subject to Semi-Annual Monitoring and Reporting Requirements:

a. Broad Creek-

	BST Results:	Fecal Bacteria Results: (<i>Enterococcus</i> CFU/100ml)
BRC001 – downstream (Henson Creek)	Too few bacteria for BST source determination	<10
BRC002 – upstream (Henson Creek)	Too few bacteria for BST source determination	<10

b. Cabin John-

	BST Results:	Fecal Bacteria Results: (<i>Enterococcus</i> CFU/100ml)
CBJ001 – downstream	Human – 0% (0%) Avian – 41% (42%) Canine – 5% (5%) Deer – 15% (13%) Misc. Wildlife – 23% (24%) Non-human Unknown – 16% (16%) Bacteroides – Negative	90 (88)
	Too few bacteria for BST source determination Bacteroides – Negative	
CBJ002 – upstream	Too few bacteria for BST source determination	<10
	Bacteroides – Negative	

Note: Values in parentheses for station CBJ001 are for field duplicate sample.

c. Horsepen-		Fecal Bacteria Results: (<i>Enterococcus</i> CFU/100ml)
	BST Results:	
HSP001 – downstream	Human – 16% Avian – 32% Canine – 7% Deer – 11% Horse – 12% Misc. Wildlife – 13% Non-human Unknown – 9% Bacteroides – Positive	275
HSP002 – upstream	Too few bacteria for BST source determination Bacteroides – Negative	<10 (<10)

Note: Value in parentheses for station HSP002 is for field duplicate sample.

d. Indian Creek-		Fecal Bacteria Results: (<i>Enterococcus</i> CFU/100ml)
	BST Results:	
INC001 – downstream	Human – 0% Avian – 35% Canine – 9% Deer – 9% Horse – 17% Misc. Wildlife – 17% Non-human Unknown – 13%	25
INC002 – upstream	Human – 0% Avian – 30% Canine – 11% Deer – 14% Horse – 13% Misc. Wildlife – 23% Non-human Unknown – 9%	28

e. Little Falls-		Fecal Bacteria Results: (<i>Enterococcus</i> CFU/100ml)
	BST Results:	
LFS001 – downstream	Human – 0% Avian – 29% Canine – 11% Deer – 13% Misc. Wildlife – 24% Non-human Unknown – 23%	43
LFS002 – upstream	Human – 0% Avian – 33% Canine – 9% Deer – 12% Misc. Wildlife – 27% Non-human Unknown – 19%	20

f. Lower Anacostia-		Fecal Bacteria Results: (<i>Enterococcus</i> CFU/100ml)
	BST Results:	
ANA001 – downstream	Human – 0% Avian – 47% Canine – 8% Deer – 12% Misc. Wildlife – 19% Non-human Unknown – 14%	53
ANA002 – upstream	Human – 0% Avian – 43% Canine – 12% Deer – 10% Misc. Wildlife – 14% Non-human Unknown – 21%	15

g. Lower Beaverdam Creek-		Fecal Bacteria Results: (<i>Enterococcus</i> CFU/100ml)
	BST Results:	
LBD001 – downstream	Human – 7% Avian – 37% Canine – 12% Deer – 8% Misc. Wildlife – 21% Non-human Unknown – 15% Bacteroides – Positive	148
LBD002 – upstream	Human – 13% Avian – 34% Canine – 17% Deer – 11% Misc. Wildlife – 17% Non-human Unknown – 8% Bacteroides – Positive	1,025

h. Muddy Branch-		Fecal Bacteria Results: (<i>Enterococcus</i> CFU/100ml)
	BST Results:	
MDB001 – downstream	Human – 0% Avian – 43% Canine – 10% Deer – 9% Misc. Wildlife – 21% Non-human Unknown – 17%	40
MDB002 – upstream	Too few bacteria for BST source determination	15 (<10)

Note: Value in parentheses for station MDB002 is for field duplicate sample.

i. Northeast Branch-		Fecal Bacteria Results: (<i>Enterococcus</i> CFU/100ml)
BST Results:		
NEB001 – upstream	Too few bacteria for BST source determination	<10
NEB002 – downstream	Human – 0% Avian – 37% Canine – 12% Deer – 14% Misc. Wildlife – 24% Non-human Unknown – 13%	15
j. Northwest Branch-		Fecal Bacteria Results: (<i>Enterococcus</i> CFU/100ml)
BST Results:		
NWA001 – downstream	Human – 0% Avian – 35% Canine – 11% Deer – 16% Misc. Wildlife – 22% Non-human Unknown – 16% Bacteroides – Negative	20
NWA002 – upstream	Human – 0% Avian – 39% Canine – 7% Deer – 12% Misc. Wildlife – 27% Non-human Unknown – 15% Bacteroides – Negative	25
k. Oxon Run-		Fecal Bacteria Results: (<i>Enterococcus</i> CFU/100ml)
BST Results:		
OXN001 – downstream	Human – 0% (0%) Avian – 44% (41%) Canine – 14% (13%) Deer – 9% (12%) Misc. Wildlife – 20% (19%) Non-human Unknown – 13% (15%) Bacteroides – Negative (Negative)	243 (315)
OXN002 – upstream (Watts Branch)	Human – 0% Avian – 46% Canine – 10% Deer – 11% Misc. Wildlife – 27% Non-human Unknown – 6% Bacteroides – Negative	70

Note: Values in parentheses for station OXN001 are for field duplicate sample.

l. Paint Branch-		Fecal Bacteria Results: (<i>Enterococcus</i> CFU/100ml)
BST Results:		
PNT001 – downstream	Human – 0% Avian – 42% Canine – 14% Deer – 15% Horse – 6% Misc. Wildlife – 14% Non-human Unknown – 9%	35
PNT002 – upstream	Too few bacteria for BST source determination	<10

m. Parkway-		Fecal Bacteria Results: (<i>Enterococcus</i> CFU/100ml)
BST Results:		
PKY001 – downstream (Bear Branch)	Human – 5% Avian – 45% Canine – 12% Deer – 12% Misc. Wildlife – 19% Non-human Unknown – 7%	93
	Bacteroides – Negative	
PKY002 – upstream (Walker Branch)	Human – 0% Avian – 39% Canine – 13% Deer – 9% Misc. Wildlife – 21% Non-human Unknown – 18%	30
	Bacteroides – Negative	

n. Piscataway-		Fecal Bacteria Results: (<i>Enterococcus</i> CFU/100ml)
BST Results:		
PSW001 – downstream	Human – 0% Avian – 46% Canine – 10% Deer – 14% Misc. Wildlife – 19% Non-human Unknown – 11%	58
PSW002 – upstream	Too few bacteria for BST source determination	<10

o. Rock Creek-		Fecal Bacteria Results: (<i>Enterococcus</i> CFU/100ml)
BST Results:		
RKC001 – downstream	Human – 0% Avian – 39% Canine – 7% Deer – 15% Misc. Wildlife – 22%	60

	Non-human Unknown – 17%	
RKC002 – upstream	Too few bacteria for BST source determination	<10

p. Seneca Creek- Fecal Bacteria Results:
BST Results: (Enterococcus CFU/100ml)

SNC001 – downstream	Too few bacteria for BST source determination	<10
SNC002 – upstream	Human – 0% Avian – 37% Canine – 9% Deer – 13% Misc. Wildlife – 18% Non-human Unknown – 23%	28

q. Sligo Creek- Fecal Bacteria Results:
BST Results: (Enterococcus CFU/100ml)

SLC001 – downstream	Human – 7% Avian – 33% Canine – 9% Deer – 14% Misc. Wildlife – 19% Non-human Unknown – 18%	825
	Bacteroides – Negative	
SLC002 – upstream	Human – 0% Avian – 39% Canine – 11% Deer – 9% Misc. Wildlife – 21% Non-human Unknown – 20%	38
	Bacteroides – Negative	

r. Upper Beaverdam Creek- Fecal Bacteria Results:
BST Results: (Enterococcus CFU/100ml)

UBD001 – downstream	Too few bacteria for BST source determination	<10
UBD002 – upstream	Too few bacteria for BST source determination	<10

s. Watts Branch- Fecal Bacteria Results:
BST Results: (Enterococcus CFU/100ml)

WTB001 – downstream	Too few bacteria for BST source determination	<10
WTB002 – upstream	Too few bacteria for BST source determination	<10

t. Western Branch-		Fecal Bacteria Results: (<i>Enterococcus</i> CFU/100ml)
BST Results:		
WNB001 – downstream	Too few bacteria for BST source determination	<10
WNB002 – upstream	Too few bacteria for BST source determination	<10

Basins Subject to Annual Monitoring and Reporting Requirements-

a. Dulles Interceptor-		Fecal Bacteria Results: (<i>Enterococcus</i> CFU/100ml)
BST Results:		
DSI001	Too few bacteria for BST source determination	<10

b. Mattawoman-		Fecal Bacteria Results: (<i>Enterococcus</i> CFU/100ml)
BST Results:		
MTW001	Too few bacteria for BST source determination	17

c. Monacacy-		Fecal Bacteria Results: (<i>Enterococcus</i> CFU/100ml)
BST Results:		
MCY001	Too few bacteria for BST source determination	<10 (<10)

d. Patuxent Center-		Fecal Bacteria Results: (<i>Enterococcus</i> CFU/100ml)
BST Results:		
PTC001 (Mill Branch)	Too few bacteria for BST source determination	<10

e. Patuxent North-		Fecal Bacteria Results: (<i>Enterococcus</i> CFU/100ml)
BST Results:		
PTN001 (Hawlings River)	Too few bacteria for BST source determination	<10

f. Rock Run-		Fecal Bacteria Results: (<i>Enterococcus</i> CFU/100ml)
BST Results:		
RCM001	Too few bacteria for BST source determination	<10

OTHER MATTERS TO BE BROUGHT TO THE ATTENTION OF EPA, MDE AND THE CITIZENS GROUPS:

As indicated in the text under Article Two, B.5- Water Quality Monitoring (WQM) Plan, under the Polymerase Chain Reaction (PCR) testing protocol for the approved WQM Plan, human source bacteria were identified in one or more samples from four sewer basins. In light of the rapid evolution of Bacterial Source Tracking (BST) technologies, the WQM Plan recommends a periodic re-evaluation of the results of the PCR testing protocol and the methodologies being used. The Virginia Tech laboratory that provides the BST testing services, and which is at the forefront of BST methods development, has recently noted that the current library-based PCR testing protocol may, from time to time, result in false positives where reported human percentage allocations are below 10%. In order to ensure that WSSC receives and presents the most accurate analysis of the presence of human source bacteria, the Virginia Tech laboratory performed additional library-independent human *Bacteroides* gene testing on a subset of the March 2011 samples. This additional testing revealed false positives in two of the basins sampled, Parkway and Sligo Creek, where the reported percentage allocations were 5% and 7%, respectively. Consequently, application of this additional testing for the Second Quarter of 2011 leads to the conclusion that human source bacteria were identified in one or more samples from only two sewer basins.