

Bacterial Source Tracking Analyses to Support Virginia's TMDLs

Shellfish Stations

Prepared by

MapTech, Inc.

in cooperation with

New River Highlands RC&D

for

Virginia Department of Environmental Quality

Contract #12186

December 2006



MapTech, Inc
3154 State Street
Blacksburg, VA 24060
(540)961-7864



CONTENTS

CONTENTS.....	i
FIGURES.....	ii
TABLES.....	iii
ACKNOWLEDGEMENTS.....	vi
1. INTRODUCTION.....	1-1
2. OBJECTIVES.....	2-1
3. METHODS.....	3-1
3.1 Collection of Known Sources.....	3-1
3.2 Development of Known-Source Libraries.....	3-3
3.3 BST Analyses.....	3-3
4. KNOWN-SOURCE LIBRARY DEVELOPMENT.....	4-1
5. RESULTS.....	5-1
5.1 Results for Piedmont Region.....	5-2
5.2 Results for Tidewater Region.....	5-22
6. DISCUSSION.....	6-1
REFERENCES.....	R-1
APPENDIX A.....	A-1

FIGURES

Figure 3.1 Locations of known-source sampling conducted to support this year's and previous years' BST analyses..... 3-2

Figure 3.2 Spatial distribution of impaired segments identified by region. 3-4

Figure 5.1 Bacterial sampling stations in VADEQ's Piedmont Region. 5-2

Figure 5.2 Bacterial sampling stations in VADEQ's Tidewater Region. 5-22

TABLES

Table 3.1	Source samples collected for BST library development.	3-3
Table 3.2	Distribution of stations sampled by VDH-DSS in support of this study.	3-5
Table 4.1	Results of known-source library development.	4-1
Table 5.1	Summary of VDH-DSS bacterial sampling in VADEQ’s Piedmont Region.	5-3
Table 5.2	Bacterial Source Tracking for Potomac River: Gardner Creek at Station 6-3.	5-4
Table 5.3	Bacterial Source Tracking for Potomac River: Jackson Creek at Station 6-5.	5-4
Table 5.4	Bacterial Source Tracking for Potomac River: Jackson Creek at Station 6-6.	5-5
Table 5.5	Bacterial Source Tracking for Potomac River: Bonum Creek at Station 6-8.	5-5
Table 5.6	Bacterial Source Tracking for Potomac River: Bonum Creek at Station 6-9.	5-6
Table 5.7	Bacterial Source Tracking for Potomac River: Cod Creek at Station 9-3.	5-6
Table 5.8	Bacterial Source Tracking for Potomac River: Cod Creek at Station 9-5.	5-7
Table 5.9	Bacterial Source Tracking for Potomac River: Code Creek at Station 9-6.	5-7
Table 5.10	Bacterial Source Tracking for Potomac River: Hull Creek at Station 9-16.	5-8
Table 5.11	Bacterial Source Tracking for Potomac River: Rogers Creek at Station 9-9.1Y.	5-8
Table 5.12	Bacterial Source Tracking for Potomac River: Bridgeman Creek at Station 9-10.	5-9
Table 5.13	Bacterial Source Tracking for Potomac River: Cubitt Creek at Station 9-19.	5-9
Table 5.14	Bacterial Source Tracking for Great Wicomico-Piankatank Rivers: Owens Pond at Station 11-5.	5-10
Table 5.15	Bacterial Source Tracking for Great Wicomico-Piankatank Rivers: Little Taskmakers Creek at Station 11-1A.	5-10
Table 5.16	Bacterial Source Tracking for Lower Rappahannock River: Millenbeck Prong at Station 21-8.	5-11

Bacterial Source Tracking Analyses to Support Virginia’s TMDLs

Table 5.17	Bacterial Source Tracking for Lower Rappahannock River: Ewells Prong at Station 21-9.....	5-11
Table 5.18	Bacterial Source Tracking for Lower Rappahannock River: Myer Creek at Station 21-17X.....	5-12
Table 5.19	Bacterial Source Tracking for Lower Rappahannock River: Taylor Creek at Station 21-15B.	5-12
Table 5.20	Bacterial Source Tracking for Lower Rappahannock River: Hills Creek at Station 21-23.....	5-13
Table 5.21	Bacterial Source Tracking for Lower Rappahannock River: Bells Creek at Station 21-24.....	5-13
Table 5.22	Bacterial Source Tracking for Lower Rappahannock River: Eastern Branch at Station 21-30A.....	5-14
Table 5.23	Bacterial Source Tracking for Lower Rappahannock River: Eastern Branch at Station 21-31.....	5-14
Table 5.24	Bacterial Source Tracking for Lower Rappahannock River: Eastern Branch at Station 21-33.....	5-15
Table 5.25	Bacterial Source Tracking for Lower Rappahannock River: Western Branch at Station 21-46.	5-15
Table 5.26	Bacterial Source Tracking for Lower Rappahannock River: Senior Branch at Station 21-42.	5-16
Table 5.27	Bacterial Source Tracking for Lower Rappahannock River: Western Branch at Station 21-49.	5-16
Table 5.28	Bacterial Source Tracking for Lower Rappahannock River: Western Branch at Station 21-51.	5-17
Table 5.29	Bacterial Source Tracking for Great Wicomico-Piankatank Rivers: Millford Haven at Station 36-12.....	5-17
Table 5.30	Bacterial Source Tracking for Great Wicomico-Piankatank Rivers: Queens Creek at Station 37-6.	5-18
Table 5.31	Bacterial Source Tracking for Great Wicomico-Piankatank Rivers: Billups Creek at Station 37-23.4.....	5-18
Table 5.32	Bacterial Source Tracking for Great Wicomico-Piankatank Rivers: Stutts Creek at Station 37-26.2.	5-19
Table 5.33	Bacterial Source Tracking for Great Wicomico-Piankatank Rivers: Morris Creek at Station 37-27.	5-19
Table 5.34	Bacterial Source Tracking for Great Wicomico-Piankatank Rivers: Horn Harbor at Station 39-8.	5-20
Table 5.35	Bacterial Source Tracking for Great Wicomico-Piankatank Rivers: Horn Harbor at Station 39-10.	5-20

Bacterial Source Tracking Analyses to Support Virginia’s TMDLs

Table 5.36	Bacterial Source Tracking for Great Wicomico-Piankatank Rivers: Doctors Creek at Station 39-C.....	5-21
Table 5.37	Bacterial Source Tracking for York River: Upper York River at Station 49-207.	5-21
Table 5.38	Summary of VDH-DSS bacterial sampling in VADEQ’s Tidewater Region.	5-23
Table 5.39	Bacterial Source Tracking for York River: Adams Creek at Station 48-21.	5-24
Table 5.40	Bacterial Source Tracking for York River: Poropotank River at Station 48-5.	5-24
Table 5.41	Bacterial Source Tracking for York River: Skimino Creek at Station 50-4.	5-25
Table 5.42	Bacterial Source Tracking for York River: Carter Creek at Station 50-19.	5-25
Table 5.43	Bacterial Source Tracking for York River: Taskinas Creek at Station 50-22.	5-26
Table 5.44	Bacterial Source Tracking for York River: Ware Creek at Station 50-23.....	5-26
Table 5.45	Bacterial Source Tracking for Lower James River: Warwick and James Rivers 57 & 58 at Station 57-E57.....	5-27
Table 5.46	Bacterial Source Tracking for Chowan-Roanoke Rivers: Dey Cove/Milldam Creek at Station 71-4A.....	5-27
Table 5.47	Bacterial Source Tracking for Great Wicomico-Piankatank Rivers: Linkhorn Bay at Station 71-9.	5-28
Table A.1	False-positive and correct classification rates for twelve BST libraries developed in support of VADEQ’s Phase-IV BST Program.	A-2
Table A.2	Species sampled for 7 libraries developed in support of VADEQ’s Phase-VII BST Program.....	A-2

ACKNOWLEDGEMENTS

Charles Hagedorn, Ph.D., Crop and Soil Environmental Sciences, Virginia Tech (CSES)

MapTech's Environmental Diagnostic Laboratory

Charles Martin, Virginia Department of Environmental Quality (VADEQ)

Jutta Schneider, VADEQ

Roger Stewart, VADEQ

Regional VADEQ Offices

Robert Wittman, Virginia Department of Health (VDH)

Regional VDH Offices

Thank you to the many state agency representatives and stakeholders who assisted with sample collection.

MapTech, Inc. of Blacksburg, Virginia, conducted this study with funding provided by New River Highlands RC & D (Contract # 12186), made available through a grant from the Virginia Department of Environmental Quality.

1. INTRODUCTION

EPA's document, *Guidance for Water Quality-Based Decisions: The TMDL Process* (USEPA, 1999) states:

According to section 303(d) of the Clean Water Act and EPA water quality planning and management regulations, States are required to identify waters that do not meet or are not expected to meet water quality standards even after technology-based or other required controls are in place. The water bodies are considered water quality-limited and require TMDLs.

. . . A TMDL, or total maximum daily load, is a tool for implementing State water quality standards and is based on the relationship between pollution sources and in-stream water quality conditions. The TMDL establishes the allowable loadings or other quantifiable parameters for a water body and thereby provides the basis for States to establish water quality-based controls. These controls should provide the pollution reduction necessary for a water body to meet water quality standards.

The purpose of this project is to use bacterial source tracking to identify sources of *E. coli* to support the development of fecal bacteria TMDLs for impaired segments in Virginia. In fulfilling the state requirement for the development of a TMDL, a systematic process will be utilized to establish the maximum allowable bacteria loading for each waterbody to meet the applicable standard, allocate that load among pollutant contributors, and provide a basis for taking actions needed to restore water quality.

Bacterial Source Tracking (BST) methods can be subdivided into three basic groups: Molecular, Biochemical, and Chemical. Molecular (genotype) are typically referred to as "DNA fingerprinting" and are based on the unique genetic makeup of different strains, or subspecies, of fecal bacteria. Biochemical (phenotype) methods are based on an effect of an organism's genes that actively produce a biochemical response under controlled conditions. The type and intensity of the response is what is actually measured. Chemical methods are based on finding chemical compounds that are associated with

Bacterial Source Tracking Analyses to Support Virginia's TMDLs

human wastewaters, and generally are restricted to determining if sources of pollution are human or not.

Hagedorn's (Hagedorn et al., 1999) Antibiotic Resistance Analysis (ARA) technique was used for this project because it has been demonstrated to be a reliable procedure for confirming the presence of human, livestock, wildlife and pet sources. Compared to DNA fingerprinting, biochemical profiling is much quicker, typically allows for many more isolates to be analyzed (*e.g.*, hundreds per week vs. a few dozen per week for DNA analysis), is more economical, has survived limited court testing, and has undergone rigorous peer review from the scientific community. Additionally, observation of an increased number of isolates allows for an estimate of the relative proportions of the fecal indicator (*e.g.*, *E. coli*) originating from different sources.

2. OBJECTIVES

BST was used to identify sources of *E. coli*, and the relative percentage contribution from four source groups (*i.e.*, livestock, wildlife, human and pets) to support the development of fecal bacteria TMDLs for impairments located throughout Virginia. BST results will be used to improve public awareness of the problem, to improve model calibration/validation of bacteria concentrations and to provide a more equitable allocation of loads to source classes. This report presents the results of water quality sampling conducted in Virginia's shellfish producing waters. A companion report, *Bacterial Source Tracking Analyses to Support Virginia's TMDLs Non-Shellfish Stations*, presents the results of sampling conducted in Virginia's non-shellfish waters.

The specific objectives of the project were to:

1. collect fecal samples from known sources in seven areas (HUCs),
2. use collected samples to develop a known-source library for each impairment area; and,
3. for this report, perform BST analyses on bacterial isolates collected from plates produced by Department of Shellfish Sanitation in order to assess impaired segments. The BST analyses were conducted using the libraries developed for objective 2.

3. METHODS

Hagedorn's ARA method has been extensively and successfully used by MapTech, and separates fecal sources based on patterns of antibiotic resistance in the *enterococci* or *E. coli*. For this study, *E. coli* was the indicator organism analyzed. The premise of ARA is that fecal bacteria from each source (*e.g.*, human, livestock, wildlife, and pets) will have different resistance patterns to the battery of antibiotics and concentrations used in the analysis. Hagedorn's method for *E. coli* tests each isolate on 28 different combinations of antibiotic type and concentration. Confidence in BST techniques is measured by the level of separation of isolates from known sources, represented as the percentage of isolates that are accurately separated into respective source types (*i.e.*, Average Rate of Correct Classification – ARCC). Additional analyses can be applied to test the specificity of the library. These analyses are discussed further in Section 4 of this document. The ARA method, like other methods (*e.g.*, molecular), requires the collection of source samples from feces of known sources to build a source library. Known-source samples from the four source classes were collected, analyzed, and entered into known-source libraries.

3.1 Collection of Known Sources

Known-source samples were collected in seven HUCs associated with fecal-bacteria impaired waters throughout Virginia (Figure 3.1). In HUCs where known-source samples had not previously been collected to support VADEQ's BST program (newly sampled HUCs), a total of 60 samples were collected. In HUCs where known-source sampling was completed within the past two years 20 known-source samples were collected. In HUCs where known-source sampling was completed more than two years previous 40 known-source samples were collected. Each set of source samples was distributed evenly between human, livestock, wildlife, and pets (Table 3.1). Specific species within each source category (*e.g.*, deer, raccoon, poultry, beef, etc.) that were selected to represent the sources in each region were identified through field observation, discussion with local stakeholders, and review of available data (*e.g.*, Virginia Agricultural Statistics). From each sample, up to 8 isolates were analyzed using BST to create a known-source library of 480 isolates for each newly sampled HUC, and to

Bacterial Source Tracking Analyses to Support Virginia's TMDLs

increase known-source libraries by 160-240 isolates in updated HUCs. To date, approximately 8,630 fecal samples have been collected to support VADEQ's BST program, resulting in over 135,974 isolates analyzed. In total 278 fecal samples were collected for this study, resulting in 2,002 isolates analyzed.

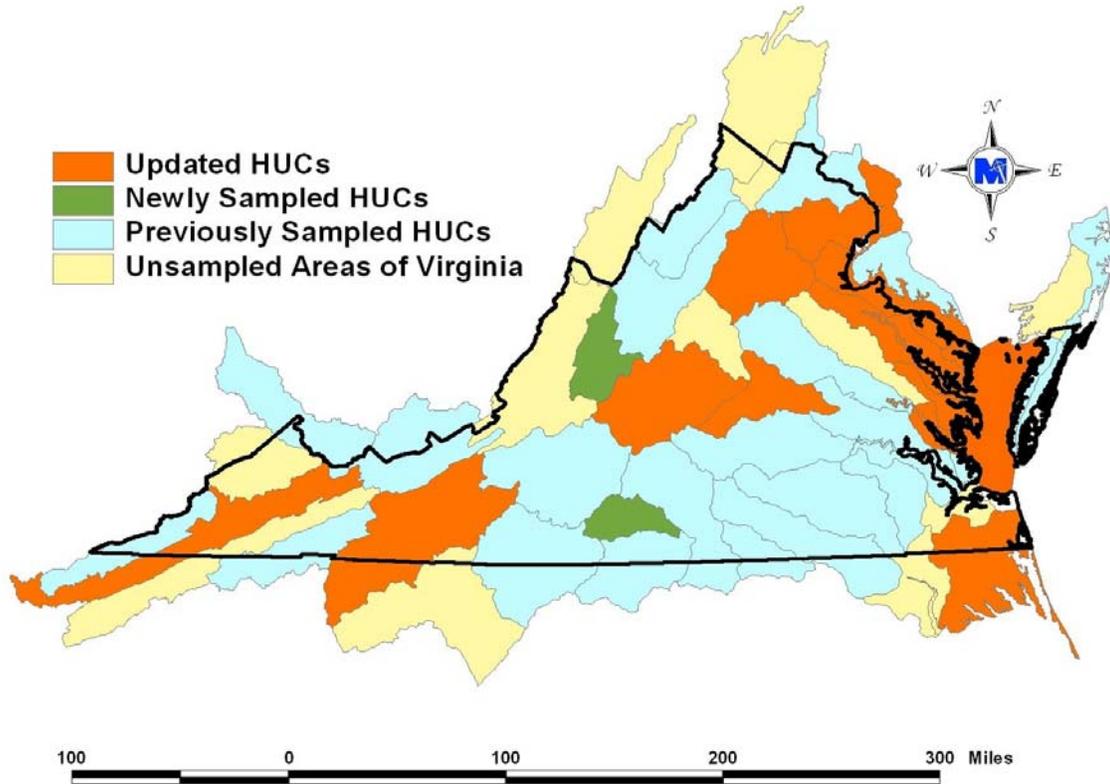


Figure 3.1 Locations of known-source sampling conducted to support this year's and previous years' BST analyses

Table 3.1 Source samples collected for BST library development.

Source	Source Species	Number of Samples Collected in Newly Sampled HUCs	Additional Samples Collected in Updated HUCs (none within past 2 years)	Additional Samples Collected in Updated HUCs (within past 2 years)
Human	Septic Systems, Portable Toilets, ...	15	10	5
Livestock	Dairy, Beef, Horse, Sheep, Broilers, Turkeys, Swine, Waste Storage Pits, ...	15	10	5
Wildlife	Deer, Raccoon, Muskrat, Duck, Goose, ...	15	10	5
Pets	Dogs & Cats	15	10	5
Total		60	40	20

3.2 Development of Known-Source Libraries

An appropriate known-source library was selected for each of the impairments to complete objective 2. A predictive model was developed from each library using logistic regression. A known-source library must be large enough to prevent an over-specified fit to the library. However, known-source responses to ARA analyses have been observed to vary geographically. The characteristics of this variance has not been well defined, so the regional libraries developed for this study were combined in a stepwise procedure and analyzed to measure the resulting specificity and the predictive accuracy of the combined libraries, as detailed in Section 4 of this document.

3.3 BST Analyses

For objective 3, water quality monitoring sites were identified and sampled by the granting agency (Figure 3.2 and Table 3.2). The contract began in July 2005 and shellfish samples started in the fall of 2005. At the conclusion of the study, most sites will have been sampled monthly for up to one year. Samples were received in the form of plates used in enumeration of *E. coli* concentrations. BST was run on bacteria isolated from these plates. Bacteria were analyzed using Hagedorn's ARA methodology, yielding the percentage of isolates classified as human, livestock, wildlife, and pets. Up to 24

Bacterial Source Tracking Analyses to Support Virginia's TMDLs

bacterial isolates were analyzed per sample, limited only by the number of isolates available from the enumeration process.

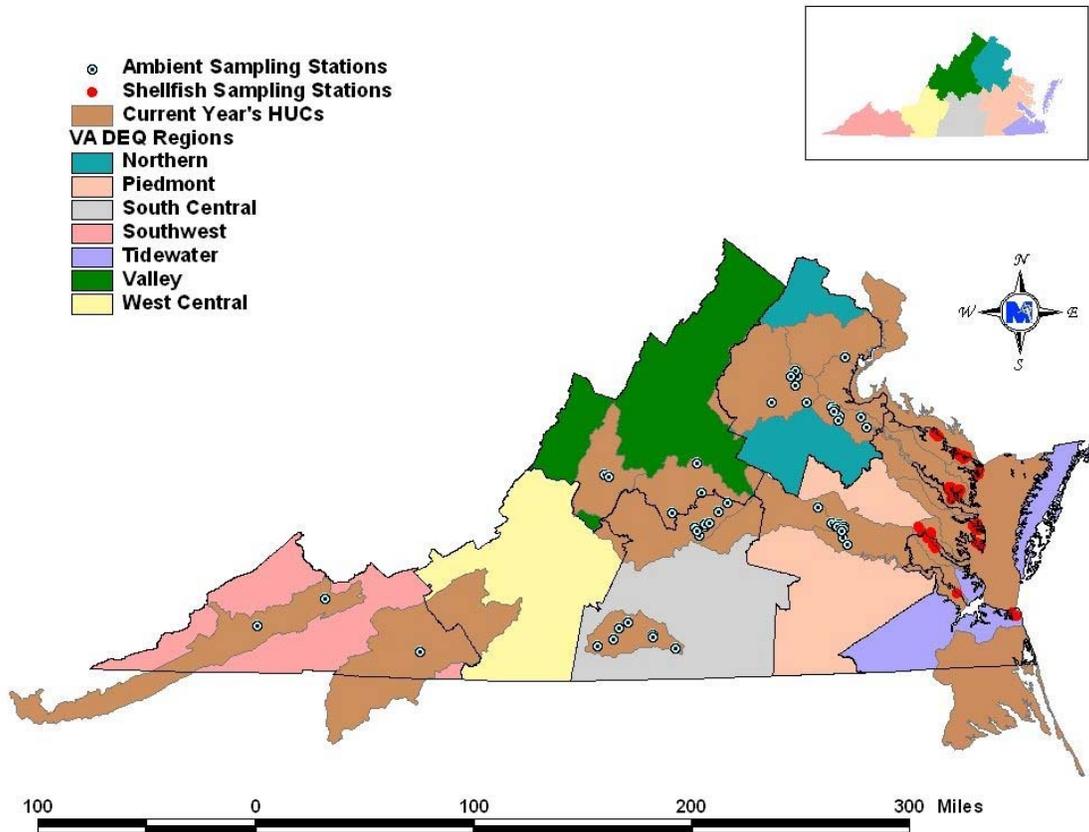


Figure 3.2 Spatial distribution of impaired segments identified by region.

Bacterial Source Tracking Analyses to Support Virginia's TMDLs

Table 3.2 Distribution of stations sampled by VDH-DSS in support of this study.

Waterbody	Hydrologic Unit
Potomac River: Gardner Creek	A33E
Potomac River: Jackson Creek	A33E
Potomac River: Jackson Creek	A33E
Bonum Creek	A33E
Bonum Creek	A33E
Potomac River: Cod Creek	A34E
Potomac River: Cod Creek	A34E
Potomac River: Cod Creek	A34E
Potomac River: Hull Creek	A34E
Rogers Creek	A34E
Bridgeman Creek	A34E
Potomac River: Cubitt Creek	A34E
Ches Bay: Owens Pond	C01E
Ches Bay: Little Taskmakers Creek	C01E
Corrotoman River: Millenbeck Pro	E26E
Corrotoman River: Ewells Prong	E26E
Corrotoman River: Myer Creek	E26E
Corrotoman River: Taylor Creek	E26E
Hills Creek	E26E
Bells Creek	E26E
Eastern Branch	E26E
Eastern Branch	E26E
Eastern Branch	E26E
Corrotoman River: Western Branch	E26E
Corrotoman River: Senior Creek	E26E
Corrotoman River: Western Branch	E26E
Corrotoman River: Western Branch	E26E
Milford Haven	C04E
Queens Creek	C04E
Billups Creek	C03E
Stutts Creek	C03E
Morris Creek	C03E
Horn Harbor	C04E
Horn Harbor	C04E
Doctors Creek	C04E
Upper York River	F25E
Adams Creek	F26E
Poropotank River	F26E
York River: Skimino Creek	F26E
York River: Carter Creek	F26E
York River: Taskinas Creek	F26E
York River: Ware Creek	F26E
Warwick and James Rivers: 57&58	G11E
Dey Cove/Mill Dam Creek	C08E
Linkhorn Bay	C08E

4. KNOWN-SOURCE LIBRARY DEVELOPMENT

As discussed in Section 3, a predictive model was developed from each library using logistic regression. The regional libraries developed for this study were combined in a stepwise procedure and analyzed to measure the resulting specificity and the predictive accuracy of the combined libraries. The specificity and predictive accuracy were assessed through three analyses. First, the ARCC was calculated for the library. Second, a randomization test was performed by randomly assigning source categories to samples and assessing the ARCC for the randomized library. Ten randomizations were performed and the results averaged. The expected result of randomization of four source categories is an ARCC of 25%, indicating a completely random result. Greater values for the randomized ARCC indicate a more specified model. Third, a jackknifing routine was conducted; where data from each whole fecal sample were individually withheld during development of the statistical model, then the model was tested for predictive accuracy on the withheld sample. In combining regional libraries a balance was sought between minimizing the randomized ARCC and maximizing the jackknifed ARCC. Table 4.1 shows the resulting analyses on the finalized libraries.

Table 4.1 Results of known-source library development.

Known-Source Library	ARCC (%)	Randomized ARCC (%)	Jackknifed ARCC (%)
02070011	74.4	37.1	68.1
02080101	80.6	38.2	73.8
02080102	75.4	37.6	69.2
02080104	72.2	35.5	66.9
02080107	67.4	36.0	61.8
02080206	69.1	38.3	58.4
03010205	71.6	37.3	67.1

5. RESULTS

The results of the water quality analyses for VADEQ's 2005-2006 BST sampling in shellfish waters are reported in this section. The proportions reported are formatted to indicate statistical significance (*i.e.*, **BOLD** numbers indicate a statistically significant result). The statistical significance was determined through 2 tests. The first was based on the sample size. A z-test was used to determine if the proportion was significantly different from zero ($\alpha = 0.10$). Second the rate of false positives was calculated for each source category in each library, and a proportion was not considered significantly different from zero unless it was greater than the false-positive rate plus three standard deviations.

5.1 Results for Piedmont Region

The results of the water quality analyses for VADEQ's Piedmont Region (Figure 5.1) are reported in the following tables. Table 5.1 indicates the number of samples analyzed in the 2005-2006 sampling phase. The results of the BST analysis are reported in Tables 5.2 through 5.37.

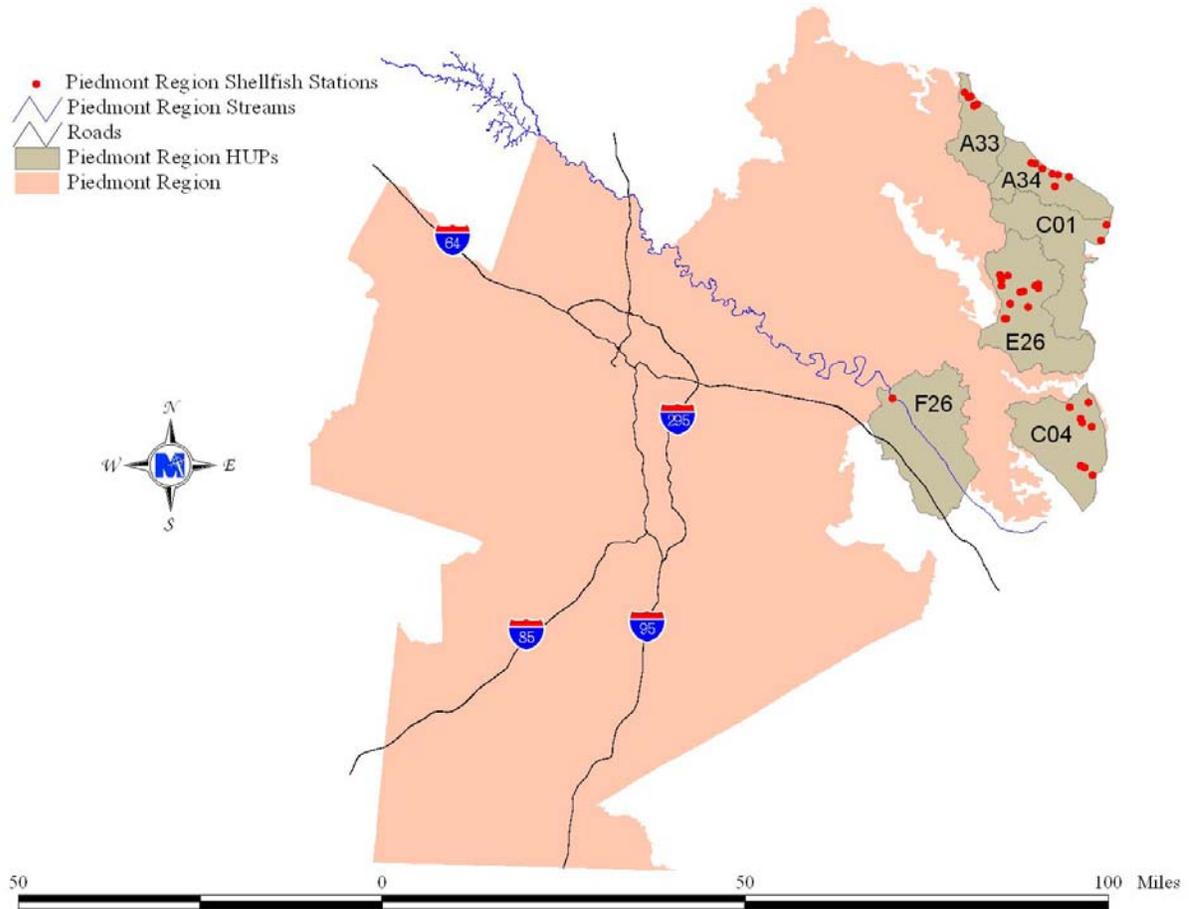


Figure 5.1 Bacterial sampling stations in VADEQ's Piedmont Region.

Bacterial Source Tracking Analyses to Support Virginia's TMDLs

Table 5.1 Summary of VDH-DSS bacterial sampling in VADEQ's Piedmont Region.

Station ID	HUP	County	Impairment	# Times Plates Received
6-3	A33E	Westmoreland	Potomac River: Gardner Creek	12
6-5	A33E	Westmoreland	Potomac River: Jackson Creek	11
6-6	A33E	Westmoreland	Potomac River: Jackson Creek	11
6-8	A33E	Westmoreland	Bonum Creek	12
6-9	A33E	Westmoreland	Bonum Creek	11
9-3	A34E	Northumberland	Potomac River: Cod Creek	11
9-5	A34E	Northumberland	Potomac River: Cod Creek	10
9-6	A34E	Northumberland	Potomac River: Cod Creek	11
9-16	A34E	Northumberland	Potomac River: Hull Creek	11
9-9.1Y	A34E	Northumberland	Rogers Creek	11
9-10	A34E	Northumberland	Bridgeman Creek	11
9-19	A34E	Northumberland	Potomac River: Cubitt Creek	11
11-5	C01E	Northumberland	Ches Bay: Owens Pond	11
11-1A	C01E	Northumberland	Ches Bay: Little Taskmakers Creek	11
21-8	E26E	Lancaster	Corrotoman River: Millenbeck Pro	11
21-9	E26E	Lancaster	Corrotoman River: Ewells Prong	12
21-17X	E26E	Lancaster	Corrotoman River: Myer Creek	11
21-15B	E26E	Lancaster	Corrotoman River: Taylor Creek	12
21-23	E26E	Lancaster	Hills Creek	11
21-24	E26E	Lancaster	Bells Creek	12
21-30A	E26E	Lancaster	Eastern Branch	12
21-31	E26E	Lancaster	Eastern Branch	12
21-33	E26E	Lancaster	Eastern Branch	11
21-46	E26E	Lancaster	Corrotoman River: Western Branch	11
21-42	E26E	Lancaster	Corrotoman River: Senior Creek	11
21-49	E26E	Lancaster	Corrotoman River: Western Branch	12
21-51	E26E	Lancaster	Corrotoman River: Western Branch	12
36-12	C04E	Mathews	Milford Haven	11
37-6	C04E	Mathews	Queens Creek	12
37-23.4	C03E	Mathews	Billups Creek	12
37-26.2	C03E	Mathews	Stutts Creek	12
37-27	C03E	Mathews	Morris Creek	12
39-8	C04E	Mathews	Horn Harbor	12
39-10	C04E	Mathews	Horn Harbor	12
39-C	C04E	Mathews	Doctors Creek	12
49-207	F25E	King William	Upper York River	12

Bacterial Source Tracking Analyses to Support Virginia's TMDLs

Table 5.2 Bacterial Source Tracking for Potomac River: Gardner Creek at Station 6-3.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
6-3	10/20/05	D4901	A33E	24	0%	0%	100%	0%
6-3	11/8/05	D4953	A33E	24	0%	0%	25%	75%
6-3	12/20/05	D5107	A33E	5	0%	0%	20%	80%
6-3	1/19/06	D5235	A33E	24	67%	0%	0%	33%
6-3	2/2/06	D5297	A33E	11	18%	0%	18%	64%
6-3	3/7/06	D5458	A33E	NVI	NVI	NVI	NVI	NVI
6-3	4/4/06	D5615	A33E	24	0%	4%	33%	63%
6-3	5/31/06	D5903	A33E	22	27%	18%	23%	32%
6-3	6/1/06	D5908	A33E	24	54%	17%	25%	4%
6-3	7/13/06	D6112	A33E	24	0%	0%	29%	71%
6-3	8/14/06	D6274	A33E	24	4%	0%	8%	88%
6-3	9/28/06	D6438	A33E	24	46%	8%	4%	42%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Table 5.3 Bacterial Source Tracking for Potomac River: Jackson Creek at Station 6-5.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
6-5	10/20/05	D4902	A33E	24	4%	8%	80%	8%
6-5	11/8/05	D4954	A33E	24	4%	0%	96%	0%
6-5	1/19/06	D5236	A33E	24	46%	0%	4%	50%
6-5	2/2/06	D5298	A33E	11	18%	9%	27%	46%
6-5	3/7/06	D5459	A33E	2	50%	0%	50%	0%
6-5	4/4/06	D5616	A33E	24	54%	0%	0%	46%
6-5	5/31/06	D5904	A33E	20	10%	0%	85%	5%
6-5	6/1/06	D5909	A33E	24	4%	4%	17%	75%
6-5	7/13/06	D6113	A33E	24	17%	4%	4%	75%
6-5	8/14/06	D6275	A33E	24	4%	25%	38%	33%
6-5	9/28/06	D6439	A33E	21	42%	10%	24%	24%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Bacterial Source Tracking Analyses to Support Virginia's TMDLs

Table 5.4 Bacterial Source Tracking for Potomac River: Jackson Creek at Station 6-6.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
6-6	10/20/05	D4903	A33E	24	0%	4%	88%	8%
6-6	11/8/05	D4955	A33E	24	0%	0%	100%	0%
6-6	1/19/06	D5237	A33E	24	67%	0%	0%	33%
6-6	2/2/06	D5299	A33E	15	0%	7%	27%	66%
6-6	3/7/06	D5460	A33E	10	70%	0%	30%	0%
6-6	4/4/06	D5617	A33E	24	46%	4%	17%	33%
6-6	5/31/06	D5905	A33E	24	8%	0%	42%	50%
6-6	6/1/06	D5910	A33E	24	0%	17%	25%	58%
6-6	7/13/06	D6114	A33E	24	38%	4%	0%	58%
6-6	8/14/06	D6276	A33E	24	8%	0%	8%	84%
6-6	9/28/06	D6440	A33E	24	4%	0%	12%	84%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Table 5.5 Bacterial Source Tracking for Bonum Creek at Station 6-8.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
6-8	10/20/05	D4904	A33E	24	0%	33%	59%	8%
6-8	11/8/05	D4956	A33E	24	0%	4%	84%	12%
6-8	12/20/05	D5108	A33E	14	0%	7%	21%	72%
6-8	1/19/06	D5238	A33E	24	8%	4%	38%	50%
6-8	2/2/06	D5300	A33E	8	0%	76%	12%	12%
6-8	3/7/06	D5461	A33E	1	100%	0%	0%	0%
6-8	4/4/06	D5618	A33E	24	79%	4%	0%	17%
6-8	5/31/06	D5906	A33E	23	26%	13%	39%	22%
6-8	6/1/06	D5911	A33E	22	0%	36%	28%	36%
6-8	7/13/06	D6115	A33E	24	0%	0%	0%	100%
6-8	8/14/06	D6277	A33E	21	0%	5%	10%	85%
6-8	9/28/06	D6441	A33E	24	0%	0%	17%	83%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Bacterial Source Tracking Analyses to Support Virginia's TMDLs

Table 5.6 Bacterial Source Tracking for Bonum Creek at Station 6-9.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
6-9	10/20/05	D4905	A33E	24	0%	54%	46%	0%
6-9	11/8/05	D4957	A33E	24	0%	4%	96%	0%
6-9	1/19/06	D5239	A33E	24	0%	8%	12%	80%
6-9	2/2/06	D5301	A33E	14	0%	29%	7%	64%
6-9	3/7/06	D5462	A33E	2	50%	0%	0%	50%
6-9	4/4/06	D5619	A33E	24	54%	8%	17%	21%
6-9	5/31/06	D5907	A33E	24	29%	63%	8%	0%
6-9	6/1/06	D5912	A33E	24	17%	25%	12%	46%
6-9	7/13/06	D6116	A33E	24	8%	0%	42%	50%
6-9	8/14/06	D6278	A33E	24	8%	0%	4%	88%
6-9	9/28/06	D6442	A33E	24	8%	67%	8%	17%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Table 5.7 Bacterial Source Tracking for Potomac River: Cod Creek at Station 9-3.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
9-3	10/25/05	D4922	A34E	24	0%	46%	33%	21%
9-3	11/8/05	D4946	A34E	24	0%	0%	38%	62%
9-3	12/7/05	D5046	A34E	24	50%	0%	17%	33%
9-3	1/23/06	D5251	A34E	24	54%	4%	0%	42%
9-3	2/21/06	D5401	A34E	16	0%	19%	6%	75%
9-3	3/6/06	D5453	A34E	2	100%	0%	0%	0%
9-3	4/19/06	D5719	A34E	23	79%	0%	4%	17%
9-3	6/15/06	D5992	A34E	24	4%	4%	63%	29%
9-3	7/17/06	D6117	A34E	5	0%	0%	0%	100%
9-3	8/16/06	D6290	A34E	24	0%	4%	96%	0%
9-3	9/13/06	D6369	A34E	24	17%	71%	8%	4%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Bacterial Source Tracking Analyses to Support Virginia's TMDLs

Table 5.8 Bacterial Source Tracking for Potomac River: Cod Creek at Station 9-5.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
9-5	10/25/05	D4923	A34E	24	0%	4%	71%	25%
9-5	11/8/05	D4947	A34E	24	4%	8%	33%	55%
9-5	12/7/05	D5047	A34E	23	74%	0%	0%	26%
9-5	1/23/06	D5252	A34E	19	58%	0%	0%	42%
9-5	2/21/06	D5402	A34E	1	0%	0%	0%	100%
9-5	4/19/06	D5720	A34E	24	54%	0%	17%	29%
9-5	6/15/06	D5993	A34E	24	38%	12%	33%	17%
9-5	7/17/06	D6118	A34E	8	12%	0%	0%	88%
9-5	8/16/06	D6291	A34E	24	0%	71%	17%	12%
9-5	9/13/06	D6370	A34E	23	35%	39%	13%	13%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Table 5.9 Bacterial Source Tracking for Potomac River: Cod Creek at Station 9-6.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
9-6	10/25/05	D4924	A34E	24	4%	33%	25%	38%
9-6	11/8/05	D4948	A34E	24	0%	0%	62%	38%
9-6	12/7/05	D5048	A34E	24	21%	0%	33%	46%
9-6	1/23/06	D5253	A34E	19	0%	0%	26%	74%
9-6	2/21/06	D5403	A34E	3	0%	67%	0%	33%
9-6	3/6/06	D5454	A34E	4	75%	0%	0%	25%
9-6	4/19/06	D5721	A34E	24	79%	4%	0%	17%
9-6	6/15/06	D5994	A34E	24	42%	4%	33%	21%
9-6	7/17/06	D6119	A34E	24	29%	0%	21%	50%
9-6	8/16/06	D6292	A34E	24	0%	75%	0%	25%
9-6	9/13/06	D6371	A34E	24	75%	17%	0%	8%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Bacterial Source Tracking Analyses to Support Virginia's TMDLs

Table 5.10 Bacterial Source Tracking for Potomac River: Hull Creek at Station 9-16.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
9-16	10/25/05	D4927	A34E	24	0%	41%	38%	21%
9-16	11/8/05	D4951	A34E	24	0%	0%	54%	46%
9-16	12/7/05	D5051	A34E	24	67%	0%	12%	21%
9-16	1/23/06	D5256	A34E	24	0%	0%	4%	96%
9-16	2/21/06	D5406	A34E	3	0%	0%	0%	100%
9-16	3/6/06	D5456	A34E	2	0%	0%	50%	50%
9-16	4/19/06	D5724	A34E	18	89%	0%	0%	11%
9-16	6/15/06	D5997	A34E	24	59%	8%	8%	25%
9-16	7/17/06	D6122	A34E	24	8%	4%	71%	17%
9-16	8/16/06	D6295	A34E	24	17%	45%	0%	38%
9-16	9/13/06	D6374	A34E	24	75%	25%	0%	0%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Table 5.11 Bacterial Source Tracking for Rogers Creek at Station 9-9.1Y.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
9-9.1Y	10/25/05	D4925	A34E	24	17%	29%	12%	42%
9-9.1Y	11/8/05	D4949	A34E	24	0%	0%	75%	25%
9-9.1Y	12/7/05	D5049	A34E	24	75%	0%	8%	17%
9-9.1Y	1/23/06	D5254	A34E	24	8%	0%	12%	80%
9-9.1Y	2/21/06	D5404	A34E	16	6%	0%	88%	6%
9-9.1Y	4/19/06	D5722	A34E	24	84%	0%	4%	12%
9-9.1Y	6/15/06	D5995	A34E	24	38%	0%	21%	41%
9-9.1Y	7/17/06	D6120	A34E	2	0%	0%	50%	50%
9-9.1Y	8/16/06	D6293	A34E	8	50%	50%	0%	0%
9-9.1Y	9/13/06	D6372	A34E	24	33%	46%	4%	17%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Bacterial Source Tracking Analyses to Support Virginia's TMDLs

Table 5.12 Bacterial Source Tracking for Bridgeman Creek at Station 9-10.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
9-10	10/25/05	D4926	A34E	24	0%	12%	67%	21%
9-10	11/8/05	D4950	A34E	24	0%	0%	4%	96%
9-10	12/7/05	D5050	A34E	24	29%	0%	42%	29%
9-10	1/23/06	D5255	A34E	24	0%	0%	4%	96%
9-10	2/21/06	D5405	A34E	2	0%	0%	100%	0%
9-10	3/6/06	D5455	A34E	6	33%	0%	0%	67%
9-10	4/19/06	D5723	A34E	24	79%	0%	0%	21%
9-10	6/15/06	D5996	A34E	24	63%	8%	21%	8%
9-10	7/17/06	D6121	A34E	5	0%	20%	80%	0%
9-10	8/16/06	D6294	A34E	11	27%	46%	0%	27%
9-10	9/13/06	D6373	A34E	24	63%	21%	4%	12%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Table 5.13 Bacterial Source Tracking for Potomac River: Cubitt Creek at Station 9-19.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
9-19	10/25/05	D4928	A34E	24	0%	25%	21%	54%
9-19	11/8/05	D4952	A34E	24	0%	0%	4%	96%
9-19	12/7/05	D5052	A34E	24	50%	0%	12%	38%
9-19	1/23/06	D5257	A34E	24	8%	0%	21%	71%
9-19	2/21/06	D5407	A34E	1	0%	0%	0%	100%
9-19	3/6/06	D5457	A34E	12	17%	0%	25%	58%
9-19	4/19/06	D5725	A34E	10	90%	0%	0%	10%
9-19	6/15/06	D5998	A34E	24	75%	4%	0%	21%
9-19	7/17/06	D6123	A34E	6	0%	33%	50%	17%
9-19	8/16/06	D6296	A34E	6	0%	50%	0%	50%
9-19	9/13/06	D6375	A34E	23	87%	9%	0%	4%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Bacterial Source Tracking Analyses to Support Virginia's TMDLs

Table 5.14 Bacterial Source Tracking for Chesapeake Bay: Owens Pond at Station 11-5.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
11-5	10/24/05	D4930	C01E	24	25%	71%	0%	4%
11-5	11/22/05	D5022	C01E	23	70%	4%	17%	9%
11-5	12/9/05	D5067	C01E	13	31%	61%	0%	8%
11-5	1/24/06	D5259	C01E	2	100%	0%	0%	0%
11-5	2/6/06	D5326	C01E	NVI	NVI	NVI	NVI	NVI
11-5	4/20/06	D5727	C01E	4	0%	75%	0%	25%
11-5	5/2/06	D5765	C01E	8	63%	25%	12%	0%
11-5	6/1/06	D5914	C01E	24	29%	55%	4%	12%
11-5	7/5/06	D6059	C01E	16	37%	25%	19%	19%
11-5	8/2/06	D6214	C01E	3	33%	67%	0%	0%
11-5	9/12/06	D6368	C01E	24	12%	21%	63%	4%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Table 5.15 Bacterial Source Tracking for Chesapeake Bay: Little Taskmakers Creek at Station 11-1A.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
11-1A	10/24/05	D4929	C01E	23	0%	100%	0%	0%
11-1A	11/22/05	D5021	C01E	23	57%	26%	4%	13%
11-1A	12/9/05	D5066	C01E	24	21%	42%	4%	33%
11-1A	1/24/06	D5258	C01E	7	71%	0%	0%	29%
11-1A	2/6/06	D5325	C01E	NVI	NVI	NVI	NVI	NVI
11-1A	3/7/06	D5463	C01E	7	29%	57%	14%	0%
11-1A	4/20/06	D5726	C01E	24	71%	4%	8%	17%
11-1A	5/2/06	D5764	C01E	16	44%	44%	0%	12%
11-1A	6/1/06	D5913	C01E	24	46%	21%	29%	4%
11-1A	7/5/06	D6058	C01E	24	38%	29%	8%	25%
11-1A	8/2/06	D6213	C01E	14	21%	21%	14%	44%
11-1A	9/12/06	D6367	C01E	24	21%	67%	12%	0%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Bacterial Source Tracking Analyses to Support Virginia's TMDLs

Table 5.16 Bacterial Source Tracking for Corrotoman River: Millenbeck Prong at Station 21-8.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
21-8	10/11/05	D4841	E26E	24	8%	17%	42%	33%
21-8	11/9/05	D4958	E26E	24	0%	8%	63%	29%
21-8	12/8/05	D5062	E26E	12	0%	33%	67%	0%
21-8	1/9/06	D5170	E26E	3	0%	33%	0%	67%
21-8	2/22/06	D5414	E26E	5	20%	80%	0%	0%
21-8	4/5/06	D5620	E26E	23	52%	39%	0%	9%
21-8	5/18/06	D5850	E26E	4	0%	0%	75%	25%
21-8	6/19/06	D5999	E26E	24	38%	50%	4%	8%
21-8	7/18/06	D6149	E26E	11	0%	18%	9%	73%
21-8	8/3/06	D6215	E26E	24	96%	4%	0%	0%
21-8	9/14/06	D6376	E26E	24	8%	25%	38%	29%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Table 5.17 Bacterial Source Tracking for Corrotoman River: Ewells Prong at Station 21-9.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
21-9	10/11/05	D4842	E26E	24	4%	4%	67%	25%
21-9	11/9/05	D4959	E26E	24	0%	17%	50%	33%
21-9	12/8/05	D5063	E26E	18	0%	28%	72%	0%
21-9	1/9/06	D5171	E26E	15	0%	27%	46%	27%
21-9	2/22/06	D5415	E26E	1	0%	100%	0%	0%
21-9	3/8/06	D5472	E26E	1	0%	0%	100%	0%
21-9	4/5/06	D5621	E26E	23	48%	30%	9%	13%
21-9	5/18/06	D5851	E26E	11	0%	0%	100%	0%
21-9	6/19/06	D6000	E26E	20	0%	0%	65%	35%
21-9	7/18/06	D6150	E26E	9	0%	78%	0%	22%
21-9	8/3/06	D6216	E26E	2	50%	50%	0%	0%
21-9	9/14/06	D6377	E26E	24	17%	59%	12%	12%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Bacterial Source Tracking Analyses to Support Virginia's TMDLs

Table 5.18 Bacterial Source Tracking for Corrotoman River: Myer Creek at Station 21-17X.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
21-17X	10/11/05	D4844	E26E	24	0%	8%	84%	8%
21-17X	11/9/05	D4961	E26E	24	0%	4%	46%	50%
21-17X	12/8/05	D5065	E26E	24	0%	8%	75%	17%
21-17X	1/9/06	D5173	E26E	2	0%	50%	50%	0%
21-17X	2/22/06	D5417	E26E	3	0%	67%	0%	33%
21-17X	4/5/06	D5623	E26E	23	22%	4%	26%	48%
21-17X	5/18/06	D5853	E26E	20	0%	0%	25%	75%
21-17X	6/19/06	D6002	E26E	6	0%	0%	50%	50%
21-17X	7/18/06	D6152	E26E	16	0%	0%	50%	50%
21-17X	8/3/06	D6218	E26E	6	17%	17%	66%	0%
21-17X	9/14/06	D6379	E26E	17	0%	0%	65%	35%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Table 5.19 Bacterial Source Tracking for Corrotoman River: Taylor Creek at Station 21-15B.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
21-15B	10/11/05	D4843	E26E	24	0%	12%	80%	8%
21-15B	11/9/05	D4960	E26E	21	0%	19%	57%	24%
21-15B	12/8/05	D5064	E26E	24	0%	17%	58%	25%
21-15B	1/9/06	D5172	E26E	4	0%	50%	0%	50%
21-15B	2/22/06	D5416	E26E	NVI	NVI	NVI	NVI	NVI
21-15B	3/8/06	D5473	E26E	2	0%	0%	0%	100%
21-15B	4/5/06	D5622	E26E	21	38%	0%	48%	14%
21-15B	5/18/06	D5852	E26E	8	25%	0%	63%	12%
21-15B	6/19/06	D6001	E26E	7	0%	0%	86%	14%
21-15B	7/18/06	D6151	E26E	3	0%	33%	0%	67%
21-15B	8/3/06	D6217	E26E	6	33%	50%	0%	17%
21-15B	9/14/06	D6378	E26E	24	29%	50%	21%	0%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Bacterial Source Tracking Analyses to Support Virginia's TMDLs

Table 5.20 Bacterial Source Tracking for Hills Creek at Station 21-23.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
21-23	10/11/05	D4845	E26E	24	0%	8%	0%	92%
21-23	11/9/05	D4962	E26E	24	0%	8%	38%	54%
21-23	12/8/05	D5053	E26E	24	0%	38%	21%	41%
21-23	1/9/06	D5174	E26E	6	17%	33%	17%	33%
21-23	2/22/06	D5418	E26E	1	0%	100%	0%	0%
21-23	4/5/06	D5606	E26E	24	25%	21%	29%	25%
21-23	5/18/06	D5854	E26E	12	8%	25%	67%	0%
21-23	6/19/06	D6003	E26E	24	88%	4%	8%	0%
21-23	7/18/06	D6140	E26E	24	0%	29%	8%	63%
21-23	8/3/06	D6219	E26E	24	50%	21%	25%	4%
21-23	9/14/06	D6380	E26E	24	4%	67%	12%	17%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Table 5.21 Bacterial Source Tracking for Bells Creek at Station 21-24.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
21-24	10/11/05	D4846	E26E	24	0%	0%	0%	100%
21-24	11/9/05	D4963	E26E	24	0%	12%	59%	29%
21-24	12/8/05	D5054	E26E	24	0%	8%	42%	50%
21-24	1/9/06	D5175	E26E	1	0%	0%	0%	100%
21-24	2/22/06	D5419	E26E	3	0%	67%	33%	0%
21-24	3/8/06	D5474	E26E	1	0%	0%	100%	0%
21-24	4/5/06	D5607	E26E	11	37%	18%	27%	18%
21-24	5/18/06	D5855	E26E	18	0%	28%	66%	6%
21-24	6/19/06	D6004	E26E	5	20%	20%	20%	40%
21-24	7/18/06	D6141	E26E	17	0%	58%	18%	24%
21-24	8/3/06	D6220	E26E	24	12%	38%	46%	4%
21-24	9/14/06	D6381	E26E	24	21%	45%	17%	17%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Bacterial Source Tracking Analyses to Support Virginia's TMDLs

Table 5.22 Bacterial Source Tracking for Eastern Branch at Station 21-30A.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
21-30A	10/11/05	D4847	E26E	24	0%	33%	8%	59%
21-30A	11/9/05	D4964	E26E	24	0%	4%	84%	12%
21-30A	12/8/05	D5055	E26E	24	4%	4%	46%	46%
21-30A	1/9/06	D5176	E26E	24	4%	58%	21%	17%
21-30A	2/22/06	D5420	E26E	6	17%	83%	0%	0%
21-30A	3/8/06	D5475	E26E	2	0%	50%	50%	0%
21-30A	4/5/06	D5608	E26E	24	0%	42%	8%	50%
21-30A	5/18/06	D5856	E26E	24	0%	42%	29%	29%
21-30A	6/19/06	D6005	E26E	24	21%	50%	17%	12%
21-30A	7/18/06	D6142	E26E	24	0%	33%	17%	50%
21-30A	8/3/06	D6221	E26E	24	38%	8%	46%	8%
21-30A	9/14/06	D6382	E26E	24	0%	0%	100%	0%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Table 5.23 Bacterial Source Tracking for Eastern Branch at Station 21-31.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
21-31	10/11/05	D4848	E26E	24	0%	12%	17%	71%
21-31	11/9/05	D4965	E26E	24	0%	21%	58%	21%
21-31	12/8/05	D5056	E26E	24	4%	17%	38%	41%
21-31	1/9/06	D5177	E26E	10	10%	70%	0%	20%
21-31	2/22/06	D5421	E26E	7	0%	57%	43%	0%
21-31	3/8/06	D5476	E26E	1	0%	100%	0%	0%
21-31	4/5/06	D5609	E26E	24	0%	38%	17%	45%
21-31	5/18/06	D5857	E26E	23	0%	39%	44%	17%
21-31	6/19/06	D6006	E26E	24	8%	68%	12%	12%
21-31	7/18/06	D6143	E26E	21	0%	48%	33%	19%
21-31	8/3/06	D6222	E26E	24	17%	25%	54%	4%
21-31	9/14/06	D6383	E26E	24	4%	0%	79%	17%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Bacterial Source Tracking Analyses to Support Virginia's TMDLs

Table 5.24 Bacterial Source Tracking for Eastern Branch at Station 21-33.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
21-33	10/11/05	D4849	E26E	24	0%	12%	0%	88%
21-33	11/9/05	D4966	E26E	24	0%	0%	79%	21%
21-33	12/8/05	D5057	E26E	24	0%	21%	17%	62%
21-33	1/9/06	D5178	E26E	8	12%	51%	12%	25%
21-33	2/22/06	D5422	E26E	3	0%	100%	0%	0%
21-33	4/5/06	D5610	E26E	24	0%	42%	12%	46%
21-33	5/18/06	D5858	E26E	23	0%	48%	17%	35%
21-33	6/19/06	D6007	E26E	21	19%	81%	0%	0%
21-33	7/18/06	D6144	E26E	24	0%	42%	16%	42%
21-33	8/3/06	D6223	E26E	16	0%	38%	62%	0%
21-33	9/14/06	D6384	E26E	24	29%	33%	38%	0%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Table 5.25 Bacterial Source Tracking for Corrotoman River: Western Branch at Station 21-46.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
21-46	10/11/05	D4851	E26E	24	0%	50%	29%	21%
21-46	11/9/05	D4968	E26E	24	0%	33%	59%	8%
21-46	12/8/05	D5059	E26E	22	0%	0%	32%	68%
21-46	1/9/06	D5180	E26E	6	1%	33%	33%	33%
21-46	2/22/06	D5424	E26E	3	0%	67%	33%	0%
21-46	4/5/06	D5612	E26E	24	21%	42%	4%	33%
21-46	5/18/06	D5860	E26E	14	0%	21%	79%	0%
21-46	6/19/06	D6009	E26E	8	38%	12%	50%	0%
21-46	7/18/06	D6146	E26E	24	0%	25%	42%	33%
21-46	8/3/06	D6225	E26E	4	0%	0%	25%	75%
21-46	9/14/06	D6386	E26E	16	0%	0%	75%	25%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Bacterial Source Tracking Analyses to Support Virginia's TMDLs

Table 5.26 Bacterial Source Tracking for Corrotoman River: Senior Branch at Station 21-42.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
21-42	10/11/05	D4850	E26E	24	4%	17%	21%	58%
21-42	11/9/05	D4967	E26E	24	0%	8%	80%	12%
21-42	12/8/05	D5058	E26E	23	0%	0%	17%	83%
21-42	1/9/06	D5179	E26E	7	0%	72%	14%	14%
21-42	2/22/06	D5423	E26E	5	0%	60%	20%	20%
21-42	4/5/06	D5611	E26E	23	0%	35%	9%	56%
21-42	5/18/06	D5859	E26E	20	5%	50%	30%	15%
21-42	6/19/06	D6008	E26E	24	21%	54%	4%	21%
21-42	7/18/06	D6145	E26E	24	4%	46%	38%	12%
21-42	8/3/06	D6224	E26E	24	12%	17%	59%	12%
21-42	9/14/06	D6385	E26E	24	38%	33%	17%	12%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Table 5.27 Bacterial Source Tracking for Corrotoman River: Western Branch at Station 21-49.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
21-49	10/11/05	D4852	E26E	23	4%	22%	13%	61%
21-49	11/9/05	D4969	E26E	24	0%	4%	75%	21%
21-49	12/8/05	D5060	E26E	24	0%	66%	17%	17%
21-49	1/9/06	D5181	E26E	23	0%	35%	56%	9%
21-49	2/22/06	D5425	E26E	3	0%	100%	0%	0%
21-49	3/8/06	D5477	E26E	1	0%	0%	100%	0%
21-49	4/5/06	D5613	E26E	24	0%	50%	25%	25%
21-49	5/18/06	D5861	E26E	23	0%	43%	48%	9%
21-49	6/19/06	D6010	E26E	24	25%	63%	8%	4%
21-49	7/18/06	D6147	E26E	24	4%	25%	21%	50%
21-49	8/3/06	D6226	E26E	24	17%	29%	42%	12%
21-49	9/14/06	D6387	E26E	24	4%	4%	92%	0%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Bacterial Source Tracking Analyses to Support Virginia's TMDLs

Table 5.28 Bacterial Source Tracking for Corrotoman River: Western Branch at Station 21-51.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
21-51	10/11/05	D4853	E26E	22	5%	5%	27%	63%
21-51	11/9/05	D4970	E26E	24	25%	4%	42%	29%
21-51	12/8/05	D5061	E26E	24	0%	62%	21%	17%
21-51	1/9/06	D5182	E26E	15	0%	74%	13%	13%
21-51	2/22/06	D5426	E26E	1	0%	100%	0%	0%
21-51	3/8/06	D5478	E26E	6	17%	33%	17%	33%
21-51	4/5/06	D5614	E26E	24	0%	76%	12%	12%
21-51	5/18/06	D5862	E26E	23	9%	74%	17%	0%
21-51	6/19/06	D6011	E26E	24	33%	43%	12%	12%
21-51	7/18/06	D6148	E26E	24	8%	29%	25%	38%
21-51	8/3/06	D6227	E26E	24	30%	33%	33%	4%
21-51	9/14/06	D6388	E26E	24	4%	0%	84%	12%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Table 5.29 Bacterial Source Tracking for Millford Haven at Station 36-12.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
36-12	10/12/05	D4898	C04E	24	25%	63%	4%	8%
36-12	11/28/05	D5023	C04E	18	89%	0%	11%	0%
36-12	12/12/05	D5092	C04E	13	46%	0%	54%	0%
36-12	1/11/06	D5234	C04E	NVI	NVI	NVI	NVI	NVI
36-12	3/23/06	D5569	C04E	8	75%	0%	0%	25%
36-12	4/24/06	D5738	C04E	19	58%	5%	11%	26%
36-12	5/22/06	D5870	C04E	16	94%	0%	6%	0%
36-12	6/5/06	D5930	C04E	24	80%	12%	4%	4%
36-12	7/19/06	D6157	C04E	24	71%	0%	4%	25%
36-12	8/17/06	D6289	C04E	24	4%	0%	96%	0%
36-12	9/18/06	D6403	C04E	7	100%	0%	0%	0%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Bacterial Source Tracking Analyses to Support Virginia's TMDLs

Table 5.30 Bacterial Source Tracking for Queens Creek at Station 37-6.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
37-6	10/12/05	D4894	C04E	23	100%	0%	0%	0%
37-6	11/28/05	D5024	C04E	7	100%	0%	0%	0%
37-6	12/12/05	D5093	C04E	24	75%	21%	0%	4%
37-6	1/26/06	D5260	C04E	3	100%	0%	0%	0%
37-6	2/8/06	D5327	C04E	NVI	NVI	NVI	NVI	NVI
37-6	3/23/06	D5570	C04E	2	100%	0%	0%	0%
37-6	4/24/06	D5739	C04E	24	54%	4%	17%	25%
37-6	5/22/06	D5866	C04E	24	100%	0%	0%	0%
37-6	6/5/06	D5931	C04E	23	57%	22%	17%	4%
37-6	7/19/06	D6153	C04E	5	100%	0%	0%	0%
37-6	8/17/06	D6297	C04E	24	58%	0%	21%	21%
37-6	9/18/06	D6399	C04E	8	62%	38%	0%	0%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Table 5.31 Bacterial Source Tracking for Billups Creek at Station 37-23.4.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
37-23.4	10/12/05	D4895	C03E	24	38%	50%	8%	4%
37-23.4	11/28/05	D5025	C03E	11	55%	9%	0%	36%
37-23.4	12/12/05	D5094	C03E	18	11%	11%	22%	56%
37-23.4	1/26/06	D5261	C03E	4	50%	50%	0%	0%
37-23.4	2/8/06	D5328	C03E	6	17%	17%	33%	33%
37-23.4	3/23/06	D5571	C03E	5	80%	20%	0%	0%
37-23.4	4/24/06	D5740	C03E	23	53%	13%	30%	4%
37-23.4	5/22/06	D5867	C03E	23	17%	44%	17%	22%
37-23.4	6/5/06	D5932	C03E	15	13%	67%	7%	13%
37-23.4	7/19/06	D6154	C03E	8	50%	38%	0%	12%
37-23.4	8/17/06	D6298	C03E	23	30%	17%	30%	23%
37-23.4	9/18/06	D6400	C03E	8	0%	63%	25%	12%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Bacterial Source Tracking Analyses to Support Virginia's TMDLs

Table 5.32 Bacterial Source Tracking for Great Stutts Creek at Station 37-26.2.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
37-26.2	10/12/05	D4896	C03E	24	4%	42%	8%	46%
37-26.2	11/28/05	D5026	C03E	12	67%	8%	17%	8%
37-26.2	12/12/05	D5095	C03E	16	100%	0%	0%	0%
37-26.2	1/26/06	D5262	C03E	23	100%	0%	0%	0%
37-26.2	2/8/06	D5329	C03E	2	100%	0%	0%	0%
37-26.2	3/23/06	D5572	C03E	4	25%	0%	0%	75%
37-26.2	4/24/06	D5741	C03E	13	85%	0%	0%	15%
37-26.2	5/22/06	D5868	C03E	24	83%	0%	17%	0%
37-26.2	6/5/06	D5933	C03E	22	76%	14%	5%	5%
37-26.2	7/19/06	D6155	C03E	24	54%	0%	8%	38%
37-26.2	8/17/06	D6299	C03E	24	0%	33%	29%	38%
37-26.2	9/18/06	D6401	C03E	24	75%	0%	25%	0%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Table 5.33 Bacterial Source Tracking for Morris Creek at Station 37-27.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
37-27	10/12/05	D4897	C03E	22	14%	36%	5%	45%
37-27	11/28/05	D5027	C03E	3	100%	0%	0%	0%
37-27	12/12/05	D5096	C03E	8	100%	0%	0%	0%
37-27	1/26/06	D5263	C03E	21	95%	0%	5%	0%
37-27	2/8/06	D5330	C03E	9	89%	11%	0%	0%
37-27	3/23/06	D5573	C03E	7	86%	0%	0%	14%
37-27	4/24/06	D5742	C03E	15	67%	0%	33%	0%
37-27	5/22/06	D5869	C03E	13	53%	8%	31%	8%
37-27	6/5/06	D5934	C03E	23	30%	9%	13%	48%
37-27	7/19/06	D6156	C03E	8	75%	0%	0%	25%
37-27	8/17/06	D6300	C03E	24	8%	25%	55%	12%
37-27	9/18/06	D6402	C03E	7	86%	0%	14%	0%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Bacterial Source Tracking Analyses to Support Virginia's TMDLs

Table 5.34 Bacterial Source Tracking for Horn Harbor at Station 39-8.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
39-8	10/31/05	D4939	C04E	3	33%	67%	0%	0%
39-8	11/14/05	D4997	C04E	2	50%	50%	0%	0%
39-8	12/12/05	D5098	C04E	12	0%	75%	0%	25%
39-8	1/26/06	D5265	C04E	1	0%	100%	0%	0%
39-8	2/9/06	D5332	C04E	10	10%	20%	0%	70%
39-8	3/27/06	D5575	C04E	24	96%	4%	0%	0%
39-8	4/10/06	D5661	C04E	19	21%	36%	32%	11%
39-8	5/25/06	D5891	C04E	8	38%	12%	25%	25%
39-8	6/7/06	D5936	C04E	12	42%	33%	0%	25%
39-8	7/6/06	D6061	C04E	24	21%	4%	54%	21%
39-8	8/7/06	D6271	C04E	8	38%	24%	0%	38%
39-8	9/18/06	D6405	C04E	18	11%	77%	6%	6%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Table 5.35 Bacterial Source Tracking for Horn Harbor at Station 39-10.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
39-10	10/31/05	D4940	C04E	9	45%	33%	11%	11%
39-10	11/14/05	D4998	C04E	6	33%	0%	50%	17%
39-10	12/12/05	D5099	C04E	24	8%	67%	0%	25%
39-10	1/26/06	D5266	C04E	21	76%	24%	0%	0%
39-10	2/9/06	D5333	C04E	19	37%	11%	0%	52%
39-10	3/27/06	D5576	C04E	14	86%	7%	0%	7%
39-10	4/10/06	D5662	C04E	24	33%	47%	8%	12%
39-10	5/25/06	D5892	C04E	15	13%	40%	0%	47%
39-10	6/7/06	D5937	C04E	22	40%	23%	5%	32%
39-10	7/6/06	D6062	C04E	24	17%	0%	83%	0%
39-10	8/7/06	D6272	C04E	8	12%	25%	0%	63%
39-10	9/18/06	D6406	C04E	19	5%	58%	5%	32%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Bacterial Source Tracking Analyses to Support Virginia's TMDLs

Table 5.36 Bacterial Source Tracking for Doctors Creek at Station 39-C.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
39-C	10/31/05	D4938	C04E	24	17%	66%	0%	17%
39-C	11/14/05	D4996	C04E	24	67%	17%	12%	4%
39-C	12/12/05	D5097	C04E	17	18%	70%	0%	12%
39-C	1/26/06	D5264	C04E	12	92%	0%	0%	8%
39-C	2/9/06	D5331	C04E	6	0%	33%	0%	67%
39-C	3/27/06	D5574	C04E	4	100%	0%	0%	0%
39-C	4/10/06	D5660	C04E	24	55%	29%	4%	12%
39-C	5/25/06	D5890	C04E	24	67%	17%	12%	4%
39-C	6/7/06	D5935	C04E	24	84%	12%	0%	4%
39-C	7/6/06	D6060	C04E	24	33%	4%	42%	21%
39-C	8/7/06	D6270	C04E	24	12%	59%	21%	8%
39-C	9/18/06	D6404	C04E	24	17%	79%	4%	0%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Table 5.37 Bacterial Source Tracking for Upper York River at Station 49-207.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
49-207	10/12/05	D4862	F25E	24	8%	63%	17%	12%
49-207	11/28/05	D5016	F25E	8	25%	25%	50%	0%
49-207	12/12/05	D5084	F25E	22	63%	5%	14%	18%
49-207	1/9/06	D5185	F25E	4	75%	25%	0%	0%
49-207	2/22/06	D5410	F25E	4	25%	0%	50%	25%
49-207	3/8/06	D5468	F25E	NVI	NVI	NVI	NVI	NVI
49-207	4/5/06	D5598	F25E	NVI	NVI	NVI	NVI	NVI
49-207	5/23/06	D5873	F25E	6	67%	0%	0%	33%
49-207	6/20/06	D6037	F25E	15	20%	13%	47%	20%
49-207	7/5/06	D6065	F25E	24	71%	8%	17%	4%
49-207	8/2/06	D6208	F25E	24	8%	29%	12%	51%
49-207	9/14/06	D6392	F25E	24	12%	17%	46%	25%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

5.2 Results for Tidewater Region

The results of the water quality analyses for VADEQ's Tidewater Region (Figure 5.2) are reported in the following tables. Table 5.38 indicates the number of samples analyzed in the 2005-2006 sampling phase. The results of the BST analysis are reported in Tables 5.39 through 5.47.

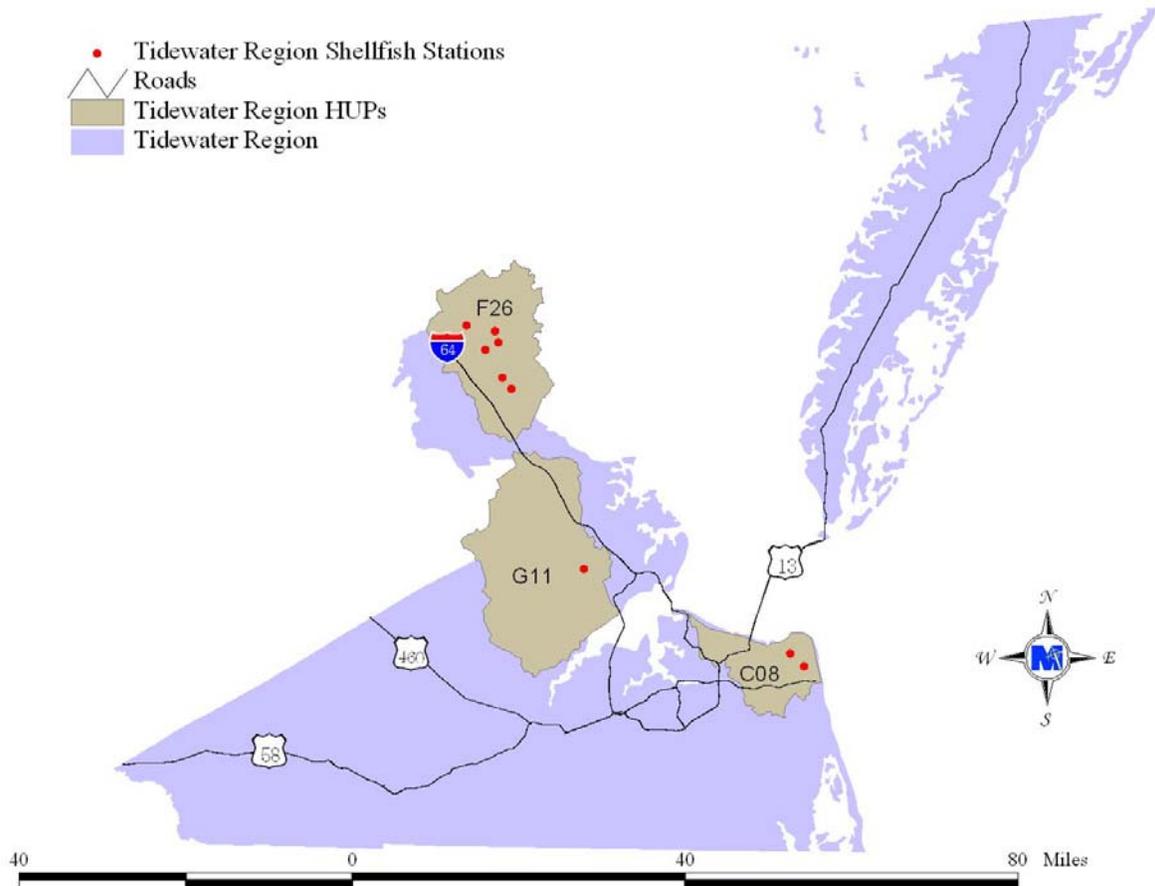


Figure 5.2 Bacterial sampling stations in VADEQ's Tidewater Region.

Bacterial Source Tracking Analyses to Support Virginia's TMDLs

Table 5.38 Summary of VDH-DSS bacterial sampling in VADEQ's Tidewater Region.

Station ID	HUP	County	Impairment	# Times Plates Received
48-21	F26E	Gloucester	Adams Creek	12
48-5	F26E	King and Queen	Poropotank River	12
50-4	F26E	James City, York	York River: Skimino Creek	11
50-19	F26E	York	York River: Carter Creek	11
50-22	F26E	James City	York River: Taskinas Creek	9
50-23	F26E	New Kent	York River: Ware Creek	10
57-E57	G11E	Newport News	Warwick and James Rivers: 57&58	6
71-4A	C08E	Virginia Beach	Dey Cove/Mill Dam Creek	11
71-9	C08E	Virginia Beach	Linkhorn Bay	9

Bacterial Source Tracking Analyses to Support Virginia's TMDLs

Table 5.39 Bacterial Source Tracking for Adams Creek at Station 48-21.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
48-21	10/12/05	D4861	F26E	24	8%	84%	8%	0%
48-21	11/28/05	D5015	F26E	16	38%	31%	12%	19%
48-21	12/12/05	D5083	F26E	24	17%	29%	21%	33%
48-21	01/9/06	D5184	F26E	NVI	NVI	NVI	NVI	NVI
48-21	2/22/06	D5409	F26E	4	50%	25%	25%	0%
48-21	3/8/06	D5467	F26E	NVI	NVI	NVI	NVI	NVI
48-21	4/5/06	D5597	F26E	7	100%	0%	0%	0%
48-21	5/23/06	D5872	F26E	23	26%	35%	13%	26%
48-21	6/20/06	D6036	F26E	24	58%	0%	25%	17%
48-21	7/5/06	D6064	F26E	24	79%	0%	17%	4%
48-21	8/2/06	D6207	F26E	24	29%	25%	12%	34%
48-21	9/14/06	D6391	F26E	24	4%	12%	29%	55%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Table 5.40 Bacterial Source Tracking for Poropotank River at Station 48-5.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
48-5	10/12/05	D4860	F26E	24	12%	76%	12%	0%
48-5	11/28/05	D5014	F26E	24	71%	25%	4%	0%
48-5	12/12/05	D5082	F26E	24	12%	63%	8%	17%
48-5	1/9/06	D5183	F26E	1	100%	0%	0%	0%
48-5	2/22/06	D5408	F26E	2	0%	100%	0%	0%
48-5	3/8/06	D5466	F26E	2	0%	100%	0%	0%
48-5	4/5/06	D5596	F26E	24	17%	71%	8%	4%
48-5	5/23/06	D5871	F26E	24	4%	71%	21%	4%
48-5	6/20/06	D6035	F26E	24	17%	33%	25%	25%
48-5	7/5/06	D6063	F26E	24	58%	0%	42%	0%
48-5	8/2/06	D6206	F26E	24	38%	0%	38%	24%
48-5	9/14/06	D6390	F26E	24	4%	33%	46%	17%

BOLD type indicates a statistically significant value. NVI – No viable isolates.

NVI – No viable isolates.

Bacterial Source Tracking Analyses to Support Virginia's TMDLs

Table 5.41 Bacterial Source Tracking for York River: Skimino Creek at Station 50-4.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
50-4	10/12/05	D4863	F26E	24	0%	75%	8%	17%
50-4	11/28/05	D5017	F26E	18	56%	11%	11%	22%
50-4	1/9/06	D5186	F26E	9	56%	22%	11%	11%
50-4	2/22/06	D5411	F26E	1	0%	0%	0%	100%
50-4	3/8/06	D5469	F26E	1	0%	100%	0%	0%
50-4	4/5/06	D5599	F26E	23	26%	4%	26%	44%
50-4	5/23/06	D5874	F26E	11	64%	18%	9%	9%
50-4	6/20/06	D6038	F26E	24	8%	33%	8%	51%
50-4	7/5/06	D6066	F26E	24	0%	0%	100%	0%
50-4	8/2/06	D6209	F26E	24	17%	21%	33%	29%
50-4	9/14/06	D6393	F26E	24	25%	8%	12%	55%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Table 5.42 Bacterial Source Tracking for York River: Carter Creek at Station 50-19.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
50-19	10/12/05	D4864	F26E	24	4%	55%	33%	8%
50-19	11/28/05	D5018	F26E	12	58%	17%	17%	8%
50-19	1/9/06	D5187	F26E	7	71%	29%	0%	0%
50-19	2/22/06	D5412	F26E	7	57%	0%	29%	14%
50-19	3/8/06	D5470	F26E	2	0%	100%	0%	0%
50-19	4/5/06	D5600	F26E	20	65%	15%	0%	20%
50-19	5/23/06	D5875	F26E	21	61%	10%	10%	19%
50-19	6/20/06	D6039	F26E	21	29%	29%	29%	13%
50-19	7/5/06	D6067	F26E	24	8%	4%	88%	0%
50-19	8/2/06	D6210	F26E	24	0%	58%	25%	17%
50-19	9/14/06	D6394	F26E	24	12%	47%	8%	33%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Bacterial Source Tracking Analyses to Support Virginia's TMDLs

Table 5.43 Bacterial Source Tracking for York River: Taskinas Creek at Station 50-22.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
50-22	10/12/05	D4865	F26E	24	4%	0%	84%	12%
50-22	11/28/05	D5019	F26E	5	80%	20%	0%	0%
50-22	1/9/06	D5188	F26E	1	100%	0%	0%	0%
50-22	4/5/06	D5601	F26E	7	86%	0%	0%	14%
50-22	5/23/06	D5876	F26E	7	14%	14%	43%	29%
50-22	6/20/06	D6040	F26E	20	40%	10%	30%	20%
50-22	7/5/06	D6068	F26E	10	0%	0%	100%	0%
50-22	8/2/06	D6211	F26E	3	0%	33%	0%	67%
50-22	9/14/06	D6395	F26E	21	10%	61%	29%	0%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Table 5.44 Bacterial Source Tracking for York River: Ware Creek at Station 50-23.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
50-23	10/12/05	D4866	F26E	24	8%	0%	88%	4%
50-23	11/28/05	D5020	F26E	16	57%	12%	12%	19%
50-23	2/22/06	D5413	F26E	6	66%	17%	17%	0%
50-23	3/8/06	D5471	F26E	1	0%	100%	0%	0%
50-23	4/5/06	D5602	F26E	16	69%	6%	6%	19%
50-23	5/23/06	D5877	F26E	15	13%	13%	27%	47%
50-23	6/20/06	D6041	F26E	24	29%	12%	21%	38%
50-23	7/5/06	D6069	F26E	24	0%	0%	100%	0%
50-23	8/2/06	D6212	F26E	24	21%	29%	8%	42%
50-23	9/14/06	D6396	F26E	21	19%	71%	5%	5%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Bacterial Source Tracking Analyses to Support Virginia's TMDLs

Table 5.45 Bacterial Source Tracking for Warwick and James Rivers 57 & 58 at Station 57-E57.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
57-E57	10/12/05	D4867	G11E	4	0%	75%	25%	0%
57-E57	1/9/06	D5189	G11E	1	100%	0%	0%	0%
57-E57	4/5/06	D5603	G11E	NVI	NVI	NVI	NVI	NVI
57-E57	5/23/06	D5878	G11E	NVI	NVI	NVI	NVI	NVI
57-E57	8/1/06	D6205	G11E	1	0%	0%	0%	100%
57-E57	9/5/06	D6340	G11E	NVI	NVI	NVI	NVI	NVI

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Table 5.46 Bacterial Source Tracking for Dey Cove/Milldam Creek at Station 71-4A.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
71-4A	10/26/05	D4931	C08E	24	59%	33%	8%	0%
71-4A	12/12/05	D5085	C08E	2	0%	100%	0%	0%
71-4A	1/10/06	D5190	C08E	2	100%	0%	0%	0%
71-4A	2/6/06	D5323	C08E	7	14%	72%	0%	14%
71-4A	3/7/06	D5464	C08E	NVI	NVI	NVI	NVI	NVI
71-4A	4/4/06	D5604	C08E	20	30%	45%	20%	5%
71-4A	5/22/06	D5879	C08E	12	33%	50%	17%	0%
71-4A	6/21/06	D6042	C08E	24	33%	29%	17%	21%
71-4A	7/19/06	D6158	C08E	15	13%	80%	0%	7%
71-4A	8/7/06	D6231	C08E	13	15%	77%	0%	8%
71-4A	9/18/06	D6397	C08E	24	29%	63%	4%	4%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

Bacterial Source Tracking Analyses to Support Virginia's TMDLs

Table 5.47 Bacterial Source Tracking for Linkhorn Bay at Station 71-9.

Station ID	Date of Sample	Lab ID	HUP ID	Number of Isolates	Wildlife	Human	Livestock	Pet
71-9	10/26/05	D4932	C08E	18	60%	28%	6%	6%
71-9	12/12/05	D5086	C08E	7	86%	14%	0%	0%
71-9	1/10/06	D5191	C08E	1	100%	0%	0%	0%
71-9	2/6/06	D5324	C08E	NVI	NVI	NVI	NVI	NVI
71-9	3/7/06	D5465	C08E	NVI	NVI	NVI	NVI	NVI
71-9	4/4/06	D5605	C08E	NVI	NVI	NVI	NVI	NVI
71-9	5/22/06	D5880	C08E	4	50%	0%	25%	25%
71-9	7/19/06	D6159	C08E	10	90%	0%	0%	10%
71-9	9/18/06	D6398	C08E	22	86%	5%	9%	0%

BOLD type indicates a statistically significant value.

NVI – No viable isolates.

6. DISCUSSION

Results of the 2005-2006 VADEQ BST program have been presented in this report. The ARCCs achieved during the library development stage are acceptable and there does not appear to be a high level of over-fitting. Based on the sample size targeted in each sample (*i.e.*, 24 isolates), there is 90% confidence that the proportions measured in each sample are within 15% of the actual proportions in the sampled population (*i.e.*, all bacteria in the stream at the time of sampling). Because a fixed-frequency sampling scheme was used, samples are not biased toward a particular flow regime and can therefore be combined to estimate the actual proportions contributed by the different sources over the entire year with greater precision (*i.e.*, 90% confidence that the estimate is within 5% of the actual proportions). Additionally, the statistical analyses applied to determine a significant difference from zero give a good indication of presence and absence of each source in each sample. All of these data are valuable for use in improving public awareness of the problem, improving model calibration/validation, and providing a more equitable allocation of loads to source classes.

In spite of the high quality of the data collected, care should be taken in using these data. These data represent, at most, 12 instantaneous observations at each station and may not be representative of long-term conditions. The hydrologic conditions during this period may not reflect either average or critical conditions. Additionally, the dynamics of the bacterial community are not well understood, so care should be taken in extrapolating from the in-stream condition to activities in the watershed. As with any other monitoring program, the data should not be viewed in a vacuum. Local knowledge of the sources involved, historical water quality records, and the hydrologic conditions during sampling should all be considered in any interpretation of this data.

REFERENCES

Hagedorn, C., S. L. Robinson, J. R. Filtz, S. M. Grubbs, T. A. Angier, and R. B. Reneau, Jr. 1999. Using antibiotic resistance patterns in the fecal streptococci to determine sources of fecal pollution in a rural Virginia watershed. *Appl. Environ. Microbiol.* 65:5522-5531.

USEPA. 1999. Guidance for Water Quality-Based Decisions: The TMDL Process. <http://www.epa.gov/OWOW/tmdl/decisions/dec1c.html>

APPENDIX A

Bacterial Source Tracking Analyses supplemental Report

Bacterial Source Tracking Analyses to Support Virginia's TMDLs

Table A.1 False-positive and correct classification rates for twelve BST libraries developed in support of VADEQ's Phase-IV BST Program.

Library	False-Positive Rates				Rate of Correct Classification			
	Wildlife	Human	Livestock	Pet	Wildlife	Human	Livestock	Pet
02070011	9.5%	5.5%	11.9%	7.3%	64.7%	80.3%	75.5%	77.0%
02080101	6.0%	4.0%	8.4%	7.1%	69.0%	88.5%	80.8%	84.1%
02080102	8.8%	12.4%	10.2%	13.2%	63.1%	86.6%	74.7%	83.2%
02080104	8.3%	6.5%	14.9%	7.3%	55.3%	83.1%	73.2%	77.2%
02080107	10.2%	7.2%	16.3%	9.4%	62.0%	80.0%	65.5%	65.6%
02080206	13.5%	6.9%	12.2%	8.7%	67.6%	82.9%	60.3%	65.9%
03010205	7.7%	6.7%	11.2%	9.9%	52.4%	82.5%	78.2%	79.0%

Table A.2 Species sampled for 7 libraries developed in support of VADEQ's Phase-VII BST Program.

Source Category	Species	02070011	02080101	02080102	02080104	02080107	02080206	03010205
Human	Human	x	x	x	x	x	x	x
Livestock	Beef	x	x	x	x	x	x	x
	Dairy	x	x	x	x	x	x	x
	Goat						x	
	Horse	x	x	x	x	x	x	x
	Poultry	x	x	x	x	x	x	x
	Swine	x	x	x	x	x	x	x
Pet	Cat	x	x	x	x	x	x	x
	Dog	x	x	x	x	x	x	x
Wildlife	Bear	x	x	x	x	x	x	x
	Deer	x	x	x	x	x	x	x
	Fox	x	x	x	x	x	x	x
	Goose	x	x	x	x	x	x	x
	Muskrat	x	x	x	x	x	x	x
	Otter	x	x	x	x	x	x	x
	Raccoon	x	x	x	x	x	x	x
	Skunk	x	x	x	x	x	x	x
Squirrel	x	x	x	x	x	x	x	

*Sources identified for each library indicates that at least one sample were collected within the geographic regions listed for that library.