Total Maximum Daily Loads of Fecal Bacteria for the Upper Monocacy River Basin in Carroll and Frederick Counties, Maryland

FINAL

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Submitted to:

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September 2009

EPA Submittal Date: October 3, 2007
EPA Approval Date: December 3, 2009

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Table of Contents

List of Figures

List of Tables

List of Abbreviations

ARCC	Average rates of correct classification
ARA	Antibiotic Resistance Analysis
BMP	Best Management Practice
BST	Bacteria Source Tracking
cfs	Cubic Feet per Second
CFR	Code of Federal Regulations
CFU	Colony Forming Units
COMAR	Code of Maryland Regulations
CSO	Combined Sewer Overflow
CSS	Combined Sewer System
CWA	Clean Water Act
DNR	Department of Natural Resources
EPA	Environmental Protection Agency
GIS	Geographic Information System
LA	Load Allocation
MACS	Maryland Agricultural Cost Share Program
MDE	Maryland Department of the Environment
MDP	Maryland Department of Planning
MGD	Millions of Gallons per Day
ml	Milliliter(s)
MOS	Margin of Safety
MPN	Most Probable Number
MPR	Maximum Practicable Reduction
MS4	Municipal Separate Storm Sewer System
MST	Microbial Source Tracking
NPDES	National Pollutant Discharge Elimination System
NRCS	National Resources Conservation Service
RCC	Rates of Correct Classification
RESAC	Mid-Atlantic Regional Earth Science Applications Center
SSO	Sanitary Sewer Overflows
SW	Stormwater
STATSGO	State Soil Geographic Database
TMDL	Total Maximum Daily Load
USGS	United States Geological Survey
WQIA	Water Quality Improvement Act
WLA	Wasteload Allocation
WQLS	Water Quality Limited Segment
WWTP	Wastewater Treatment Plant

EXECUTIVE SUMMARY

This document, upon approval by the U.S. Environmental Protection Agency (EPA), establishes a Total Maximum Daily Load (TMDL) for fecal bacteria in the Upper Monocacy River watershed (basin number 02-14-03-03). Section 303(d) of the federal Clean Water Act (CWA) and the EPA's implementing regulations direct each state to identify and list waters, known as water quality limited segments (WQLSs), in which current required controls of a specified substance are inadequate to achieve water quality standards. For each WQLS, states are required to either establish a Total Maximum Daily Load (TMDL) of the specified substance that the waterbody can receive without violating water quality standards or demonstrate that water quality standards are being met.

The Maryland Department of the Environment (MDE) has identified the Upper Monocacy River in the State of Maryland's 303(d) List as impaired by the following (years listed in parentheses): nutrients (1996), sediments (1996), impacts to biological communities (2002) and fecal bacteria (2002). The Upper Monocacy River mainstem in Maryland (MD), the MD portions of tributaries Toms Creek and Piney Creek, and the tributary Double Pipe Creek (entirely in MD) have been designated as Use IV-P waters (Water Contact Recreation, Protection of Aquatic Life, Recreational Trout Waters and Public Water Supply). The tributaries Tuscarora Creek, Fishing Creek, Hunting Creek, and Owens Creek, all located within MD, are designated as Use III-P (Water Contact Recreation, Protection of Aquatic Life, Non-tidal Cold Water and Public Water Supply). See Code of Maryland Regulations (COMAR) 26.08.02.08P. This document proposes to establish a TMDL for fecal bacteria in the Upper Monocacy River watershed in Maryland that will allow for attainment of the beneficial use designation of primary contact recreation. The listings for nutrients, sediments, and impacts to biological communities will be addressed separately at a future date. A data solicitation for fecal bacteria was conducted by MDE in 2003, and all readily available data from the past five years were considered. A separate fecal bacteria TMDL has been developed for Double Pipe Creek, which is a discrete MD 8-digit basin (basin number 02-14-03-01) and, as such, has been listed separately in the 303(d) list. The Double Pipe Creek TMDL and its allocations are described in detail in another MD TMDL document, which is pending EPA approval. Since Double Pipe Creek is a major tributary of the Upper Monocacy River, the Double Pipe Creek TMDL is accounted for herein as an upstream load allocation. To account for portions of subwatersheds located in a Pennsylvania (PA), a PA upstream load allocation, determined to be necessary in order to meet MD water quality standards in the MD portion of the watershed, is also included in this TMDL. Appendix E of this report provides further explanation of the upstream loads.

For this TMDL analysis, the Upper Monocacy River watershed has been divided into nine subwatersheds, within which lie the mainstem of the river and tributaries Rock Creek and Marsh Creek (located primarily in PA), Toms Creek and Piney Creek (in both MD and PA), and Owens Creek, Hunting Creek, Fishing Creek, and Tuscarora Creek (entirely in MD). The pollutant loads set forth in this document are for these nine subwatersheds, which are identified by the MDE monitoring stations located in them that provide the data used to assess flows and loads for each subwatershed. To establish baseline and allowable pollutant loads for this TMDL, a flow duration curve approach was employed, using flow strata estimated from United States Geological Survey (USGS) daily flow monitoring data and bacteria monitoring data. The sources of fecal bacteria are estimated at nine representative stations in the Upper Monocacy

River watershed where samples were collected for one year. Multiple antibiotic resistance analysis (ARA) source tracking was used to determine the relative proportion of domestic animal (pets and human associated animals), human (human waste), livestock (agriculture-related animals), and wildlife (mammals and waterfowl) source categories.

The allowable load is determined by estimating a baseline load from current monitoring data. The baseline load is estimated using a long-term geometric mean and weighting factors from the flow duration curve. The TMDL for fecal bacteria entering the Upper Monocacy River watershed is established after considering three different hydrological conditions: high flow and low flow annual conditions, and an average seasonal condition (the period between May 1st and September 30th when water contact recreation is more prevalent). This allowable load is reported in units of Most Probable Number (MPN)/day and represents a long-term load estimated over a variety of hydrological conditions.

Two scenarios were developed, with the first assessing if attainment of current water quality standards could be achieved by applying maximum practicable reductions (MPRs), and the second applying higher reductions than MPRs. Scenario solutions were based on an optimization method where the objective was to minimize the overall risk to human health, assuming that the risk varies over the four bacteria source categories. In eight of the nine subwatersheds of the Upper Monocacy River watershed, it was estimated that water quality standards could not be attained with MPRs. Thus, for these subwatersheds, the second scenario with higher maximum reductions was applied.

The fecal bacteria long-term annual average TMDL for the Upper Monocacy River watershed is 1,353,850 billion MPN *E. coli*/year. The TMDL allocation for the Upper Monocacy River 8-digit basin in MD is 496,234 billion MPN *E. coli*/year. The maximum daily load for the MD 8-digit basin is 57,734 billion MPN/day. The MD long-term annual average TMDL allocation represents a reduction of approximately 75% from the MD baseline load of 1,985,054 billion MPN *E. coli*/year.

The Upper Monocacy MD 8-digit portion of the TMDL is distributed between a load allocation (LA_{UM}) for nonpoint sources and waste load allocations (WLA_{UM}) for point sources, including National Pollutant Discharge Elimination System (NPDES) wastewater treatment plants (WWTPs) and NPDES regulated stormwater discharges, including county municipal separate storm sewer systems (MS4s). The margin of safety (MOS) has been incorporated using a conservative assumption by estimating the loading capacity of the stream based on a water quality endpoint concentration more stringent than the applicable MD water quality standard criterion. The *E. coli* water quality criterion concentration was reduced by 5%, from 126 MPN *E. coli*/100ml to 119.7 MPN *E. coli*/100ml.

The long-term annual average allocations in MD are as follows: the LA_{UM} is 438,751 billion MPN *E. coli*/year. The Stormwater (SW) WLA_{UM} is 51,816 billion MPN *E. coli*/year and the WWTP WLA_{UM} is 5,667 billion MPN *E. coli*/year. In addition to these allocation categories for the MD portion of the Upper Monocacy watershed, the TMDL also includes load allocations to account for two upstream loads to the Upper Monocacy MD 8-digit basin. One is the upstream load allocation for the portion of the watershed located in PA (LA_{PA}). The second upstream load allocation is for Double Pipe Creek (LA_{DP}). The LA_{PA}, determined to be necessary in order to meet MD water quality standards in the MD portion of the Upper Monocacy River watershed, is estimated as 575,448 billion MPN *E. coli*/year. This represents a reduction of approximately 61% from the PA baseline load of 1,474,162 billion MPN *E. coli*/year. The LA_{DP} is equivalent to the Double Pipe Creek fecal bacteria TMDL of 282,168 billion MPN *E. coli*/year.

The maximum daily loads for the watershed in MD, estimated using predicted long-term annual average TMDL allocation concentrations (after source controls), are allocated as follows: the LA_{UM} is 53,225 billion MPN *E. coli*/day. The SW WLA_{UM} is 4,461 billion MPN *E. coli*/day and the WWTP WLA_{UM} is 48 billion MPN *E. coli*/day.

Once EPA has approved a TMDL, and it is known what measures must be taken to reduce pollution levels, implementation of best management practices (BMPs) is expected to take place. MDE intends for the required reductions to be implemented in an iterative process that first addresses those sources with the largest impacts to water quality and creating the greatest risks to human health, with consideration given to ease and cost of implementation. In addition, follow-up monitoring plans will be established to track progress and to assess the implementation efforts. As previously stated, water quality standards cannot be attained in eight out of nine Upper Monocacy River subwatersheds, using the MPR scenario. MPRs may not be sufficient in subwatersheds where wildlife is a significant component or where very high reductions of fecal bacteria loads are required to meet water quality standards. In these cases, it is expected that the MPR scenario will be the first stage of TMDL implementation. Progress will be made through the iterative implementation process described above, and the situation will be reevaluated in the future.

1.0 INTRODUCTION

This document, upon approval by the U.S. Environmental Protection Agency (EPA), establishes a Total Maximum Daily Load (TMDL) for fecal bacteria in the Upper Monocacy River watershed (basin number 02-14-03-03). Section 303(d)(1)(C) of the federal Clean Water Act (CWA) and the U.S. Environmental Protection Agency's (EPA) implementing regulations direct each state to develop a TMDL for each impaired water quality limited segment (WQLS) on the Section 303(d) List, taking into account seasonal variations and a protective margin of safety (MOS) to account for uncertainty. A TMDL reflects the total pollutant loading of the impairing substance a waterbody can receive and still meet water quality standards.

TMDLs are established to achieve and maintain water quality standards. A water quality standard is the combination of a designated use for a particular body of water and the water quality criteria designed to protect that use. Designated uses include activities such as swimming, drinking water supply, and shellfish propagation and harvest. Water quality criteria consist of narrative statements and numeric values designed to protect the designated uses. Criteria may differ among waters with different designated uses.

The Maryland Department of the Environment (MDE) has identified the Upper Monocacy River in the State of Maryland's 303(d) List as impaired by the following (years listed in parentheses): nutrients (1996), sediments (1996), impacts to biological communities (2002) and fecal bacteria (2002). The Upper Monocacy River mainstem in Maryland (MD), the MD portions of tributaries Toms Creek and Piney Creek, and the tributary Double Pipe Creek (entirely in MD) have been designated as Use IV-P waters (Water Contact Recreation, Protection of Aquatic Life, Recreational Trout Waters and Public Water Supply). The tributaries Tuscarora Creek, Fishing Creek, Hunting Creek, and Owens Creek, all located within MD, are designated as Use III-P (Water Contact Recreation, Protection of Aquatic Life, Non-tidal Cold Water and Public Water Supply). See Code of Maryland Regulations (COMAR) 26.08.02.08P. This document proposes to establish a TMDL for fecal bacteria in the Upper Monocacy River watershed in MD that will allow for attainment of the beneficial use designation of primary contact recreation. The listings for nutrients, sediments, and impacts to biological communities will be addressed separately at a future date. A data solicitation for fecal bacteria was conducted by MDE in 2003, and all readily available data from the past five years were considered. A separate fecal bacteria TMDL has been developed for Double Pipe Creek, which is a discrete Maryland 8-digit basin (basin number 02-14-03-01) and, as such, has been listed separately in the 303(d) list. The Double Pipe Creek TMDL and its allocations are described in detail in another TMDL document, which is pending EPA approval. Since Double Pipe Creek is a major tributary of the Upper Monocacy River, the Double Pipe Creek TMDL is accounted for herein as an upstream load allocation (LA_{DP}). To account for portions of subwatersheds located in a Pennsylvania (PA), a PA upstream load allocation (LA_{PA}), determined to be necessary in order to meet MD water quality standards in the MD portion of the watershed, is also included in this TMDL. Appendix E of this report provides further explanation of the upstream loads.

Fecal bacteria are microscopic single-celled organisms (primarily fecal coliform and fecal streptococci) found in the wastes of warm-blooded animals. Their presence in water is used to assess the sanitary quality of water for body-contact recreation, for consumption of molluscan bivalves (shellfish), and for drinking water. Excessive amounts of fecal bacteria in surface water used for recreation are known to indicate an increased risk of pathogen-induced illness to humans. Infections due to pathogen-contaminated recreation waters include gastrointestinal, respiratory, eye, ear, nose, throat, and skin diseases (US EPA 1986).

In 1986, EPA published "Ambient Water Quality Criteria for Bacteria," in which three indicator organisms were assessed to determine their correlation with swimming-associated illnesses. Fecal coliform, *E. coli* and enterococci were the indicators used in the analysis. Fecal coliform bacteria are a subgroup of total coliform bacteria and *E. coli* bacteria are a subgroup of fecal coliform bacteria. Most *E. coli* are harmless and are found in great quantities in the intestines of people and warm-blooded animals. However, certain pathogenic strains may cause illness. Enterococci are a subgroup of bacteria in the fecal streptococcus group. Fecal coliform, *E. coli* and enterococci can all be classified as fecal bacteria. The results of the EPA study demonstrated that fecal coliform showed less correlation to swimming-associated gastroenteritis than did either *E. coli* or enterococci.

Based on EPA's guidance (US EPA 1986), adopted by Maryland in 2004, the State has revised the bacteria water quality criteria and it is now based on water column limits for either *E. coli* or enterococci. Because multiple monitoring datasets are available within this watershed for various pathogen indicators, the general term fecal bacteria will be used to refer to the impairing substance throughout this document. The TMDL will be based on the pathogen indicator organisms specified in MD's current bacteria water quality criteria, either *E. coli* or enterococci. The indicator organism used in the Upper Monocacy River TMDL analysis was *E. coli*.

2.0 SETTING AND WATER QUALITY DESCRIPTION

2.1 General Setting

Location

The Upper Monocacy River watershed is located in Carroll and Frederick Counties in MD (Figure 2.1.1). The drainage area of the Upper Monocacy River considered in this analysis is approximately 462 square miles (295,638 acres), and lies west of the Westminster metropolitan area. The Upper Monocacy River and its tributaries flow through several small towns, including Thurmont, Taneytown, and Emmitsburg. The basin receives drainage from the Double Pipe Creek basin, as well as from areas in PA. The headwaters of the Upper Monocacy originate in Pennsylvania (PA), just north of Gettysburg, flowing south toward the town of Emmitsburg, MD, and eventually emptying into the Middle Potomac River near the town of Dickerson. The town of Gettysburg in Adams County, PA, is centrally located between two large streams (Rock Creek and Marsh Creek) that drain to the Upper Monocacy River basin.

The Upper Monocacy River basin includes the following tributaries: Fishing Creek, Hunting Creek, Marsh Creek, Owens Creek, Toms Creek, Piney Creek, Rock Creek, Tuscarora Creek and Double Pipe Creek. Marsh Creek and Rock Creek are located almost entirely in PA. Toms Creek and Piney Creek flow through both PA and MD, and the other tributaries are located entirely in MD. There are two major drainage areas comprising the Double Pipe Creek watershed: Big Pipe Creek and Little Pipe Creek. These branches and tributaries are free-flowing (non-tidal) streams, and flow into the Monocacy River.

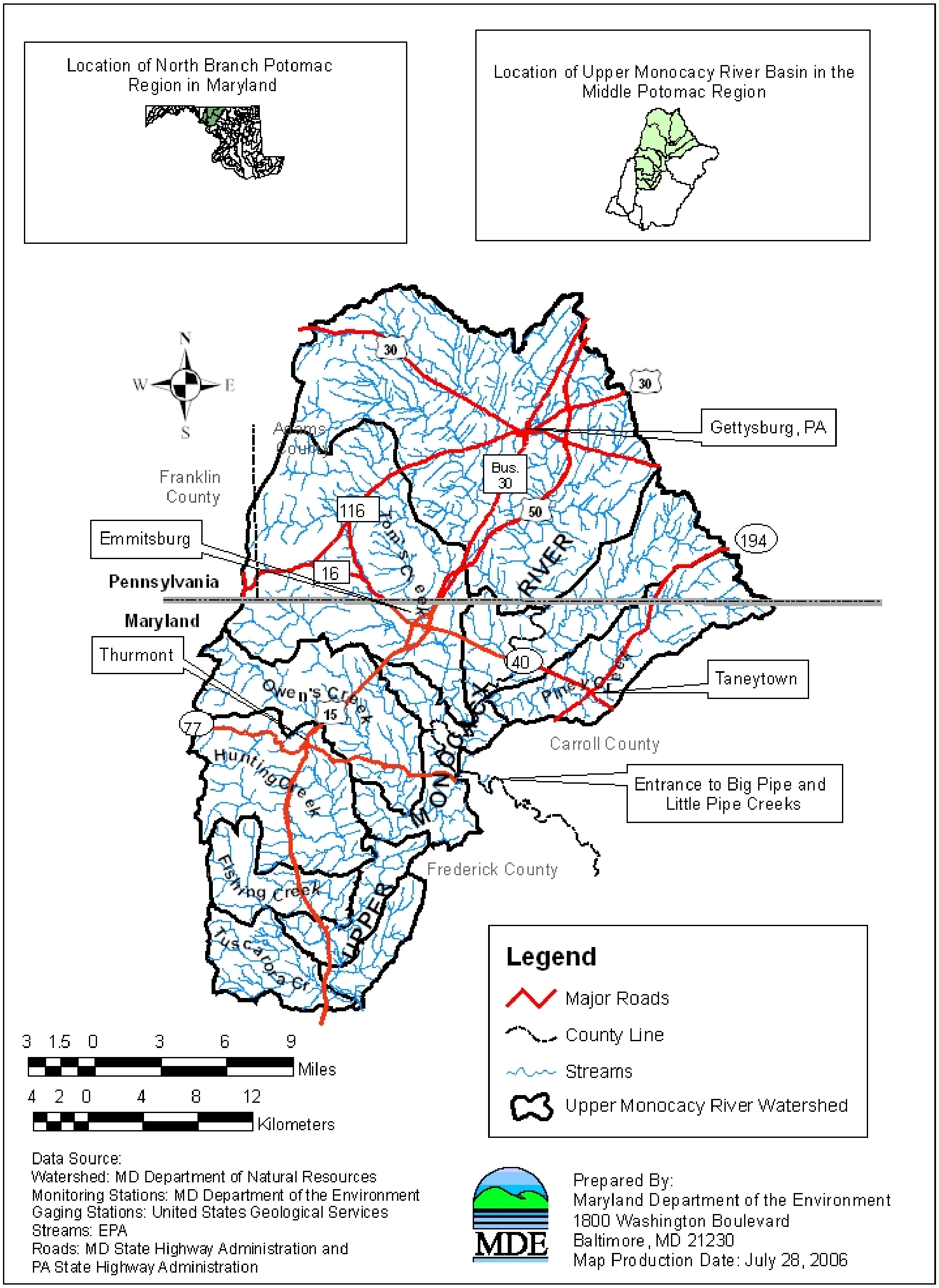

Figure 2.1.1: Location Map of the Upper Monocacy River Watershed

Land Use

The 2002 Maryland Department of Planning (MDP) land use/land cover data shows that MD's portion of the Upper Monocacy River watershed can be characterized as primarily forest and crop land. Forested areas are mostly in the western portion of the watershed where the Catoctin Mountain Park and Frederick Municipal Forest are located. Regional Earth Science Application Center (RESAC) land use/land cover was used to estimate the land use for the PA portion of Upper Monocacy River watershed. RESAC shows that the watershed is also primarily forest and pasture in the Pennsylvania portion of the basin. The three major urban areas are Thurmont, Taneytown, and Emmitsburg (MDE 2002).

The land use percentage distribution for the Upper Monocacy River watershed is shown in Table 2.1.1, and spatial distributions for each land use are shown in Figure 2.1.2. The land use of the Double Pipe Creek watershed is discussed in a separate TMDL document and is not included in the following table. The land use percentage distribution for the Double Pipe Creek watershed is Forest (19.4%), Urban (12.2%), Crops (57%), Pasture (11.3%) and Water (0.1%).

Table 2.1.1: Land Use Percentage Distribution for the Upper Monocacy River Watershed

Land Type	Maryland Acreage	Maryland %	Pennsylvania Acreage	%
Forest	61,464	41	63,418	44
Urban	13,785	9	11,560	8
Agricultural	67,954	45	16,127	11
Pasture	6,326	4	54,334	37
Water	487	0.3	184	0.1
Totals	**150,016**	**100**	**145,623**	**100**

Note: Land Use does not include the Double Pipe Creek watershed.

Population

The total population in the Upper Monocacy River watershed is estimated to be 587,306 people. Figure 2.1.3 illustrates the population density in the watershed. The human population and the number of households were estimated based on a weighted average from the GIS 2000 U. S. Census Block and the MDP Land Use 2002 Cover and the RESAC for PA that includes the Upper Monocacy River watershed. Since the Upper Monocacy River watershed is a sub-area of the Census Block, percentages of each land use within the watershed were used to extract the areas from the 2000 Census Block. Table 2.1.2 shows the number of dwellings per acre in the Upper Monocacy River watershed. The number of dwellings per acre was derived from information for residential density (low, medium, high) from the MDP land use cover and RESAC.

Table 2.1.2: Number of Dwellings Per Acre

Land use Code	Dwelling Per Acres
Low Density Residential	1
Medium Density Residential	5
High Density Residential	8

Based on the number of households from the Total Population from the Census Block and the number of dwellings per acre from the MDP Land Use Cover and RESAC, population per sub-watershed was estimated (see Table 2.1.3). Note that the nine subwatersheds are identified by the MDE monitoring stations located in the mainstem of the river (3) and in the main tributaries (6) partially or entirely within MD (except for Double Pipe Creek), and are listed by flow from upstream to downstream.

Table 2.1.3: Total Population Per Subwatershed in the Upper Monocacy River Watershed

Tributary	Station	Population
Upper Monocacy River	MON0575	37,338
Piney Creek	PIN0000	77,050
Toms Creek	TOM0011	78,879
Owens Creek	OWN0007	61,497
Upper Monocacy River	MON0355	68,342
Hunting Creek	HUN0009	112,184
Fishing Creek	FIS0012	40,978
Upper Monocacy River	MON0269	40,219
Tuscarora Creek	TUS0007	70,819
	TOTAL	587,306

Note: Population does not include the Double Pipe Creek watershed.

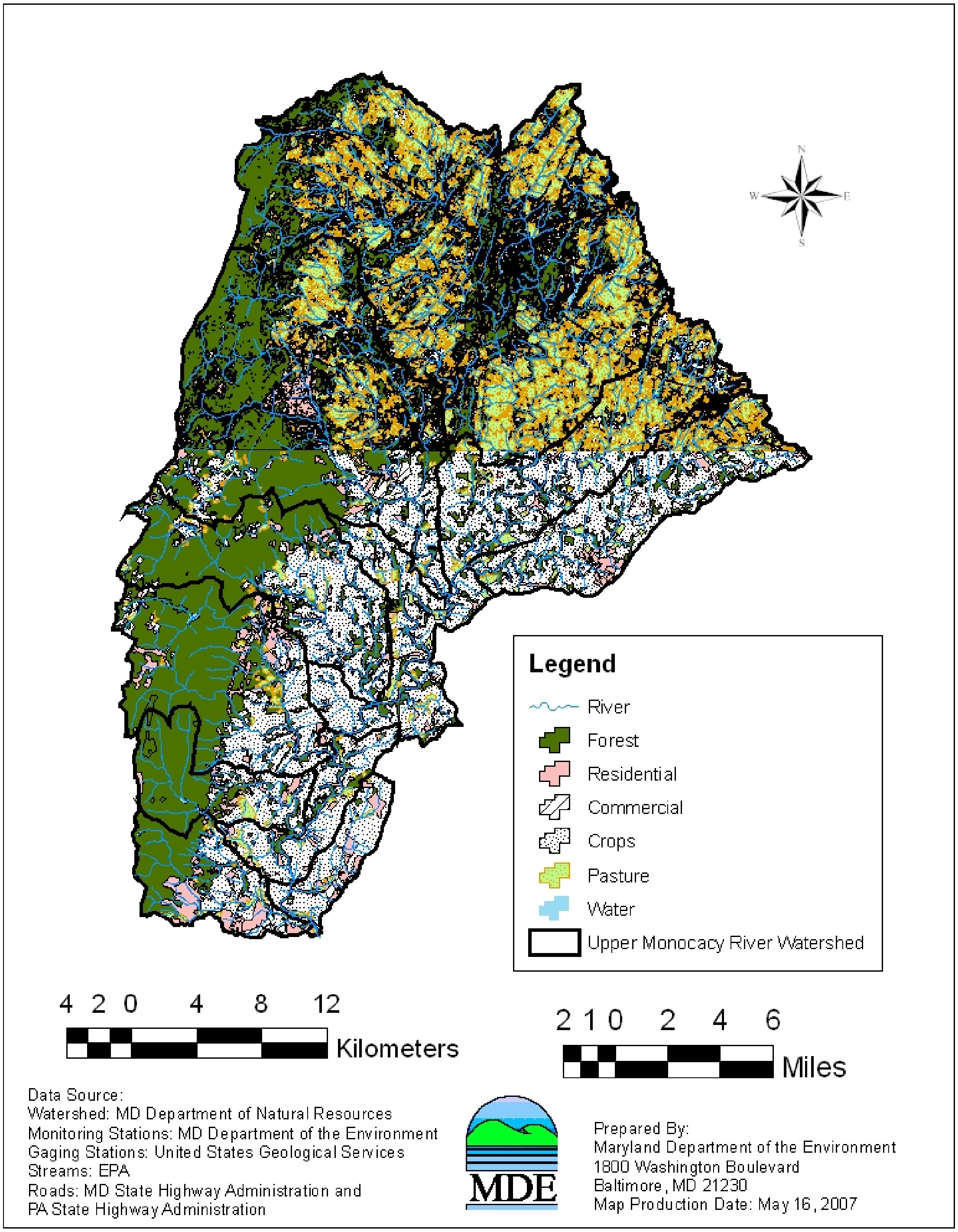

Figure 2.1.2: Land Use of the Upper Monocacy River Watershed

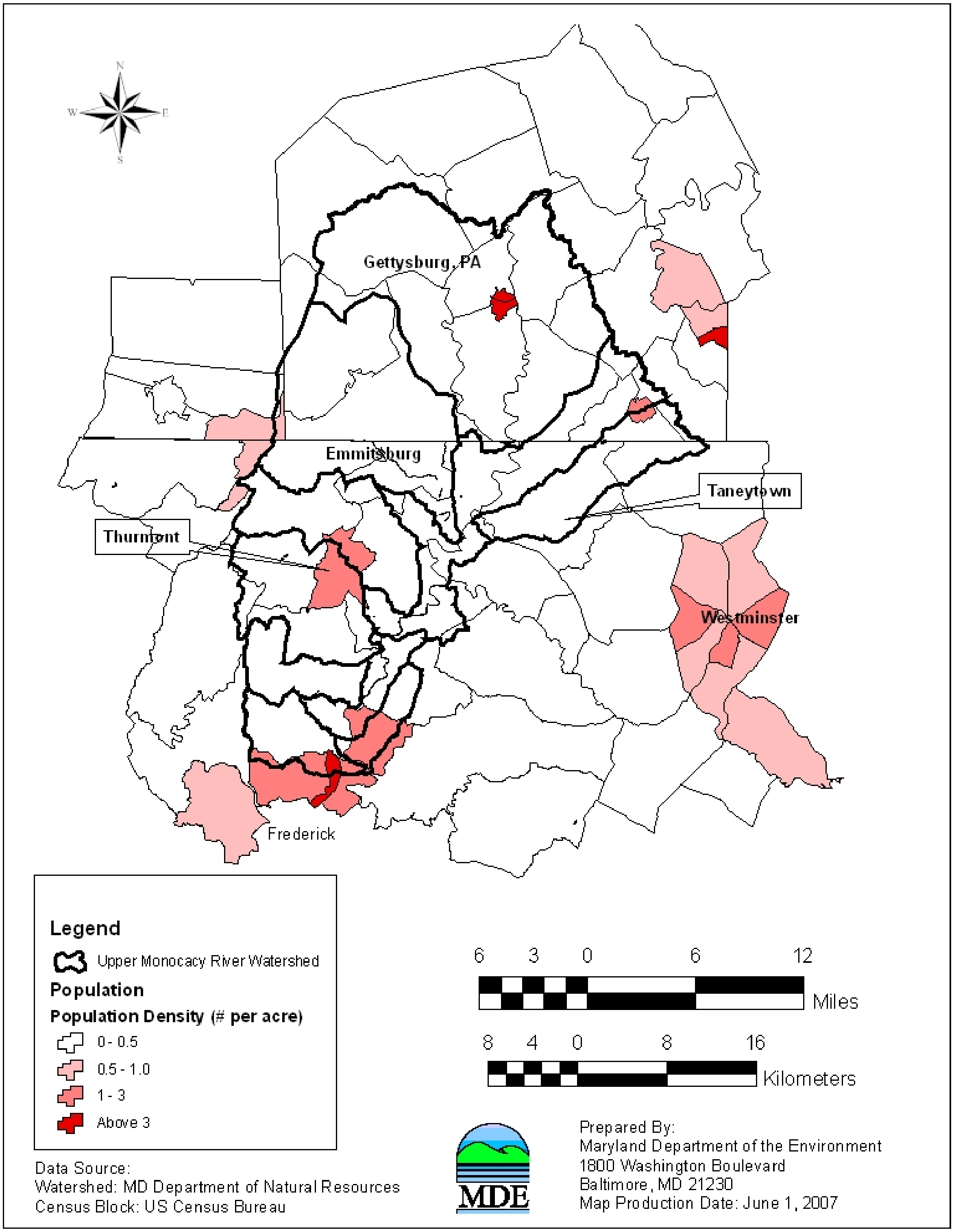

Figure 2.1.3: Population Density in the Upper Monocacy River Watershed

2.2 Water Quality Characterization

EPA's guidance document, "Ambient Water Quality Criteria for Bacteria" (1986), recommended that states use *E. coli* (for fresh water) or enterococci (for fresh or salt water) as pathogen indicators. Fecal bacteria, *E. coli*, and enterococci were assessed as indicator organisms for predicting human health impacts. A statistical analysis found that the highest correlation to gastrointestinal illness was linked to elevated levels of *E. coli* and enterococci in fresh water (enterococci in salt water).

As per EPA's guidance, Maryland has adopted the new indicator organisms, *E. coli* and enterococci, for the protection of public health in Use I, II, and IV waters. These bacteria listings were originally assessed using fecal coliform bacteria. The analysis was based on a geometric mean of the monitoring data, where the result had to be less than or equal to 200 MPN/100ml. From EPA's analysis (US EPA 1986), this fecal coliform geometric mean target equates to an approximate risk of 8 illnesses per 1,000 swimmers at fresh water beaches and 19 illnesses per 1,000 swimmers at marine beaches (enterococci only), which is consistent with MDE's revised Use I bacteria criteria. Therefore, the original 303(d) List fecal coliform listings can be addressed using the refined bacteria indicator organisms to ensure that risk levels are acceptable.

Bacteria Monitoring

Table 2.2.1 lists the historical monitoring data for the Upper Monocacy River watershed. MDE conducted monitoring sampling from November 2003 through November 2004. There are nine MDE monitoring stations in the Upper Monocacy River watershed. In addition to the bacteria monitoring stations, there is one United States Geological Survey (USGS) gauging station used in deriving the surface flow in the Upper Monocacy River. The locations of these stations are shown in Tables 2.2.2 to 2.2.4 and in Figure 2.2.1. In Table 2.2.3, and throughout this report, the monitoring stations are listed according to flow from upstream to downstream for the mainstem of the Upper Monocacy River (3) and the tributaries Piney Creek, Toms Creek, Owens Creek, Hunting Creek, Fishing Creek, and Tuscarora Creek (6). (In addition, two monitoring stations from Double Pipe Creek were used to calculate loadings coming from Double Pipe Creek.) Observations recorded during the period 2003-2004 from the nine MDE monitoring stations in the Upper Monocacy watershed are shown in Appendix A, which also includes a table listing the monitoring results.

Bacteria counts are highly variable and results are presented on a log scale for the eleven monitoring stations for data collected for November 2003 through November 2004. Bacteria counts ranged between 10 and 7,700 MPN/100 ml.

Table 2.2.1: Historical Monitoring Data in the Upper Monocacy River Watershed

Sponsor	Location	Date	Design	Summary
MDE	MD	11/03 to 10/04	*E. coli*	6 stations 2 samples per month
MDE	MD	11/03 to 10/04	BST(ARA) (enterococci)	6 stations 1 sample per month

Table 2.2.2: Location of DNR (CORE) Monitoring Station in the Upper Monocacy River Watershed

Tributary	Monitoring Station	LATITUDE Dec-Deg	LONGITUDE Dec-Deg
Upper Monocacy River	MON0528	39^o 40.752	77^o 14.10

Table 2.2.3: Locations of MDE Monitoring Stations in the Upper Monocacy Watershed

Tributary	Monitoring Station	Observation Period	Total Observations	LATITUDE Dec-Deg	LONGITUDE Dec-Deg
Upper Monocacy	MON0575	2003 - 2004	22	39^o 42.863	77^o 12.947
Piney Creek	PIN0000	2003 - 2004	22	39^o 39.336	77^o 15.897
Toms Creek	TOM0011	2003 - 2004	22	39^o 38.894	77^o 17.336
Owens Creek	OWN0007	2003 - 2004	22	39^o 35.126	77^o 20.110
Upper Monocacy	MON0355	2003 - 2004	22	39^o 33.813	77^o 21.110
Hunting Creek	HUN0009	2003 - 2004	22	39^o 33.175	77^o 22.416
Fishing Creek	FIS0012	2003 - 2004	22	39^o 30.687	77^o 23.091
Upper Monocacy	MON0269	2003 - 2004	22	39^o 28.796	77^o 23.297
Tuscarora Creek	TUS0007	2003 - 2004	22	39^o 27.488	77^o 23.265

Table 2.2.4: Location of USGS Gauging Stations in the Upper Monocacy River Watershed

Monitoring Station	Observation Period Used in TMDL Analysis	Total Observations	LATITUDE Dec-Deg	LONGITUDE Dec-Deg
01639000	1989 – 2004	5,477	39^o 40.730’	77^o 14.070’

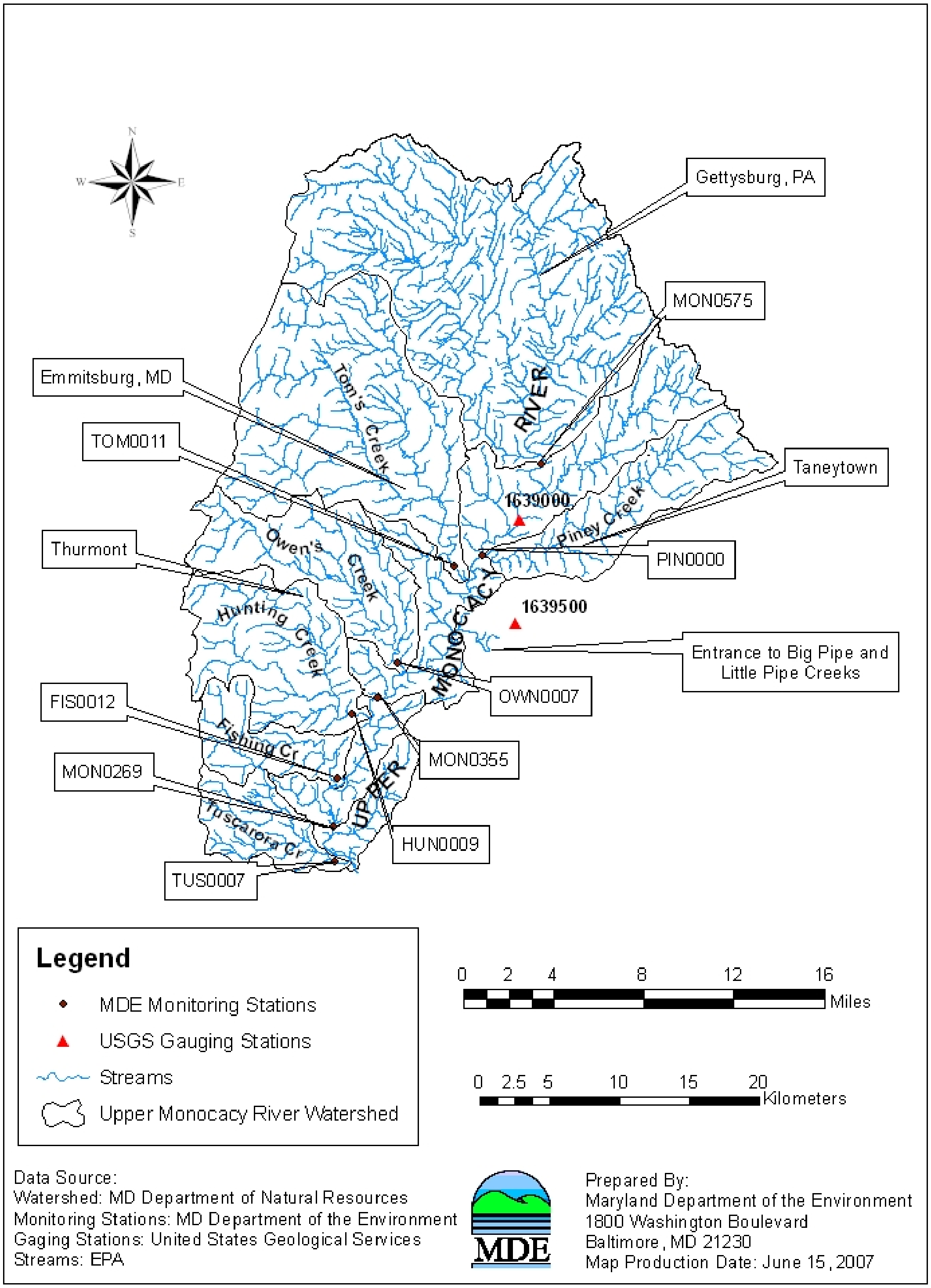

Figure 2.2.1: Monitoring Stations and Subwatersheds in the Upper Monocacy River Basin

2.3 Water Quality Impairment

Designated Uses and Water Quality Standard

The MD water quality standards Surface Water Use Designation for the MD waters of the Upper Monocacy River mainstem and its tributaries Toms Creek, Piney Creek and Double Pipe Creek is IV-P (Recreational Trout Waters and Public Water Supply). The tributaries Tuscarora Creek, Fishing Creek, Hunting Creek, and Owens Creek, all located within MD, are designated as Use III-P (Non-tidal Cold Water and Public Water Supply). See COMAR 26.08.02.08P. The Upper Monocacy River watershed was listed on Maryland's 303(d) List as impaired by fecal bacteria in 2002, due to elevated bacterial concentrations detected at CORE monitoring station MON0528, which showed a geometric mean of 386 MPN/100ml.

Water Quality Criteria

The State water quality standard for bacteria (*E. coli*) used in this study is as follows (COMAR 26.08.02.03-3):

Table 2.3.1: Bacteria Criteria Values from Table 1 COMAR 26.08.02.03-3 Water Quality Criteria Specific to Designated Uses.

Indicator	Steady-state Geometric Mean Indicator Density
Freshwater	
E. coli	126 MPN/100 ml

Interpretation of Bacteria Data for General Recreational Use

The relevant portion (for freshwater) of the listing methodology pursuant to the 2006 Integrated 303(d) List for all Use Waters - Water Contact Recreation and Protection of Aquatic Life is as follows:

Recreational Waters

A steady-state geometric mean will be calculated with available data where there are at least five representative sampling events. The data shall be from samples collected during steady-state conditions and during the beach season (Memorial Day through Labor Day) to be representative of the critical condition. If the resulting steady-state geometric mean is greater than 126 *E. coli* MPN/100 ml in freshwater, the waterbody will be listed as impaired. If fewer than five representative sampling events for an area being assessed are available, data from the previous two years will be evaluated in the same way. The single sample maximum criterion applies only to beaches and is to be used for closure and advisory decisions based on short term exceedances of the geometric mean portion of the standard.

Water Quality Assessment

Bacteria water quality impairment in Upper Monocacy River was assessed by comparing both the annual and the seasonal (May 1^{st} –September 30^{th}) steady-state geometric means of *E. coli* concentrations with the water quality criterion. Graphs illustrating these results can be found in Appendix B.

The steady-state condition is defined as unbiased sampling targeting average flow conditions and/or equally sampling or providing for unbiased sampling of high and low flows. The 1986 EPA criteria document assumed steady-state flow in determining the risk at various bacterial concentrations, and therefore the chosen criterion value also reflects steady-state conditions (EPA 1986). The steady-state geometric mean condition can be estimated either by monitoring design or more practically by statistical analysis as follows:

1. A stratified monitoring design is used where the number of samples collected is proportional to the duration of high flows, mid flows and low flows within the watershed. This sample design allows a geometric mean to be calculated directly from the monitoring data without bias.

2. Routine monitoring typically results in samples from varying hydrologic conditions (i.e., high flows, mid flows and low flows) where the numbers of samples are not proportional to the duration of those conditions. Averaging these results without consideration of the sampling conditions results in a biased estimate of the steady-state geometric mean. The potential bias of the steady-state geometric means can be reduced by weighting the samples results collected during high flow, mid flow and low flow regimes by the proportion of time each flow regime is expected to occur. This ensures that the high flow and low flow conditions are proportionally balanced.

3. If (1) the monitoring design was not stratified based on flow regime or (2) flow information is not available to weight the samples accordingly, then a geometric mean of sequential monitoring data can be used as an estimate of the steady-state geometric mean condition for the specified period.

A routine monitoring design was used to collect bacteria data in the Upper Monocacy River watershed. To estimate the steady-state geometric mean, the monitoring data were first reviewed by plotting the sample results versus their corresponding daily flow duration percentile. Graphs illustrating these results can be found in Appendix B.

To calculate the steady-state geometric mean with routine monitoring data, a conceptual model was developed by dividing the daily flow frequency for the stream segment into strata that are representative of hydrologic conditions. A conceptual continuum of flows is illustrated in Figure 2.3.1.

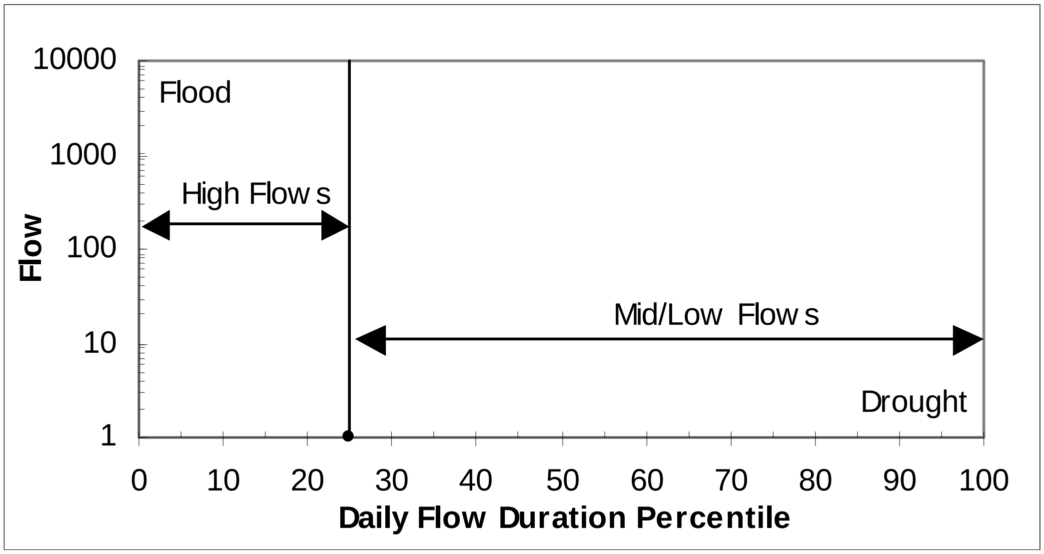

Figure 2.3.1: Conceptual Diagram of Flow Duration Zones

During high flows, a significant portion of the total stream flow is from surface flow contributions. Low flow conditions represent periods with minimal rainfall and surface runoff. There is typically a transitional mid flow period between the high and low flow durations, representative of varying contributions of surface flow inputs that result from differing rainfall volumes and antecedent soil moisture conditions. The division of the entire flow regime into strata enables the estimation of a less biased geometric mean from routine monitoring data that more closely approaches steady-state. Based on a flow analysis of several watersheds throughout Maryland, it was determined that flows within the 25^{th} to 30^{th} daily flow duration percentiles were representative of average daily flows. It is assumed for this analysis that flows higher than the 25^{th} percentile flow represent high flows, and flows lower than the 25^{th} percentile flow represent mid/low flows. A detailed method of how the flow strata were defined is presented in Appendix B.

Factors for estimating a steady-state geometric mean are based on the frequency of each flow stratum. The weighting factor accounts for the proportion of time that each flow stratum represents. The weighting factors for an average hydrological year used in the Upper Monocacy River TMDL analysis are presented in Table 2.3.2.

Table 2.3.2: Weighting Factors for Average Hydrology Year Used for Estimation of Geometric Means in the Upper Monocacy River Watershed

Flow Duration Zone	Duration Interval	Weighting Factor
High Flows	0 – 25%	0.25
Mid/Low Flows	25 – 100%	0.75

Bacteria enumeration results for samples within a specified stratum will receive their corresponding weighting factor. The steady-state geometric mean is calculated as follows:

$$M = \sum_{i=1}^{2} M_i * W_i \qquad (1)$$

where

$$M_i = \frac{\sum_{j=1}^{n_i} \log_{10}(C_{i,j})}{n_i} \qquad (2)$$

M = log weighted mean
M_i = log mean concentration for stratum i
W_i= Proportion of stratum i
$C_{i,j}$ = Concentration for sample j in stratum i
n_i = number of samples in stratum

Finally, the steady-state geometric mean concentration is estimated using the following equation:

$$C_{gm} = 10^M \qquad (3)$$

C_{gm} = Steady-state geometric mean concentration

Tables 2.3.3 and 2.3.4 present the maximum and minimum concentrations and the geometric means by stratum, and the overall steady-state geometric mean for the Upper Monocacy River subwatersheds for the annual and the seasonal (May 1st –September 30th) periods. Monitoring stations are listed by flow from upstream to downstream. For the seasonal period, only one sample in each subwatershed fell in the high flow category; and a geometric mean by flow stratum could not be calculated due to an insufficient number of samples. Therefore, in the seasonal analysis, only the overall geometric mean for the May 1st – September 30th period was applied.

Table 2.3.3: Upper Monocacy River Watershed Annual Steady-State Geometric Means by Flow Stratum per Monitoring Station

Tributary Station	Flow Stratum	# of Samples	*E. coli* Minimum Concentration (MPN/100ml)	*E. coli* Maximum Concentration (MPN/100ml)	Annual Steady-State Geometric Mean (MPN/100ml)	Annual Weighted Geometric Mean (MPN/100ml)
Upper Monocacy River MON0575	High	7	10	650	179	107
	Low	15	10	360	90	
Piney Creek PIN0000	High	7	10	1,660	230	179
	Low	15	10	1,040	165	
Toms Creek TOM0011	High	7	30	750	149	258
	Low	15	10	7,700	311	
Owens Creek OWN0007	High	7	60	580	209	204
	Low	15	10	1,190	203	
Upper Monocacy River MON0355	High	7	10	2,910	432	223
	Low	15	20	4,610	179	
Hunting Creek HUN0009	High	7	20	660	125	196
	Low	15	20	750	228	
Fishing Creek FIS0012	High	7	30	520	135	180
	Low	15	10	1,140	198	
Upper Monocacy River MON0269	High	7	30	2,180	360	178
	Low	15	10	1,600	141	
Tuscarora Creek TUS0007	High	9	20	330	126	282
	Low	13	60	1,470	368	

Table 2.3.4: Upper Monocacy River Watershed Average Seasonal (May 1st-September 30th) Period Steady-State Geometric Mean per Monitoring Station

Tributary Station	# of Samples	*E. coli* Minimum Concentration (MPN/100ml)	*E. coli* Maximum Concentration (MPN/100ml)	Average Seasonal Geometric MEAN(MPN/ 100ml)
Upper Monocacy River MON0575	10	30	410	158
Piney Creek PIN0000	10	130	1,040	334
Toms Creek TOM0011	10	179	7,700	951
Owens Creek OWN0007	10	220	1,190	407
Upper Monocacy River MON0355	10	70	1,180	212
Hunting Creek HUN0009	10	260	740	521
Fishing Creek FIS0012	10	300	1,140	558
Upper Monocacy River MON0269	10	110	840	226
Tuscarora Creek TUS0007	10	310	1,470	593

2.4 Source Assessment

Nonpoint Source Assessment

Nonpoint sources of fecal bacteria do not have one discharge point but occur over the entire length of a stream or waterbody. During rain events, surface runoff transports water and fecal bacteria over the land surface and discharges to the stream system. This transport is dictated by rainfall, soil type, land use, and topography of the watershed. Many types of nonpoint sources introduce fecal bacteria to the land surface, including the manure spreading process, direct deposition from livestock during the grazing season, and excretions from pets and wildlife. The deposition of non-human fecal bacteria directly to the stream occurs when livestock or wildlife have direct access to the waterbody. Nonpoint source contributions from human sources generally arise from failing septic systems and their associated drain fields or leaking infrastructure (i.e., sewer systems). The entire Upper Monocacy River watershed in MD is covered by two National Pollutant Discharge Elimination System (NPDES) Municipal Separate Storm Sewer System (MS4) individual permits; therefore, contributions from domestic animal and human sources will be categorized under point sources as part of a Stormwater (SW) Waste Load Allocation (WLA_{UM}). The presence of agricultural land use is significant in the watershed, and sources associated with it (i.e., livestock) contribute to the load allocation (LA_{UM}) in this analysis. Wildlife contributions will be distributed between WLAs and LAs due to the presence of wildlife in both developed and undeveloped areas of the watershed.

Sewer Systems

The MD Upper Monocacy River watershed is serviced by both sewer systems and septic systems. Sewer systems are present in the towns of Emmitsburg, Frederick, Lewistown, Taneytown, Thurmont and White Rock. Wastewater collected by these systems is treated at the Emmitsburg WWTP, Frederick WWTP, Lewistown WWTP, Taneytown WWTP, Thurmont WWTP and White Rock WWTP.

Septic Systems

On-site disposal (septic) systems are located throughout the Upper Monocacy River watershed. Table 2.4.1 presents the number of septic systems per subwatershed in the State of Maryland only. Figure 2.4.1 depicts the areas that are serviced by sewers and septic systems in MD.

Table 2.4.1: Septic Systems Per Subwatershed in the Upper Monocacy Watershed in Maryland

Tributary	Station	Septic Systems (units)
Upper Monocacy River (MD portion only)	MON0575	4
Piney Creek (MD portion only)	PIN0000	878
Toms Creek (MD portion only)	TOM0011	903
Owens Creek	OWN0007	950
Upper Monocacy River (MD portion only)	MON0355	1,036
Hunting Creek	HUN0009	1,412
Fishing Creek	FIS0012	556
Upper Monocacy River	MON0269	488
Tuscarora Creek	TUS0007	1,309
	TOTAL	7,536

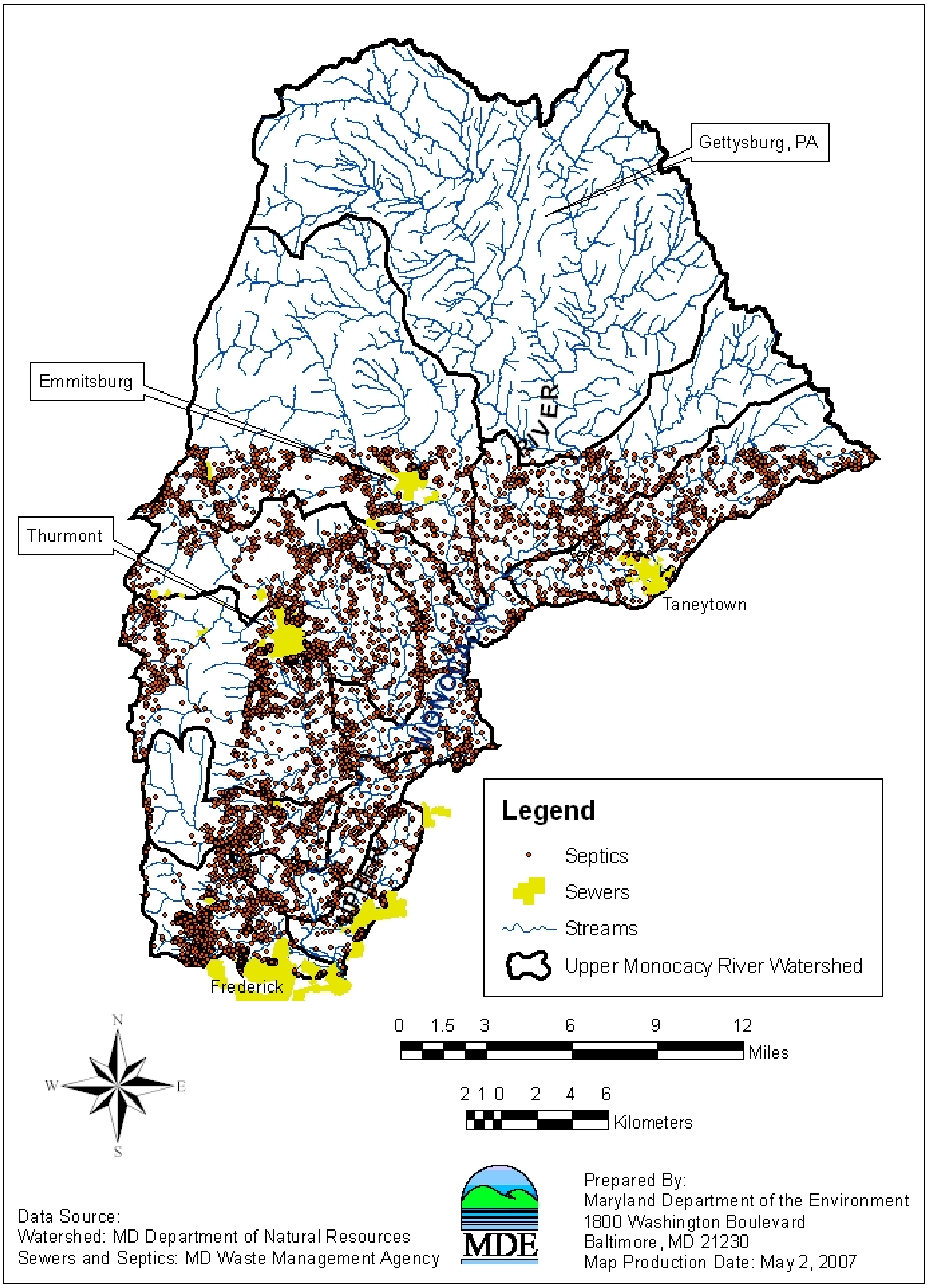

Figure 2.4.1: Sanitary Sewer Service and Septics Areas in Maryland's Portion of the Upper Monocacy River Watershed

Point Source Assessment

There are two broad types of National Pollutant Discharge Elimination System (NPDES) permits considered in this analysis, individual and general. Both types of permits include industrial and municipal categories. Individual permits are issued for industrial and municipal WWTPs and Phase I municipal separate storm sewer systems (MS4s). MDE general permits have been established for surface water discharges from: Phase II and other MS4 entities, surface coal mines, mineral mines, quarries, borrow pits, ready-mix concrete, asphalt plants, seafood processors, hydrostatic testing of tanks and pipelines, marinas, concentrated animal feeding operations, and stormwater associated with industrial activities.

NPDES Regulated Stormwater

Bacteria sources associated with MS4s are considered point sources. Stormwater runoff is an important source of water pollution, including bacterial pollution. A MS4 is a conveyance or system of conveyances (roads with drainage systems, municipal streets, catch basins, curbs, gutters, ditches, man-made channels, storm drains) designed or used for collecting or conveying stormwater and delivering it to a waterbody. MS4 programs are designed to reduce the amount of pollution that enters a waterbody from storm sewer systems to the maximum extent practicable.

Maryland's portion of the Upper Monocacy River watershed is located in Carroll and Frederick Counties, which are both jurisdictions with individual Phase I National Pollutant Discharge Elimination System (NPDES) MS4 permits. NPDES MS4 Permit numbers for these jurisdictions are MD0068331 for Carroll County and MD0068357 for Frederick County. Bacteria loads associated with these MS4s are therefore included in the Stormwater (SW) WLA_{UM} of this TMDL, which also encompasses any other NPDES regulated Phase I and Phase II stormwater discharges in the watershed, including State and federal entities.

Sanitary Sewer Overflows

Sanitary Sewer Overflows (SSOs) occur when the capacity of a separate sanitary sewer is exceeded. There are several factors that may contribute to SSOs from a sewerage system, including pipe capacity, operations and maintenance effectiveness, sewer design, age of system, pipe materials, geology and building codes. SSOs are prohibited by the facilities' permits, and must be reported to MDE's Water Management Administration in accordance with COMAR 26.08.10 to be addressed under the State's enforcement program.

There were a total of 34 SSOs reported to MDE between September 2003 and November 2004 in the Frederick County portion of the Upper Monocacy watershed. Approximately 3,165,624 gallons of SSOs were discharged through various waterways (surface water, groundwater, sanitary sewers, etc.) in the Frederick County portion of the watershed. No SSOs were reported in the Carroll County portion of the watershed. Figure 2.4.2 depicts the locations where SSOs occurred in the Maryland portion of the watershed between September 2003 and November 2004.

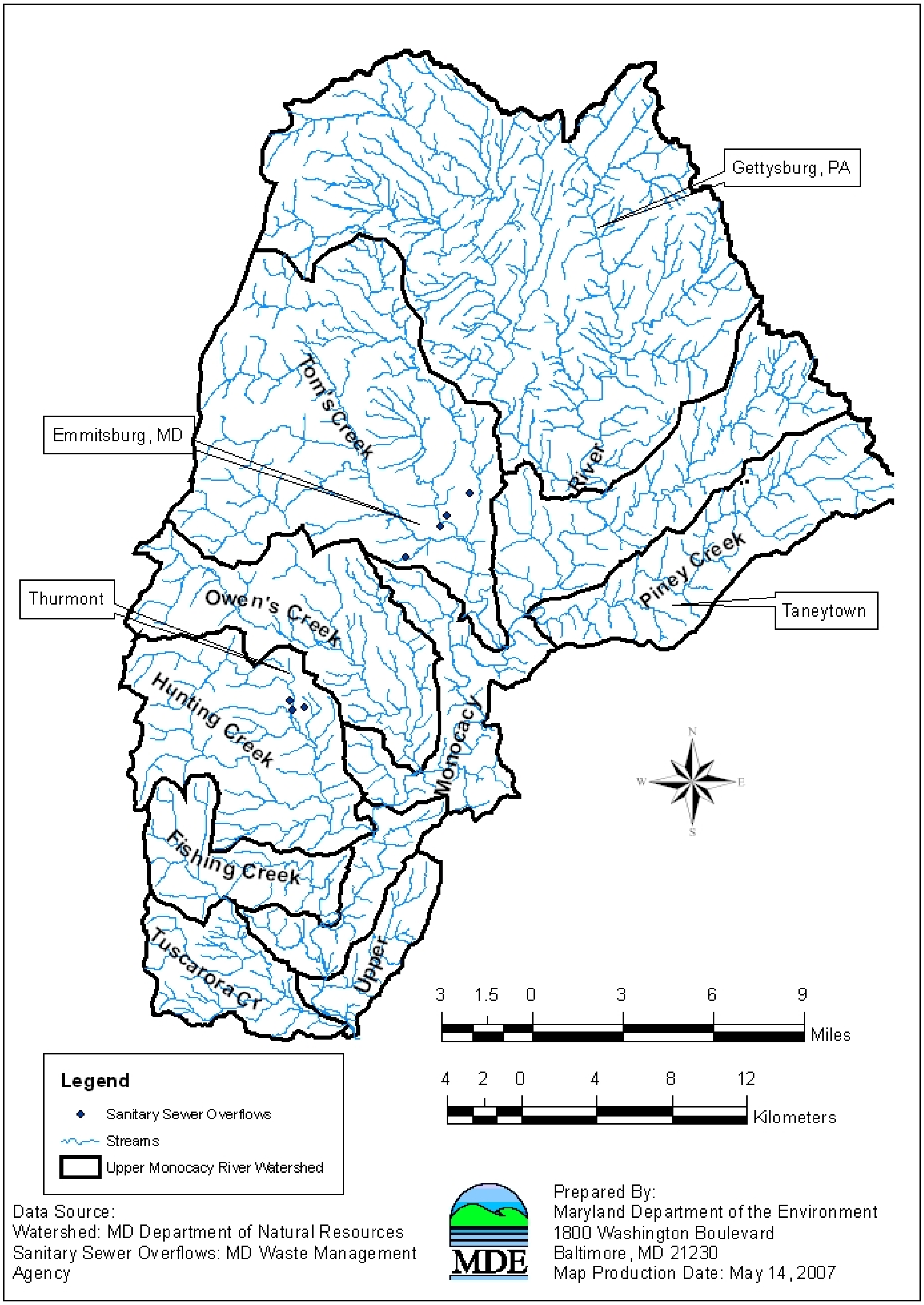

Figure 2.4.2: Sanitary Sewer Overflow Areas in the Upper Monocacy River Watershed

Municipal and Industrial Wastewater Treatment Plants (WWTPs)

Wastewater treatment plants are designed to treat wastewater before it is discharged to a stream or river. The goals of wastewater treatment are to protect the public health, protect aquatic life, and to prevent harmful substances from entering the environment.

Based on MDE's point source permitting information, there are ten active municipal and one industrial NPDES permitted point source facilities with permits regulating the discharge of fecal bacteria directly into the Upper Monocacy River watershed. Emmitsburg WWTP discharges into Toms Creek. Lewistown Elementary WWTP discharges into Fishing Creek. Taneytown WWTP discharges into Piney Creek. Thurmont WWTP discharges into Hunting Creek and White Rock WWTP discharges into Tuscarora Creek. Crestview WWTP discharges into Muddy Run. Shamrock Restaurant and Foxville Garden Naval WWTPs discharge into Owens Creek. Victor Cullen Center and St. Mary's College WWTPs discharge into Toms Creek. To this date, the Lewistown Mills WWTP Plant #1 and Plant #2 have not been built, but have future NPDES permits with maximum permitted flows of 0.005 millions of gallons per day (MGD) for each plant. The ten active WWTPs combined use an activated sludge process currently treating approximately 2.77 MGD. There is one industrial point source permitted to discharge fecal coliform into the Upper Monocacy River watershed, Shuff's Meat Market. Table 2.4.2 lists the active WWTPs in the Carroll County and Frederick County portion of the watershed. Figure 2.4.3 depicts the location of the WWTPs throughout the watershed.

Table 2.4.2: NPDES Permit Holders with Permits Regulating Fecal Bacteria Discharge in the Upper Monocacy River Watershed

Permittee	NPDES Permit No.	County / Subwatershed	Average Annual Flow (MGD)	Fecal Coliform Concentrations Annual AVG (MPN/100ml)	Fecal Coliform Load Per Day (Billion MPN/day)
Emmittsburg WWTP	MD0020257	Frederick / TOM0011	0.53	15.21	0.30
Foxville Naval WWTP	MD0025119	Frederick OWN0007	0.04	1.17	0.0016
Lewistown Mills WWTP Plant #1	Not available	Frederick / FIS0012	Future (0.005)	N/A	N/A
Lewistown Mills WWTP Plant#2	Not available	Frederick / FIS0012	Future (0.005)	N/A	N/A
Lewistown Elementary WWTP	MD0022900	Frederick / FIS0012	0.0061	22.33	0.01
Mt. St. Mary's WWTP	MD0023230	Frederick / TOM0011	0.1097	4.71	0.02
Shamrock Restaurant WWTP	MD0058050	Frederick / OWN0007	0.002	6.33	0.0005
Shuff's Meat Market WWTP	MD0050245	Frederick / HUN0009	0.001	5.86	0.0002
Taneytown WWTP	MD0020672	Carroll / PIN0000	0.88	44.13	1.47
Thurmont WWTP	MD0021121	Frederick / HUN0009	1.13	11.75	0.5
Victor Cullen Center WWTP	MD0023922	Frederick / TOM0011	0.02	1.04	0.0008
Crestview WWTP	MD0022683	Frederick / MON0269	0.0354	20	0.0268
White Rock WWTP	MD0025089	Frederick / TUS0007	0.017	20	0.013

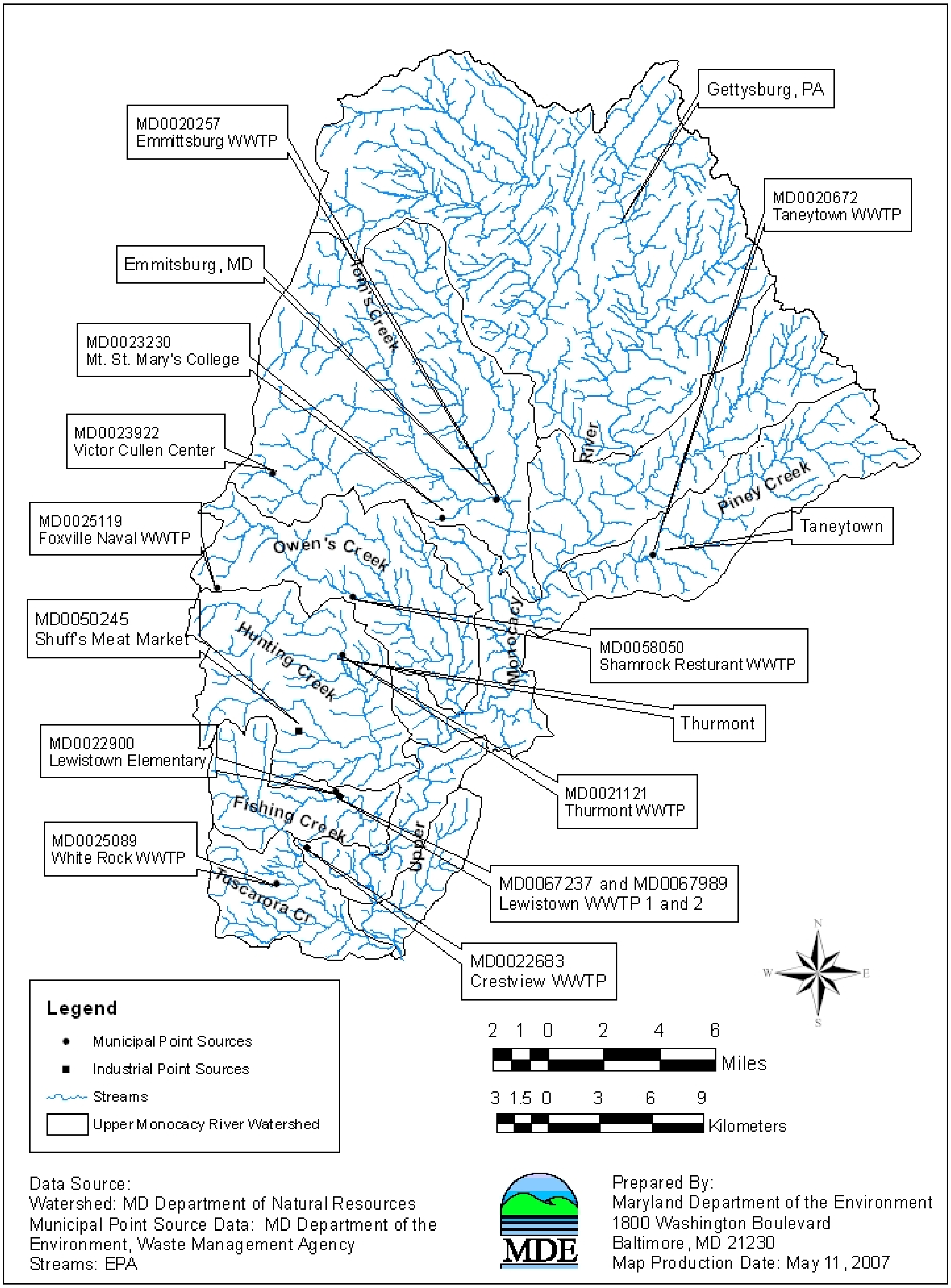

Figure 2.4.3: Permitted Point Sources Discharging Fecal Bacteria in Upper Monocacy River Watershed

Bacteria Source Tracking

Bacteria source tracking (BST) was used to identify the relative contributions from various sources of bacteria to in-stream water samples. BST monitoring was conducted at six stations throughout the Upper Monocacy River watershed, where 12 samples (one per month) were collected for a one-year duration. Sources are defined as domestic (pets and human associated animals), human (human waste), livestock (agricultural animals), and wildlife (mammals and waterfowl). To identify sources, samples are collected within the watershed from known fecal sources, and the patterns of antibiotic resistance of these known sources are compared to isolates of unknown bacteria from ambient water samples. Details of the BST methodology and data can be found in Appendix C.

An accurate representation of the expected average source at each station is estimated by using a stratified weighted mean of the identified sample results. The weighting factors are based on the $\log_{10}$ of the bacteria concentration and the percent of time that represents the high stream flow or low stream flow (See Appendix B). The procedure for calculating the stratified weighted mean of the sources per monitoring station is as follows:

1. Calculate the percentage of isolates per source per each sample date (S).
2. Calculate the weighted percentage (MS) of each source per flow strata (high/low). The weighting is based on the $\log_{10}$ bacteria concentration for the water sample.
3. The final weighted mean source percentage, for each source category, is based on the proportion of time in each flow duration zone (i.e., high flow=0.25, low flow=0.75).

The weighted mean for each source category is calculated using the following equations:

$$MS_k = \sum_{i=1}^{2} MS_{i,k} * W_i \qquad (4)$$

where

$$MS_{i,k} = \frac{\sum_{j=1}^{n_i} \log_{10}(C_{i,j}) * S_{i,j,k}}{\sum_{j=1}^{n_i} \log_{10}(C_{i,j})} \qquad (5)$$

where

$MS_{i,k}$ = Weighted mean proportion of isolates for source k in stratum i
MS_k = weighted mean proportion of isolates of source k
W_i= Proportion covered by stratum i
i = stratum
j = sample
k = Source category (1 = human, 2 = domestic, 3 = livestock, 4 = wildlife, 5 = unknown)
$C_{i,j}$ = Concentration for sample j in stratum i
$S_{i,j,k}$ = Proportion of isolates for sample j, of source k in stratum i
n_i = number of samples in stratum i

The complete distributions of the annual and seasonal periods source loads are listed in Tables 2.4.3 and 2.4.4. Details of the BST data and tables with the BST analysis results can be found in Appendix C. For the seasonal period, only one sample in each subwatershed fell in the high flow category; therefore, a distribution by flow stratum was not calculated due to an insufficient number of samples. In the seasonal analysis, a distribution of all samples was calculated and applied.

Table 2.4.3: Distribution of Fecal Bacteria Source Loads in the Upper Monocacy River Basin for the Average Annual Period

STATION	Flow Stratum	% Domestic Animals	% Human	% Livestock	% Wildlife	% Unknown
Upper Monocacy River MON0575[1]	High Flow	24.6	8.8	17.1	31.5	18.1
	Low Flow	26.8	1.1	11.5	14.6	37.2
	Weighted	26.2	11.4	18.6	17.5	26.2
Piney Creek PIN0000[1]	High Flow	19.5	18.0	28.0	13.4	21.0
	Low Flow	35.6	1.1	11.5	14.6	37.2
	Weighted	31.6	5.3	15.6	14.3	33.2
Toms Creek TOM0011[1]	High Flow	24.7	18.9	20.4	11.9	24.2
	Low Flow	15.8	9.8	31.4	8.2	34.8
	Weighted	18.0	12.0	28.6	9.0	32.1
Owens Creek OWN0007	High Flow	23.6	14.4	20.6	16.0	25.4
	Low Flow	37.9	8.9	8.7	16.1	28.5
	Weighted	34.3	10.3	11.6	16.0	27.7
Upper Monocacy River MON0355[1]	High Flow	27.0	17.4	27.2	10.8	17.7
	Low Flow	22.1	15.8	7.8	28.3	26.0
	Weighted	23.3	16.2	12.7	23.9	23.9
Hunting Creek HUN0009	High Flow	25.0	13.4	15.9	6.9	38.8
	Low Flow	30.1	11.4	17.2	18.7	22.7
	Weighted	28.8	11.9	16.8	15.7	26.7
Fishing Creek FIS0012	High Flow	19.0	17.2	13.2	15.0	35.5
	Low Flow	16.5	3.5	16.9	26.9	36.2
	Weighted	17.1	6.9	16.0	23.9	36.0
Upper Monocacy River MON0269	High Flow	32.1	10.9	19.8	10.1	26.9
	Low Flow	13.0	2.0	20.0	20.7	44.3
	Weighted	17.8	4.2	19.9	18.0	39.9
Tuscarora Creek TUS0007	High Flow	29.1	6.9	28.2	17.8	18.0
	Low Flow	11.5	2.7	35.1	15.7	35.0
	Weighted	15.8	3.7	33.3	16.3	30.8

[1]Subwatersheds partially located in Pennsylvania

Table 2.4.4: Distribution of Fecal Bacteria Source Loads in the Upper Monocacy River Basin for the Seasonal Period (May 1st – September 30th)

Tributary Station	Flow Stratum	% Domestic Animals	% Human	% Livestock	% Wildlife	% Unknown
Upper Monocacy River MON0575[1]	**Average**	37.8	11.6	17.3	9.1	24.3
Piney Creek PIN0000[1]	**Average**	35.4	3.7	9.9	10.8	40.3
Toms Creek TOM0011[1]	**Average**	21.7	6.5	26.2	5.9	39.6
Owens Creek OWN0007	**Average**	35.4	12.2	11.1	11.8	29.5
Upper Monocacy River MON0355[1]	**Average**	21.7	14.8	11.9	25.5	26.1
Hunting Creek HUN0009	**Average**	25.7	10.7	13.2	13.1	37.3
Fishing Creek FIS0012	**Average**	17.3	3.3	14.0	13.3	52.0
Upper Monocacy River MON0269	**Average**	15.2	1.8	15.4	16.0	51.6
Tuscarora Creek TUS0007	**Average**	11.5	2.7	35.1	15.7	35.0

[1]Subwatersheds partially located in Pennsylvania

3.0 TARGETED WATER QUALITY GOAL

The overall objective of the fecal bacteria TMDL set forth in this document is to establish the loading caps needed to assure attainment of water quality standards in the Upper Monocacy River watershed. These standards are described fully in Section 2.3, "Water Quality Impairment."

4.0 TOTAL MAXIMUM DAILY LOADS AND SOURCE ALLOCATION

4.1 Overview

This section provides an overview of the non-tidal fecal bacteria TMDL development, with a discussion of the many complexities involved in estimating bacteria concentrations, loads and sources. The second section presents the analysis for estimating a representative geometric mean fecal bacteria concentration and baseline loads. The third section describes the analysis framework and how the hydrological, water quality and BST data are linked together in the TMDL process. This analysis methodology is based on available monitoring data and is specific to a free-flowing stream system. The fourth section addresses the critical condition and seasonality. The fifth section presents the margin of safety. The sixth section discusses annual average TMDL loading caps and how maximum daily loads are estimated. The seventh section presents TMDL scenario descriptions. The eighth section presents the load allocations. Finally, in section nine, the TMDL equation is summarized.

To be most effective, the TMDL provides a basis for allocating loads among the known pollutant sources in the watershed so that appropriate control measures can be implemented and water quality standards achieved. By definition, the TMDL is the sum of the individual waste load allocations (WLAs) for point sources, and load allocations (LAs) for nonpoint sources, natural background sources and any upstream loads originating outside of, but flowing into, the MD 8-digit watershed assessment unit. A margin of safety (MOS) is also included and accounts for the uncertainty in the analytical procedures used for water quality modeling, as well as the limits in scientific and technical understanding of water quality in natural systems. Although this formulation suggests that the TMDL be expressed as a load, the Code of Federal Regulations (40 CFR 130.2(i)) states that the TMDL can be expressed in terms of "mass per time, toxicity or other appropriate measure."

For many reasons, bacteria are difficult to simulate in water quality models. They reproduce and die off in a non-linear fashion as a function of many environmental factors, including temperature, pH, turbidity (UV light penetration) and settling. They occur in concentrations that vary widely (i.e., over orders of magnitude) and an accurate estimation of source inputs is difficult to develop. Finally, limited data are available to characterize the effectiveness of any program or practice at reducing bacteria loads (Schueler 1999).

Bacteria concentrations, determined through laboratory analysis of in-stream water samples for bacteria indicators (e.g., enterococci), are expressed in either colony forming units (CFU) or most probable number (MPN) of colonies. The first method (US EPA 1985) is a direct estimate of the bacteria colonies (Method 1600), and the second is a statistical estimate of the number of colonies (ONPG MUG Standard Method 9223B, AOAC 991.15). Sample results indicate the extreme variability in the total bacteria counts (see Appendix A). The distribution of the sample results tends to be lognormal, with a strong positive skew of the data. Estimating loads of constituents that vary by orders of magnitude can introduce much uncertainty and result in large confidence intervals around the final results.

Estimating bacteria sources can also be problematic due to the many assumptions required and to limited available data. Lack of specific numeric and spatial location data for several source categories, from failing septic systems to domestic animals, livestock, and wildlife populations, can create many potential uncertainties in traditional water quality modeling. For this reason, MDE applies an analytical method combined with the bacteria source tracking described above for the calculation of this TMDL.

4.2 Analysis Framework

This TMDL analysis uses flow duration curves to identify flow intervals that are used as indicator of hydrological conditions (i.e., annual average and critical conditions). This analytical method, combined with water quality monitoring data and BST, provides reasonable results (Cleland 2003), a better description of water quality than traditional water quality modeling, and also meets TMDL requirements.

In brief, baseline loads are estimated first for each subwatershed by using bacteria monitoring data and long-term flow data. These baseline loads are divided into four bacteria source categories, using the results of BST analysis. Next, the percent reduction required to meet the water quality criterion in each subwatershed is estimated from the observed bacteria concentrations after determining the critical condition and accounting for seasonality. Critical condition and seasonality are determined by assessing annual and seasonal hydrological conditions for high flow and low flow periods. Finally, TMDLs for each subwatershed are estimated by applying these percent reductions.

Figure 4.2.1 illustrates how the hydrological (flow duration curve), water quality and BST data are linked together for the TMDL development.

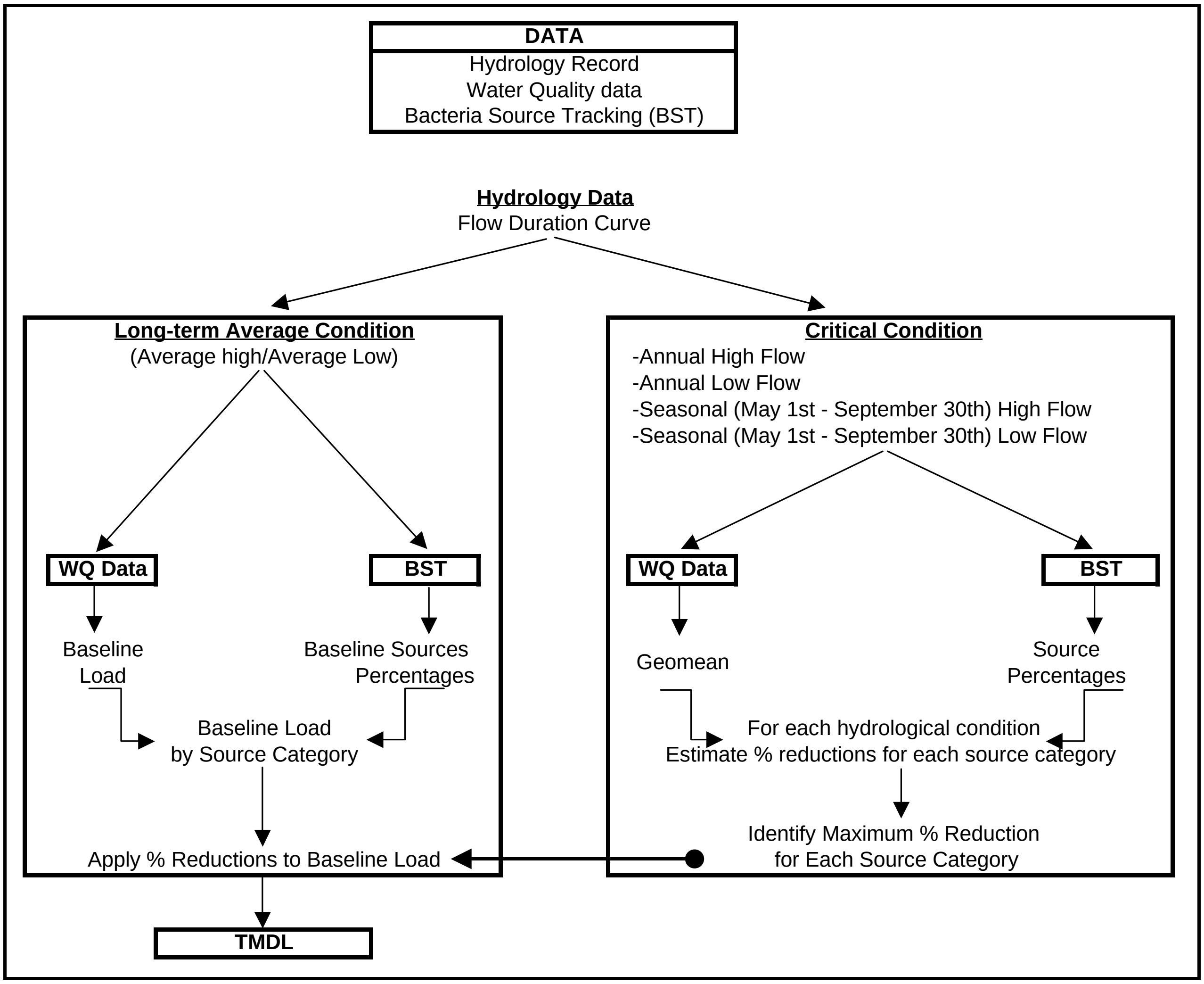

Figure 4.2.1: Diagram of Non-tidal Bacteria TMDL Analysis Framework

4.3 Estimating Baseline Loads

Baseline loads are estimated for all subwatersheds of the Upper Monocacy River, including, for computational purposes, those partially located in PA. Baseline loads estimated in this TMDL analysis are reported in long-term average annual loads, using bacteria monitoring data and long-term flow data.

To estimate baseline loads for each subwatershed of the Upper Monocacy River, geometric mean concentrations, bias correction factors and daily average flows for each stratum are first estimated.

The geometric mean concentration is calculated from the log transformation of the raw data. Statistical theory tells us that when back-transformed values are used to calculate average daily loads or total annual loads, the loads will be biased low (Richards 1998). To avoid this bias, a factor should be added to the log-concentration before it is back-transformed. There are several methods of determining this bias correction factor, ranging from parametric estimates resulting from the theory of the log-normal distribution to non-parametric estimates using a bias correction factor [Ferguson 1986; Cohn et al. 1989; Duan 1983]. There is much literature on the applicability and results from these various methods with a summary provided in Richards (1998). Each has advantages and conditions of applicability. A non-parametric estimate of the bias correction factor (Duan 1983) was used in this TMDL analysis.

With calculated geometric means and arithmetic means for each flow stratum, the bias correction factors are estimated as follows:

$$F_{1i} = A_i/C_i \qquad (6)$$

where

F_{1i} = Bias correction factor for stratum *i*
A_i = Long term annual arithmetic mean for stratum *i*
C_i = Long term annual geometric mean for stratum *i*

Daily average flows are estimated for each flow stratum using the watershed area ratio approach, since nearby long-term monitoring data are available.

The loads for each stratum are estimated as follows:

$$L_i = Q_i * C_i * F_{1i} * F_2 \qquad (7)$$

where

L_i = Daily average load (Billion MPN/day) at monitoring station for stratum *i*
Q_i = Daily average flow (cfs) for stratum *i*
C_i = Geometric mean for stratum *i*
F_{1i} = Bias correction factor for stratum *i*
F_2 = Unit conversion factor (0.0245)

Finally, for each subwatershed, the baseline load is estimated as follows:

$$L = \sum_{i=1}^{2} L_i * W_i \qquad (8)$$

L = Daily average load at station (MPN/day)
W_i= Proportion of stratum *i*

In the Upper Monocacy River watershed, a weighting factor of 0.25 for high flow and 0.75 for low/mid flows were used to estimate the annual baseline load expressed as Billion MPN *E. coli*/day.

Estimating Subwatershed Loads

Subwatersheds with more than one monitoring station were subdivided into unique watershed segments, thus allowing individual load and reduction targets to be determined for each. In the mainstem of the Upper Monocacy River watershed, two stations, MON0355 and MON0269, have upstream monitoring stations: MON0575 and MON0355, respectively (see Figure 2.2.1). The watershed segments between these stations are identified as subwatersheds by adding the extension "sub" to their downstream station names (MON0355sub and MON0269sub). Thus, there are a total of nine subwatersheds defined in this analysis.

To estimate subwatershed (i.e., MON0355sub and MON0269sub) loads, the baseline loads from the upstream watersheds, estimated from bacteria monitoring data and flow data, are multiplied by a transport factor derived from a first order decay rate and the bacteria travel time from the upstream station to the downstream station. The decay rate for *E. coli* used in the analysis was obtained from the study "Pathogen Decay in Urban Waters" by Easton et al. (2001), and was estimated by linear regression of counts of microorganisms versus time (die-off plots). The traveling time is estimated using the computer program XSECT. This program calculates flows and corresponding travel time for a stream channel using the hydraulic characteristics of the stream segment (stream length, stream slope, channel width, channel depth, floodplain slope, and Manning's number). The estimated transported loads were then subtracted from the downstream cumulative load to estimate the adjacent subwatershed load.

The general equation for the flow mass balance is:

$$\sum Q_{us} + Q_{sub} = Q_{ds} \qquad (9)$$

where

Q_{us} = Upstream flow (cfs)
Q_{sub} = Subwatershed flow (cfs)
Q_{ds} = Downstream flow (cfs)

and the general equations for bacteria loading mass balance:

$$\sum (e^{-kt} Q_{us} C_{us}) + Q_{sub} C_{sub} = Q_{ds} C_{ds} \qquad (10)$$

where

C_{us} = Upstream bacteria concentration (MPN/100ml)
k = Bacteria (*E. coli*) decay coefficient (1/day) = 0.762 day^{-1}
t = travel time from upstream watershed to outlet (days)
C_{sub} = Subwatershed bacteria concentration (MPN/100ml)
C_{ds} = Downstream bacteria concentration (MPN/100ml)

The concentrations in the subwatersheds were estimated by considering both high flow concentrations and low flow concentrations in the upstream watersheds. If the total load and average flow were used to estimate the geometric mean concentration, this estimated concentration would be biased by a correlation with flow and concentration. For example, in two strata, the steady-state geometric mean is estimated as follows:

$$L = Q_{high} W_{high} C_{high} + Q_{low} W_{low} C_{low} \quad (11)$$

where

L = Average load (MPN/day)
Q_i = Average flow for stratum *i*
W_i = Proportion of stratum *i*
C_i = Concentration for stratum *i*
n_i = number of samples in stratum *i*

The load in equation (11) is based on two concentrations. Therefore, when using the mass balance approach and the total load, it results in two unknowns, C_{high} and C_{low}, with one equation. Thus a relationship between C_{high} and C_{low}, must be estimated to solve for the concentration in both strata. This relationship is estimated using the average of the ratios estimated from the monitoring data in the upstream watersheds. Using this relationship, the following two equations result:

$$C_{low} = \frac{L}{Q_{high} R * W_{high} + Q_{low} W_{low}} \quad (12)$$

where

$$R = \frac{C_{high}}{C_{low}} \quad (13)$$

and the final geometric mean concentration is estimated as follows:

$$GM = 10^{W_{high} \log_{10}(C_{high}) + W_{low} \log_{10}(C_{low})} \quad (14)$$

Finally, to estimate the load from subwatershed MON0355sub, the transported loads, estimated as explained above, from stations MON0575, PIN0000, TOM0011 and OWN0007 and from stations BPC006 and LPC0032 located in the Double Pipe Creek watershed, are subtracted from the load measured at station MON0355. The difference is assigned to subwatershed MON0355sub. To estimate the load from subwatershed MON0269sub, the transported loads from stations MON0355, HUN0009 and FIS0012 are subtracted from the load measured at station MON0269. The difference is assigned to subwatershed MON0269sub.

Source estimates from the BST analysis are completed for each station and are based on the contribution from the upstream watershed. Given the uncertainty of in-stream bacteria processes and the complexity involved in back-calculating an accurate source transport factor, the sources for MON0355sub and MON0269sub were assigned from the analysis for MON0355 and MON0269, respectively.

Results of the baseline load calculations, including subwatersheds partially located in PA, are presented in Table 4.3.1.

Table 4.3.1: Baseline Loads Calculations

Sub-watershed	Area (sq. miles)	High Flow		Low Flow		Baseline Load (Billion MPN/year)	Weighted Geometric Mean Conc. MPN/100ml
		Q (cfs)	*E. coli* Concentration (MPN/100ml)	(cfs)	*E. coli* Concentration (MPN/100ml)		
MON0575[1]	143.3	626.1	178.8	51.6	90.0	475,859	107
PIN0000[1]	34.8	152.0	229.9	12.5	165.0	461,616	179
TOM0011[1]	88.8	387.8	148.6	31.9	310.7	944,099	258
OWN0007	39.6	173.0	209.4	14.3	203.0	137,961	205
MON0355sub[1]	68.9	300.9	549.9	24.8	276.9	959,283	329
HUN0009	41.7	182.2	125.2	15.0	227.6	127,841	196
FIS0012	18.4	80.4	135.4	6.6	198.1	59,819	180
MON0269sub	13.5	59.0	657.9	4.9	962.1	239,291	875
TUS0007	17.8	77.8	126.5	6.4	368.4	53,446	282

[1]Subwatersheds partially located in Pennsylvania

Baseline loads for subwatersheds located in both MD and PA were estimated using the ratios of the areas of the MD and PA portions to the total area of the subwatershed. The total baseline load for all subwatersheds or portions thereof located in MD is estimated as 1,985,054 billion MPN *E.coli*/year. The total baseline load for the portions of subwatersheds located in PA is 1,474,162 billion MPN E. coli/year.

4.4 Critical Condition and Seasonality

Federal regulations (40 CFR 130.7(c)(1)) require TMDLs to take into account critical conditions for stream flow, loading, and water quality parameters. The intent of this requirement is to ensure that the water quality of the waterbody is protected during times when it is most vulnerable.

For this TMDL the critical condition is determined by assessing annual and seasonal hydrological conditions for high flow and low flow periods. Seasonality is captured by assessing the time period when water contact recreation is expected (May 1st - September 30th). For this

TMDL analysis, the average hydrological condition over a 15-year period has been estimated as approximately 25% high flow and 75% low flow as defined in Appendix B. Using the definition of a high flow condition as occurring when the daily flow duration interval is less than 25% and a low flow condition as occurring when the daily flow duration interval is greater than 25%, critical hydrological condition can be estimated by the percent of high or low flows during a specific period.

Using long term flow data from USGS station 01639000, critical condition and seasonality has been determined by assessing various hydrological conditions to account for seasonal and annual averaging periods. The four conditions listed in Table 4.4.1 were used to account for the critical condition.

Table 4.4.1: Hydrological Conditions Used to Account for Critical Condition and Seasonality

Hydrological Condition		Averaging Period	Water Quality Data Used	Subwatershed	Fraction High Flow	Fraction Low Flow	Period
Annual	Average	365 days	All	All	0.25	0.75	Long Term Average
Annual	High Flow	365 days	All	All	0.48	0.52	Nov 1st,2002- Oct. 31st, 2003
Annual	Low Flow	365 days	All	All	0.03	0.97	Nov 1st,2002- Oct. 31st, 2003
Seasonal	Average	May 1st – Sept 30th	May 1st – Sept 30th	All	N/A	N/A	Long Term Average For May-Sept Period

The critical condition requirement is met by determining the maximum reduction per bacteria source that satisfies all hydrological conditions and meets the water quality standard, thereby minimizing the risk to water contact recreation. It is assumed that the reduction applied to a bacteria source category will be constant through all conditions.

The bacteria monitoring data for all stations located in the Upper Monocacy River watershed cover a sufficient temporal span (at least one year) to estimate annual conditions. However, only one bacteria sample fell within the high flow condition of the seasonal period. Geometric means could not be calculated for the high flow condition for the critical period analysis; therefore, average geometric mean and average flow were used in the critical analysis calculations.

Table 4.4.2 shows the reductions of fecal bacteria required in each subwatershed of the Upper Monocacy River to meet water quality standards for designated uses in the MD 8-digit basin. For computational purposes, the calculations include those subwatersheds partially located in PA.

Table 4.4.2: Required Reductions of Fecal Bacteria to Meet Water Quality Standards

Subwatershed	Hydrological Condition		Domestic Animals %	Human %	Livestock %	Wildlife %
MON0355[1]	Annual	Average	0.0%	0.0%	0.0%	0.0%
		High Flow	0.0%	30.6%	0.0%	0.0%
		Low Flow	0.0%	0.0%	0.0%	0.0%
	Seasonal	Average	6.0%	73.8%	43.5%	0.0%
	Maximum Source Reduction		6.0%	73.8%	43.5%	0%
PIN0000[1]	Annual	Average	32.1%	74.1%	55.1%	0.0%
		High Flow	33.1%	94.8%	49.8%	0.0%
		Low Flow	28.2%	68.9%	57.8%	0.0%
	Seasonal	Average	98.0%	94.2%	1.8%	0.0%
	Maximum Source Reduction		98%	94.8%	57.8%	0%
TOM0011[1]	Annual	Average	61.2%	85.9%	52.6%	0.0%
		High Flow	49.9%	97.2%	31.1%	0.0%
		Low Flow	68.7%	97.4%	60.7%	0.0%
	Seasonal	Average	95.3%	98.0%	98.0%	0.0%
	Maximum Source Reduction		95.3%	98%	98%	0%
OWN0007	Annual	Average	40.2%	84.7%	63.3%	1.0%
		High Flow	35.0%	96.3%	59.1%	1.0%
		Low Flow	39.0%	95.3%	66.8%	1.0%
	Seasonal	Average	82.4%	98.0%	77.1%	1.0%
	Maximum Source Reduction		82.4%	98%	77.1%	1.0%
MON0355sub[1]	Annual	Average	85.6%	98.0%	80.6%	11.1%
		High Flow	96.7%	98.0%	83.7%	0.0%
		Low Flow	92.3%	98.0%	81.5%	0.0%
	Seasonal	Average	46.3%	97.2%	64.8%	0.0%
	Maximum Source Reduction		97.9%	98%	98%	0%
HUN0009	Annual	Average	0.0%	0.0%	0.0%	0.0%
		High Flow	5.2%	91.0%	38.1%	0.0%
		Low Flow	0.0%	0.0%	0.0%	0.0%
	Seasonal	Average	98.0%	91.0%	98.0%	3.5%
	Maximum Source Reduction		98%	91%	98%	3.5%

Subwatershed	Hydrological Condition		Domestic Animals %	Human %	Livestock %	Wildlife %
FIS0012	Annual	Average	46.4%	83.4%	48.3%	0.0%
		High Flow	9.7%	98.0%	39.7%	0.0%
		Low Flow	27.0%	98.0%	98.0%	0.0%
	Seasonal	Average	98.0%	98.0%	98.0%	28.0%
	Maximum Source Reduction		98%	98%	98%	28%
MON0269sub	Annual	Average	98.0%	98.0%	98.0%	74.8%
		High Flow	98.0%	98.0%	98.0%	79.1%
		Low Flow	98.0%	98.0%	98.0%	72.4%
	Seasonal	Average	98.0%	98.0%	98.0%	93.8%
	Maximum Source Reduction		98%	98%	98%	93.8%
TUS0007	Annual	Average	98.0%	97.0%	98.0%	67.4%
		High Flow	98.0%	97.0%	98.0%	77.0%
		Low Flow	98.0%	97.0%	98.0%	59.6%
	Seasonal	Average	98.0%	97.0%	98.0%	92.4%
	Maximum Source Reduction		98%	97%	98%	92.4%

[1]Subwatersheds partially located in Pennsylvania

4.5 Margin of Safety

A margin of safety (MOS) is required as part of this TMDL in recognition of the many uncertainties in the understanding and simulation of bacteriological water quality in natural systems and in statistical estimates of indicators. As mentioned in Section 4.1, it is difficult to estimate stream loadings for fecal bacteria due to the variation in loadings across sample locations and time. Load estimation methods should be both precise and accurate to obtain the true estimate of the mean load. Refined precision in the load estimation is due to using a stratified approach along the flow duration intervals, thus reducing the variation in the estimates. Moreover, Richards (1998) reports that averaging methods are generally biased, and the bias increases as the size of the averaging window increases. Finally, accuracy in the load estimation is based on minimal bias in the final result when compared to the true value.

Based on EPA guidance, the MOS can be achieved through two approaches (EPA 1991). One approach is to reserve a portion of the loading capacity as a separate term in the TMDL (i.e., TMDL = LA + WLA + MOS). The second approach is to incorporate the MOS as conservative assumptions used in the TMDL analysis. For this TMDL, the second approach was used by estimating the loading capacity of the stream based on a reduced (more stringent) water quality criterion concentration. The *E. coli* water quality criterion concentration was reduced by 5%, from 126 *E. coli* MPN/100ml to 119.7 *E. coli* MPN/100ml.

4.6 Scenario Descriptions

Source Distribution

The final bacteria source distribution and corresponding baseline loads are derived from the source proportions listed in Table 2.4.3. For the purposes of the TMDL analysis and allocations, the percentage of sources identified as "unknown" was removed and redistributed proportionally among the known sources to total 100%. The source distribution and baseline loads used in the TMDL scenarios are presented in Table 4.6.1. As stated in Section 4.3, the source distributions for subwatersheds MON0355sub and MON0269sub, were based on the sources identified at stations MON0355 and MON0269, respectively.

Table 4.6.1: Bacteria Source Distributions and Corresponding Baseline Loads Used in the Annual Average TMDL Analysis

Subwatershed	Domestic		Human		Livestock		Wildlife		Total Billion *E. coli* MPN/year
	%	Load Billion *E. coli* MPN/year	%	Load Billion *E. coli* MPN/year	%	Load Billion *E. coli* MPN/year	%	Load Billion *E. coli* MPN/year	
MON0575[1]	35.5%	168,976	15.5%	73,564	25.2%	119,981	23.8%	113,338	475,859
PIN0000[1]	47.2%	217,991	7.9%	36,598	23.4%	108,010	21.5%	99,017	461,616
TOM0011[1]	26.6%	251,309	17.8%	167,742	42.2%	398,470	13.4%	126,578	944,099
OWN0007	47.5%	65,493	14.2%	19,598	16.1%	22,240	22.2%	30,631	137,961
MON0355sub[1]	30.6%	294,003	21.3%	203,867	16.6%	159,622	31.5%	301,790	959,283
HUN0009	39.3%	50,269	16.2%	20,749	23%	29,381	21.5%	27,442	127,841
FIS0012	26.7%	15,995	10.9%	6,502	25%	14,973	37.4%	22,349	59,819
MON0269sub	29.6%	70,848	7.0%	16,765	33.3%	79,732	30.1%	71,945	239,291
TUS0007	22.9%	12,243	5.4%	2,896	48.2%	25,751	23.5%	12,556	53,446

[1]Subwatersheds partially located in Pennsylvania

First Scenario: Fecal Bacteria Practicable Reduction Targets

The maximum practicable reduction (MPR) for each of the four source categories is listed in Table 4.6.2. These values are based on review of the available literature and best professional judgment. It is assumed that human sources would potentially have the highest risk of causing gastrointestinal illness and therefore should have the highest reduction. If a domestic WWTP is located in the upstream watershed, this is considered in the MPR so as to not violate the permitted loads. The domestic animal category includes sources from pets (e.g., dogs) and the MPR is based on an estimated success of education and outreach programs.

Table 4.6.2: Maximum Practicable Reduction Targets

Max Practicable Reduction per Source	**Human**	**Domestic**	**Livestock**	**Wildlife**
	95%	75%	75%	0%
Rationale	(a) Direct source inputs. (b) Human pathogens more prevalent in humans than animals. (c) Enteric viral diseases spread from human to human.[1]	Target goal reflects uncertainty in effectiveness of urban BMPs[2] and is also based on best professional judgment	Target goal based on sediment reductions from BMPs[3] and best professional judgment	No programmatic approaches for wildlife reduction to meet water quality standards. Waters contaminated by wild animal wastes offer a public health risk that is orders of magnitude less than that associated with human waste.[4]

[1]Health Effects Criteria for Fresh Recreational Waters. EPA-600/1-84-004. U.S. Environmental Protection Agency, Washington, DC. EPA. 1984.
[2]Preliminary Data Summary of Urban Storm Water Best Management Practices. EPA-821-R-99-012. U.S. Environmental Protection Agency, Washington, DC. EPA. 1999.
[3]Agricultural BMP Descriptions as Defined for The Chesapeake Bay Program Watershed Model. Nutrient Subcommittee Agricultural Nutrient Reduction Workshop. EPA. 2004.
[4]Environmental Indicators and Shellfish Safety. 1994. Edited by Cameron, R., Mackeney and Merle D. Pierson, Chapman & Hall.

As previously stated, these maximum practicable reduction targets are based on the available literature and best professional judgment. There is much uncertainty with estimated reductions from best management practices (BMP). The BMP efficiency for bacteria reduction ranged from –6% to +99% based on a total of 10 observations (US EPA 1999). The MPR to agricultural lands was based on sediment reductions identified by EPA (US EPA 2004).

The practicable reduction scenario was developed based on an optimization analysis whereby a subjective estimate of risk was minimized and constraints were set on maximum reduction and allowable background conditions. Risk was defined on a scale of one to five, where it was assumed that human sources had the highest risk (5), domestic animals and livestock next (3), and wildlife the lowest (1) (See Table 4.6.2). The model was defined as follows:

$$\text{Risk Score} = \text{Min} \sum_{i=1}^{4} P_j * W_j \qquad (15)$$

Where

$$P_j = \frac{(1-R_i) * Pb_j}{1-TR} \qquad (16)$$

and

$$TR = \frac{C - C_{cr}}{C} \qquad (17)$$

Therefore the risk score can be represented as:

$$Risk\ Score = Min \sum_{i=1}^{4} \left[\frac{(1-R_j) * Pb_j}{(1-\frac{C-Ccr}{C})} * W_j \right] \qquad (18)$$

where
i = hydrological condition
j = bacteria source category =human, domestic animal, livestock and wildlife
P_j = % of each source category (human, domestic animals, livestock and wildlife) in final allocation
W_j = Weigh of risk per source category = 5, 3 or 1
R_j= percent reduction applied by source category (human, domestic animals, livestock and wildlife) for the specified hydrological condition (variable)
Pb_j = original (baseline) percent distribution by source category (variable)
TR = total reduction (constant within each hydrological condition) = Target reduction
C = In-stream concentration
Ccr = Water quality criterion

The model is subject to the following constraints:

C = Ccr
$0 <= R_{human} <= 95\%$
$0 <= R_{pets} <= 75\%$
$0 <= R_{livestock} <= 75\%$
$R_{wildlife} = 0$
$P_j >= 1\%$

In eight out of nine subwatersheds, three of which are partially located in PA, the constraints of this scenario could not be satisfied, indicating there was not a practicable solution. A summary of the first scenario analysis results is presented in Table 4.6.3.

Table 4.6.3: Practicable Reduction Scenario Results

Subwatershed	Applied Reductions				Achievable ?
	Domestic %	Human %	Livestock %	Wildlife %	
MON0575[1]	75%	95%	75%	0%	Yes
PIN0000[1]	75%	95%	75%	0%	No
TOM0011[1]	75%	95%	75%	0%	No
OWN0007	75%	95%	75%	0%	No
MON0355sub[1]	75%	95%	75%	0%	No
HUN0009	75%	95%	75%	0%	No
FIS0012	75%	95%	75%	0%	No
MON0269sub	75%	95%	75%	0%	No
TUS0007	75%	95%	75%	0%	No

[1]Subwatersheds partially located in Pennsylvania

Second Scenario: Fecal Bacteria Reductions Higher than Maximum Practicable Reductions

The TMDL must specify load allocations that will meet the water quality standards. In the practicable reduction targets scenario, only one of the Upper Monocacy subwatersheds (located mostly in PA) could meet water quality standards based on MPRs.

To further develop the TMDL, a second scenario was analyzed in which the constraints on the MPRs were relaxed in the subwatersheds where water quality attainment was not achievable with MPRs. In these subwatersheds, the maximum allowable reduction was increased to 98% for all sources, including wildlife. A similar optimization procedure was used to minimize risk. Again, the objective is to minimize the sum of the risk for all conditions while meeting the scenario reduction constraints. The model was defined in the same manner as shown in the practicable reduction scenario but subject to the following constraints:

$C = Ccr$
$0 <= R_i <= 98\%$
$P_j >= 1\%$

The summary of the analysis for all subwatersheds, including those partially located in PA, is presented in Table 4.6.4.

Table 4.6.4: TMDL Scenario Results: Percent Reductions Based on Optimization Model Allowing Up to 98% Reduction

Station	Domestic %	Human %	Livestock %	Wildlife %	Target Reduction %
MON0575[1]	6.0%	73.8%	43.5%	0.0%	24.5%
PIN0000[1]	98.0%	94.8%	57.8%	0.0%	67.3%
TOM0011[1]	95.3%	98.0%	98.0%	0.0%	84.1%
OWN0007	82.4%	98.0%	77.1%	1.0%	65.7%
MON0355sub[1]	96.7%	98.0%	83.7%	11.1%	67.9%
HUN0009	98.0%	91.0%	98.0%	3.5%	76.6%
FIS0012	98.0%	98.0%	98.0%	28.0%	71.9%
MON0269sub	98.0%	98.0%	98.0%	93.8%	96.7%
TUS0007	98.0%	97.0%	98.0%	92.4%	96.6%

[1]Subwatersheds partially located in Pennsylvania

4.7 TMDL Loading Caps

The TMDL loading cap is an estimate of the assimilative capacity of the monitored watershed. Estimation of the TMDL requires knowledge of how bacteria concentrations vary with flow rate or the flow duration interval. This relationship between concentration and flow is established using the strata defined by the flow duration curve.

The TMDL loading caps are provided in billion MPN *E. coli*/day. These loading caps are for the nine subwatersheds located upstream of their respective monitoring stations: MON0575, PIN0000, TOM011, OWN0007, MON0355sub, HUN0009, FIS0012, MON0269sub, and TUS0007. Loading caps for subwatersheds of the Upper Monocacy River partially located in PA are included in the TMDL scenario. A TMDL summary for the entire Upper Monocacy watershed will include an upstream load allocation for the portion of the watershed located in PA to indicate estimated loads necessary to meet MD water quality standards in the MD 8-digit assessment unit for the Upper Monocacy River basin.

Annual Average TMDL Loading Caps

As explained in the sections above, the annual average TMDL loading caps are estimated by first determining the baseline or current condition loads for each subwatershed and the associated geometric mean from the available monitoring data. This annual average baseline load is estimated using the geometric mean concentration and the long-term annual average daily flow for each flow stratum. The loads from these two strata are then weighted to represent average conditions (see Table 4.3.1), based on the proportion of each stratum, to estimate the total long-term loading rate.

Next, the percent reduction required to meet the water quality criterion is estimated from the observed bacteria concentrations accounting for the critical conditions (See Section 4.4). A reduction in concentration is proportional to a reduction in load; thus the TMDL is equal to the current baseline load multiplied by one minus the required reduction. This reduction, estimated as explained in Section 4.4, represents the maximum reduction per source that satisfies all hydrological conditions in each subwatershed, and that is required to meet water quality standards.

$$\text{TMDL Loading Cap} = L_b * (1 - R) \qquad (19)$$

where

L_b = Current or baseline load estimated from monitoring data
R = Reduction required from baseline to meet water quality criterion.

The annual average bacteria TMDL loading caps for the subwatersheds, including those partially located in PA, are shown in Tables 4.7.1 and 4.7.2.

Table 4.7.1: Upper Monocacy River Subwatersheds Annual Average TMDL Loading Caps

Subwatershed ID	**Baseline Load *E. coli* (Billion MPN/year)**	**Long Term Average TMDL Loading Caps *E. coli* (Billion MPN/year)**	**% Target Reduction**
MON0575[1]	475,859	359,211	24.5%
PIN0000[1]	461,616	150,924	67.3%
TOM0011[1]	944,099	149,690	84.1%
OWN0007	137,961	47,338	65.7%
MON0355sub[1]	959,283	308,107	67.9%
HUN0009	127,841	29,942	76.6%
FIS0012	59,819	16,833	71.9%
MON0269sub	239,291	7,834	96.7%
TUS0007	53,446	1,802	96.6%
Total	3,459,216	1,071,682	69.0%

[1]Subwatersheds partially located in Pennsylvania

Table 4.7.2: TMDL Loading Caps by Source Category - Annual Average Conditions

Subwatershed	Domestic		Human		Livestock		Wildlife		Total Billion *E. coli* MPN/year
	%	Load Billion *E. coli* MPN/year	%	Load Billion *E. coli* MPN/year	%	Load Billion *E. coli* MPN/year	%	Load Billion *E. coli* MPN/year	
MON0575[1]	44.2%	158,797	5.4%	19,271	18.9%	67,806	31.6%	113,338	359,211
PIN0000[1]	2.9%	4,360	1.3%	1,914	30.2%	45,633	65.6%	99,017	150,924
TOM0011[1]	7.9%	11,788	2.2%	3,355	5.3%	7,969	84.6%	126,578	149,690
OWN0007	24.4%	11,540	0.8%	392	10.7%	5,083	64.1%	30,324	47,338
MON0355sub[1]	3.1%	9,635	1.3%	4,077	8.4%	25,977	87.1%	268,418	308,107
HUN0009	3.4%	1,005	6.2%	1,867	2.0%	588	88.4%	26,482	29,942
FIS0012	1.9%	320	0.8%	130	1.8%	299	95.5%	16,083	16,833
MON0269sub	18.1%	1,417	4.3%	335	20.4%	1,595	57.3%	4,487	7,834
TUS0007	13.6%	245	4.8%	87	28.6%	515	53.0%	955	1,802

[1]Subwatersheds partially located in Pennsylvania

Maximum Daily Loads

Selection of an appropriate method for translating a TMDL based on a longer time period into one using a daily time period requires decisions regarding 1) the level of resolution, and 2) the level of protection. The level of resolution pertains to the amount of detail used in specifying the maximum daily load. The level of protection represents how often the maximum daily load (MDL) is expected to be exceeded. Draft EPA/TetraTech guidance on daily loads (Limno-Tech 2007) provides three categories of options for both level of resolution and level of protection, and discusses these categories in detail.

For the Upper Monocacy River MDLs, a “representative daily load” option was selected as the level of resolution, and a value “that will be exceeded with a pre-defined probability” was selected as the level of protection. In these options, the MDLs are two single daily loads that correspond to the two flow strata, with an upper bound percentile that accounts for the variability of daily loads. The upper bound percentile and the MDLs were estimated following EPA’s “*Technical Support Document for Water Quality-Based Toxics Control*” (1991 TSD) (EPA 1991); and “*Approaches For Developing a Daily Load Expression for TMDLs Computed for Longer Term Averages*” (EPA 2006).

There are three steps to the overall process of estimating these MDLs. First, all the data available from each monitoring station are examined together by stratum and the percentile rank of the highest observed concentration (for each stratum at each station) is computed. The highest computed percentile rank is the upper bound percentile to be used in estimating the MDLs.

Secondly, the long-term annual average TMDL (see Table 4.7.1) concentrations are estimated for both high-flow and low-flow strata. This is conducted for each station using a statistical methodology (the "Statistical Theory of Rollback," or "STR," described more fully in Appendix D).

Third, based on the estimated long-term average (LTA) TMDL concentrations, the MDL for each flow stratum at each station is estimated using the upper boundary percentile computed in the first step above. Finally, MDLs are computed from these MDL concentrations and their corresponding flows.

Results of the fecal bacteria MDL analysis for the Upper Monocacy River subwatersheds, including, for computational purposes, those partially located in PA, are shown in Table 4.7.3.

Table 4.7.3: Upper Monocacy River Watershed Maximum Daily Loads Summary

Subwatershed		Maximum Daily Load by Stratum (Billion *E. coli* MPN/day)	Maximum Daily Load (Weighted) (Billion *E. coli* MPN/day)
MON0575[1]	High Flow	56,119	15,517
	Low Flow	1,983	
PIN0000[1]	High Flow	22,861	6,108
	Low Flow	523	
TOM0011[1]	High Flow	3,851	6,640
	Low Flow	7,570	
OWN0007	High Flow	3,238	1,232
	Low Flow	564	
MON0355sub[1]	High Flow	257,189	65,341
	Low Flow	1,391	
HUN0009	High Flow	3,963	1,343
	Low Flow	469	
FIS0012	High Flow	2,275	990
	Low Flow	569	
MON0269sub	High Flow	1,798	495
	Low Flow	61	
TUS0007	High Flow	101	49
	Low Flow	32	

[1]Subwatersheds partially located in Pennsylvania

See Appendix D for a more detailed explanation of the procedure for obtaining these daily loads.

4.8 TMDL Allocations

The Upper Monocacy River fecal bacteria TMDL is composed of the following components:

$$TMDL = LA_{UM} + WLA_{UM} + LA_{DP} + LA_{PA} + MOS \qquad (20)$$

LA_{UM} – Upper Monocacy Load Allocation
WLA_{UM} – Upper Monocacy Waste Load Allocation
LA_{DP} – Double Pipe Creek Load Allocation
LA_{PA} – Pennsylvania Load Allocation
MOS – Margin of Safety

The TMDL allocations for the Upper Monocacy River MD 8-digit basin include a load allocation (LA_{UM}) for certain nonpoint sources, and waste load allocations (WLA_{UM}) for point sources including WWTPs and NPDES-regulated stormwater discharges. The Stormwater (SW) WLA_{UM} includes any nonpoint source loads deemed to be transported and discharged by regulated stormwater systems. An explanation of the distribution of nonpoint source loads and point source loads to the LA_{UM} and to the SW-WLA_{UM} and WWTP-WLA_{UM} is provided in the subsections that follow.

In addition to these allocation categories for the MD 8-digit watershed, the Upper Monocacy River TMDL includes an upstream load allocation for the portion of the watershed located in PA (LA_{PA}) and an upstream load allocation for Double Pipe Creek (LA_{DP}). The LA_{PA} was calculated using the ratios of the areas of the watershed in MD and in PA to the total area of the watershed, and is presented as a "lump-sum" upstream load comprising all bacteria source categories. The portion of the Upper Monocacy watershed located in PA includes 99% of the subwatershed MON0575, 20% of the subwatershed PIN0000, 67% of TOM0011,and 29% of the subwatershed MON0355sub. The LA_{PA}, determined to be necessary in order to meet MD water quality standards in the Upper Monocacy River MD 8-digit basin, will not be distributed between nonpoint sources (LA) and point sources (WLA). The final Double Pipe Creek TMDL, determined in a separate TMDL document, constitutes the LA_{DP} from that tributary to the Upper Monocacy River. See Appendix E for further information on the upstream loads.

The margin of safety (MOS) is explicit and is incorporated in the analysis using a conservative assumption; it is not specified as a separate term. The assumption is that a 5% reduction of the criterion concentration established by MD to meet the applicable water quality standard will result in more conservative allowable loads of fecal bacteria, and thus provide the MOS. The final loads are based on average hydrological conditions, with reductions estimated based on critical hydrological conditions. The load reduction scenario results in load allocations that will achieve water quality standards. The State reserves the right to revise these allocations provided such revisions are consistent with the achievement of water quality standards.

Bacteria Source Categories and Allocation Distributions

The bacteria sources are grouped into four categories that are also consistent with divisions for various management strategies. The categories are human, domestic animal, livestock and wildlife. TMDL allocation rules are presented in Table 4.8.1. This table identifies how the TMDL will be allocated among the LA_{UM} (those nonpoint sources or portions thereof not transported and discharged by stormwater systems) and the WLA_{UM} (point sources including WWTPs, and NPDES regulated stormwater discharges). Only the final LA_{UM} or WLA_{UM} is reported in this TMDL. Note that the assignment of a small allowable human load to the Stormwater WLA_{UM} is in consideration of the possible presence of such loads in the watershed beyond the reach of the sanitary sewer systems. The term "allowable load" means the load that the waterbody can assimilate and still meet water quality standards.

Table 4.8.1: Potential Source Contributions for TMDL Allocation Categories in the Upper Monocacy River Watershed in Maryland

Source Category	Maryland TMDL Allocation Categories		
	LA	WLA	
		WWTPs	Stormwater
Human		X	X
Domestic			X
Livestock	X		
Wildlife	X		X

* These allocation distributions apply only to the portion of the watershed in MD. The LA_{PA} includes all four bacteria source categories in a single upstream load allocation.

LA_{UM}

All four bacteria source categories could potentially contribute to nonpoint source loads. For human sources, if the watershed has no MS4s or other NPDES-regulated Phase I or Phase II stormwater discharges, the nonpoint source contribution is estimated by subtracting any WWTP and/or CSO loads from the TMDL human load, and is then assigned to the LA_{UM}. However, in watersheds covered by NPDES-regulated stormwater permits, any such nonpoint sources of human bacteria (i.e., beyond the reach of the sanitary sewer systems) are assigned to the SW-WLA_{UM} (see below). There are twelve municipal WWTPs (two not yet active) and one industrial WWTP with NPDES permits regulating the discharge of bacteria in the Upper Monocacy River watershed. There are no subwatersheds with assigned NPDES CSO WLA.

Livestock loads are all assigned to the LA_{UM}. Domestic animals (pets) loads are assigned to the LA in watersheds with no MS4s or other NPDES-regulated stormwater systems. Since the entire Upper Monocacy River watershed is covered by NPDES MS4 permits, bacteria loads from domestic animal sources are assigned to the SW-WLA_{UM} in all nine subwatersheds of Upper Monocacy River. However, wildlife sources will be distributed between the LA_{UM} and the SW-WLA_{UM}, based on a ratio of the amount of pervious area in non-urban land to pervious area in urban land.

WLA_{UM}

NPDES Regulated Stormwater

Both individual and general NPDES Phase I and Phase II stormwater permits are point sources subject to WLA assignment in the TMDL. Quantification of rainfall-driven nonpoint source loads, such as those transported by stormwater through MS4s, is uncertain. EPA recognized this in its guidance document entitled "Establishing Total Maximum Daily Load (TMDL) Wasteload Allocations (WLAs) for Storm Water Sources and NPDES Permit Requirements Based on Those WLAs" (November 2002), which states that available data and information usually are not detailed enough to determine WLAs for NPDES-regulated stormwater discharges on an outfall-specific basis. Therefore, in watersheds with an existing MS4 permit, domestic animal bacteria loads are grouped together into a single $SW\text{-}WLA_{UM}$ along with other potential nonpoint source loads such as human and wildlife loads. This allowable human load in the $SW\text{-}WLA_{UM}$ is estimated by subtracting any WWTP and CSO loads (if present) from the total allowable (TMDL) human load. There are twelve municipal WWTPs (two not yet active) and one industrial WWTP with NPDES permits regulating the discharge of bacteria in the Upper Monocacy River watershed. There are no NPDES CSO permits in the watershed. The $SW\text{-}WLA_{UM}$ wildlife load is estimated as explained above. In watersheds with no existing NPDES-regulated stormwater permits, these loads will be included in the LA.

The jurisdictions within the MD portion of Upper Monocacy River watershed, Carroll County and Frederick County, are covered by individual Phase I MS4 program regulations. Based on EPA's guidance, the $SW\text{-}WLA_{UM}$ is presented as one combined load for the entire land area of each county in each subwatershed. In the future, when more detailed data and information become available, it is anticipated that MDE will revise the WLA into appropriate WLAs and LAs, and may also revise the LA accordingly. Note that the overall reductions in the TMDL will not change. The $SW\text{-}WLA_{UM}$ category includes any other Phase I and Phase II NPDES-regulated stormwater entities in the watershed, in addition to the Counties' MS4s. The $SW\text{-}WLA_{UM}$ distributions between Carroll County and Frederick County are presented in Table 4.8.2.

Table 4.8.2: Annual Average Stormwater Allocations for the Upper Monocacy River Watershed in Maryland

Station	**SW-WLA in Maryland (Billion MPN *E. Coli*/year)**			
	Carroll County	%	Frederick County	%
MON0575[1]	125	7%	1,656	93%
PIN0000[1]	9,092	100%	N/A	0%
TOM0011[1]	N/A	0%	7,346	100%
OWN0007	N/A	0%	13,008	100%
MON0355sub[1]	5,021	33%	10,194	67%
HUN0009	N/A	0%	3,170	100%
FIS0012	N/A	0%	1,301	100%
MON0269sub	N/A	0%	1,983	100%
TUS0007	N/A	0%	423	100%

[1]WLA presented only for the Maryland portion of each of these subwatersheds

Municipal and Industrial WWTPs

As explained in the source assessment section above, there are twelve municipal NPDES permitted point source facilities with permits regulating the discharge of fecal bacteria directly into the Upper Monocacy River watershed. Ten of these are active, while two others have not yet been built. There is only one industrial WWTP with a permit regulating the discharge of bacteria directly into the River. These 10 active municipal WWTPs and one industrial WWTP discharge bacteria into six subwatersheds: Piney Creek (PIN0000), Hunting Creek (HUN0009), Toms Creek (TOM0011), Owens Creek (OWN0007), Fishing Creek (FIS0012), and Tuscarora Creek (TUS0007). The WLA for each WWTP is estimated using the design flow of the plant stated in the facility's NPDES permit and the *E. coli* criterion of 126 MPN/100ml. Bacteria loads assigned to these WWTPs are allocated as the WWTP WLA.

4.9 Summary

The long-term annual average TMDL and TMDL allocations are presented in Table 4.9.1. Table 4.9.2 presents the maximum daily loads for the subwatersheds or portions thereof within the Upper Monocacy River MD 8-digit basin.

Table 4.9.1: Upper Monocacy River Watershed Annual Average TMDL

	Total Allocation	**LA**	**SW-WLA**	**WWTP-WLA**
	Billion MPN *E. coli*/year			
Upper Monocacy River (MON0575) [1]	**3,592**	1,811	1,781	N/A
Piney Creek (PIN0000) [1]	**120,740**	110,115	8,709	1,915
Toms Creek (TOM0011) [1]	**49,398**	41,500	6,226	1,671
Owens Creek (OWN0007) [1]	**47,338**	34,235	13,008	96
Upper Monocacy River (MON0355sub) [1]	**218,756**	203,541	15,215	N/A
Hunting Creek (HUN0009) [1]	**29,942**	24,993	3,170	1,779
Fishing Creek (FIS0012) [1]	**16,833**	15,476	1,301	56
Upper Monocacy River (MON0269sub) [1]	**7,834**	5,788	1,983	63

Tuscarora Creek (TUS0007)[1]	**1,802**	1,292	423	87
MD 8-Digit Total[2]	**496,234**	438,751	51,816	5,667
Double Pipe Creek Upstream Load	**282,168**			
PA Upstream Load	**575,448**			
TMDL[3]	**1,353,850**			

[1]MD portion of the subwatershed only.
[2]This total load represents the sum of the individual maximum daily loads for the MD portion of the subwatersheds presented above.
[3]The MOS is incorporated.

Table 4.9.2: MD Upper Monocacy River Watershed Maximum Daily Loads

Subwatersheds	MD 8-Digit Basin			
	MDL	LA	SW-WLA	WWTP-WLA
	Billion MPN *E. coli*/day			
Upper Monocacy River (MON0575)	**155**	78	77	N/A
Piney Creek (PIN0000)	**4,886**	4,456	414	16.3
Toms Creek (TOM0011)	**2,191**	1,841	336	14.2
Owens Creek (OWN0007)	**1,232**	808	423	0.8
Upper Monocacy River (MON0355sub)	**46,392**	43,610	2,782	N/A
Hunting Creek (HUN0009)	**1,343**	1,121	207	15.2
Fishing Creek (FIS0012)	**990**	910	79	0.5
Upper Monocacy River (MON0269sub)	**496**	366	129	0.5
Tuscarora Creek (TUS0007)	**49**	35	13	0.7
MD 8-Digit Total*	**57,734**	53,225	4,461	48.3

Double Pipe Creek Upstream Load	**8,082**
PA Upstream Load	**39,981**
TOTAL	**105,797**

*This total load represents the sum of the individual maximum daily loads for the MD portion of the subwatersheds presented above.

The long-term annual average fecal bacteria TMDL summary for the entire Upper Monocacy River watershed is presented in Table 4.9.3.

Table 4.9.3: Upper Monocacy River Watershed Annual Average TMDL Summary

TMDL Billion MPN *E. coli*/year	=	**LA_{UM}**	+	**WLA_{UM}**	+	**LA_{DP}**	+	**LA_{PA}**	+	**MOS**
		Billion MPN *E. coli*/year								
1,353,850	=	**438,751**	+	**57,483**	+	**282,168[1]**	+	**575,448[2]**	+	**Incorporated**

[1]This upstream load allocation is equivalent to the Double Pipe Creek TMDL.
[2]This upstream PA load allocation is determined to be necessary in order to meet MD water quality standards in the MD portion of the Upper Monocacy River watershed.

The fecal bacteria MDL summary for the entire Upper Monocacy River watershed is presented in Table 4.9.4.

Table 4.9.4: Upper Monocacy River Watershed Annual Average MDL Summary

MDL Billion MPN *E. coli*/day	=	**LA_{UM}**	+	**WLA_{UM}**	+	**LA_{DP}**	+	**LA_{PA}**	+	**MOS**
		Billion MPN *E. coli*/day								
105,797	=	**53,225**	+	**4,509**	+	**8,082[1]**	+	**39,981[2]**	+	**Incorporated**

[1]This upstream load allocation is equivalent to the Double Pipe Creek MDL.
[2]This upstream PA load allocation is determined to be necessary in order to meet MD water quality standards in the MD portion of the Upper Monocacy River watershed.

In certain watersheds, the goal of meeting water quality standards may require very high reductions that are not achievable with current technologies and management practices. In this situation, where there is no feasible TMDL scenario, MPRs are increased to provide estimates of the reductions required to meet water quality standards. In the Upper Monocacy River subwatersheds, water quality standards cannot be achieved with the maximum practicable reduction rates specified in Table 4.6.3. The TMDLs shown in Tables 4.9.1 and 4.9.2 represent reductions from current bacteria loadings that are beyond practical reductions. In cases where such high reductions are required to meet standards, it is expected that the first stage of implementation will be to carry out the MPR scenario.

5.0 ASSURANCE OF IMPLEMENTATION

Section 303(d) of the Clean Water Act and current EPA regulations require reasonable assurance that the TMDL load and waste load allocations can and will be implemented. In the Upper Monocacy River watershed, the TMDL analysis indicates that, for eight out of nine subwatersheds, the reduction of fecal bacteria loads from all sources including wildlife are beyond the MPR targets. These MPR targets were defined based on a literature review of BMPs effectiveness and assuming a zero reduction for wildlife sources. The Upper Monocacy River and its tributaries Toms Creek, Fishing Creek, Hunting Creek, Owens Creek, Piney Creek, Tuscarora Creek and Double Pipe Creek may not be able to attain water quality standards. The headwaters subwatershed, where Marsh Creek and Rock Creek join to form the Upper Monocacy River (Subwatershed ID MON0575), is the only watershed that could meet water quality standards with practicable reductions. The fecal bacteria load reductions required to meet water quality criteria in the remaining eight subwatersheds of the Upper Monocacy River are not feasible by implementing effluent limitations and cost-effective, reasonable BMPs to nonpoint sources. Therefore, MDE proposes a staged approach to implementation beginning with the MPR scenario, with regularly scheduled follow-up monitoring to assess the effectiveness of the implementation plan.

Additional reductions will be achieved through the implementation of BMPs; however, the literature reports considerable uncertainty concerning the effectiveness of BMPs in treating bacteria. As an example, pet waste education programs have varying results based on stakeholder involvement. Additionally, the extent of wildlife reduction associated with various BMPs methods (e.g., structural, non-structural, etc.) is uncertain. Therefore, MDE intends for the required reductions to be implemented in an iterative process that first addresses those sources with the largest impact on water quality and human health risk, with consideration given to ease of implementation and cost. The iterative implementation of BMPs in the watershed has several benefits: tracking of water quality improvements following BMP implementation through follow-up stream monitoring; providing a mechanism for developing public support through periodic updates on BMP implementation; and helping to ensure that the most cost-effective practices are implemented first.

Potential funding sources for implementation include the Maryland's Agricultural Cost Share Program (MACS), which provides grants to farmers to help protect natural resources, and the Environmental Quality and Incentives Program, which focuses on implementing conservation practices and BMPs on land involved with livestock and production. Though not directly linked, it is assumed that the nutrient management plans from the Water Quality Improvement Act of 1998 (WQIA) will have some reduction of bacteria from manure application practices.

Implementation and Wildlife Sources

It is expected that in some waters for which TMDLs will be developed, the bacteria source analysis indicates that after controls are in place for all anthropogenic sources, the waterbody will not meet water quality standards. Neither Maryland nor EPA is proposing the elimination of wildlife to allow for the attainment of water quality standards, although managing the overpopulation of wildlife remains an option for state and local stakeholders. After developing and implementing, to the maximum extent possible, a reduction goal based on the anthropogenic sources identified in the TMDL, Maryland anticipates that implementation to reduce the controllable nonpoint sources may also reduce some wildlife inputs to the waters.

REFERENCES

Cameron, R., Mackeney and Merle D. Pierson, eds. 1994. Environmental Indicators and Shellfish Safety. Chapman & Hall.

Code of Federal Regulations. 40 CFR 130.2(h), 40 CFR 130.7(c)(1). Website http://www.access.gpo.gov/nara/cfr/waisidx_04/40cfr130_04.html, last visited 06/24/06.

COMAR (Code of Maryland Regulations) 26.08.02.03-3A(1), 26.08.02.08P. Website http://www.dsd.state.md.us/comar, last visited 06/24/06.

COMAR 26.08.10. Website http://www.dsd.state.md.us/comar, last visited 07/29/06.

Cohn, T.A., L.L. DeLong, E.J. Gilroy, and R.M. Hirsch, and D.K. Wells. 1989. Estimating Constituent Loads. Water Resources Research 25: 937-942.

Duan, N. 1983. Smearing Estimate: A Nonparametric Retransformation method. Journal of the American Statistical Association 78:605-610.

Easton, J. H., M. M. Lalor, J. J. Gauthier and R. E. Pitt. 2001. Pathogen Decay in Urban Streams. In: AWRA Annual Spring Specialty Conference Proceedings: Water Quality Monitoring and Modeling, American Water Resources Association, San Antonio, TX, pp. 169-174.

Ferguson, R.I. 1986. River Loads Underestimated by Rating Curves. Water Resources Research 22: 74-76.

MDE (Maryland Department of the Environment). 2002. *2002 List of Impaired Surface Waters [303(d) List] and Integrated Assessment of Water Quality in Maryland.*

————. 2006. *2006 List of Impaired Surface Waters [303(d) List] and Integrated Assessment of Water Quality in Maryland.*

————. 2004. *2004 FINAL List of Impaired Surface Waters [303(d) List] and Integrated Assessment of Water Quality in Maryland.*

————. 2002. *2002 Bacteriological TMDL Survey of Lower Monocacy River.*

MDP (Maryland Department of Planning). 2002. 2002 Land Use, Land Cover Map Series.

————. Estimates of Septic Systems. 2003. Baltimore: Maryland Department of Planning, Comprehensive Planning Unit.

Richards, R.P. 1998. Estimation of pollutant loads in rivers and streams: A guidance document for NPS programs. Project report prepared under Grant X998397-01-0, U.S. Environmental Protection Agency, Region VIII, Denver. 108 p.

Schueler, T. 1999. "Microbes and Urban Watersheds." Watershed Protection Techniques. 3(1): 551-596.

.U.S. Department of Commerce. 2000. United States Census Bureau's GIS Coverage. Washington DC: US Bureau of the Census.

————. 1997. Census of Agriculture: Maryland State and County Data. Washington, DC: National Agricultural Statistic Service.

US EPA (U.S. Environmental Protection Agency). 1986. *Ambient Water Quality Criteria for Bacteria--1986*. EPA-440/5-84-002.

————. 1991. Guidance for water quality-based decisions: The TMDL Process, EPA 440/4-91-001.

————. 2002. *National Recommended Water Quality Criteria: 2002*. EPA-822-R-02-047. November 2002.

————. 1984. Health Effects Criteria for Fresh Recreational Waters. EPA-600/1-84-004. U.S. Environmental Protection Agency, Washington, DC. EPA.

————. 1999. Preliminary Data Summary of Urban Storm Water Best Management Practices. EPA-821-R-99-012. U.S. Environmental Protection Agency, Washington, DC.

————. 2004. Agricultural BMP Descriptions as Defined for The Chesapeake Bay Program Watershed Model. Nutrient Subcommittee Agricultural Nutrient Reduction Workshop.

————. 2003. *Implementation Guidance for Ambient Water Quality Criteria for Bacteria: Draft*, U.S. Environmental Protection Agency. Office of Water, Washington, D.C. EPA-823-B-02-003.

————. 1985. Test Methods for Eschericichia coli and Enterococci in Water by the Membrane Filter Procedure. EPA600/4-85-076. Washington, DC. NTIS PB86-158052.

USGS (U.S. Geological Survey). 1996. HYSEP: A Computer Program for Streamflow Hydrograph Separation and Analysis. USGS Water-Resource Investigations Report 96-4040.

University of Maryland, Mid-Atlantic Regional Earth Science Applications Center, version 1.05, 2000.

Versar. 2004. Development of Regional Flow Duration Curves in Maryland. Prepared for Maryland Department of the Environment.

Appendix A – Bacteria Data

Table A-1: Measured Bacteria Concentration with Daily Flow Frequency

Sampling Station Identifier	Date	Daily flow frequency	*E. Coli* MPN/100ml
FIS0012	11/03/2003	30.0292	140
FIS0012	11/17/2003	29.1165	100
FIS0012	12/01/2003	19.4597	130
FIS0012	12/15/2003	7.5758	520
FIS0012	01/06/2004	11.1355	80
FIS0012	01/21/2004	69.2041	20
FIS0012	02/04/2004	11.9022	330
FIS0012	02/18/2004	37.1303	10
FIS0012	03/02/2004	13.2713	30
FIS0012	03/16/2004	37.9518	30
FIS0012	04/06/2004	22.6725	30
FIS0012	04/20/2004	29.6276	60
FIS0012	05/11/2004	46.3673	300
FIS0012	05/25/2004	50.3834	370
FIS0012	06/08/2004	21.1391	520
FIS0012	06/22/2004	46.3673	510
FIS0012	07/07/2004	71.5955	570
FIS0012	07/20/2004	73.9686	990
FIS0012	08/10/2004	79.9562	680
FIS0012	08/24/2004	52.1723	810
FIS0012	09/08/2004	87.4589	280
FIS0012	09/21/2004	43.7203	1140
HUN0009	11/03/2003	30.0292	100
HUN0009	11/17/2003	29.1165	100
HUN0009	12/01/2003	19.4597	120
HUN0009	12/15/2003	7.5758	520

Sampling Station Identifier	Date	Daily flow frequency	*E. Coli* MPN/100ml
HUN0009	01/06/2004	11.1355	20
HUN0009	01/21/2004	69.2041	130
HUN0009	02/04/2004	11.9022	130
HUN0009	02/18/2004	37.1303	20
HUN0009	03/02/2004	13.2713	50
HUN0009	03/16/2004	37.9518	30
HUN0009	04/06/2004	22.6725	90
HUN0009	04/20/2004	29.6276	130
HUN0009	05/11/2004	46.3673	260
HUN0009	05/25/2004	50.3834	510
HUN0009	06/08/2004	21.1391	660
HUN0009	06/22/2004	46.3673	360
HUN0009	07/07/2004	71.5955	530
HUN0009	07/20/2004	73.9686	620
HUN0009	08/10/2004	79.9562	490
HUN0009	08/24/2004	52.1723	720
HUN0009	09/08/2004	87.4589	750
HUN0009	09/21/2004	43.7203	540
MON0269	11/03/2003	30.0292	300
MON0269	11/17/2003	29.1165	110
MON0269	12/01/2003	19.4597	640
MON0269	12/15/2003	7.5758	2180
MON0269	01/06/2004	11.1355	910
MON0269	01/21/2004	69.2041	10
MON0269	02/04/2004	11.9022	350
MON0269	02/18/2004	37.1303	1600
MON0269	03/02/2004	13.2713	30
MON0269	03/16/2004	37.9518	10
MON0269	04/06/2004	22.6725	70

Sampling Station Identifier	Date	Daily flow frequency	*E. Coli* MPN/100ml
MON0269	04/20/2004	29.6276	80
MON0269	05/11/2004	46.3673	130
MON0269	05/25/2004	50.3834	160
MON0269	06/08/2004	21.1391	840
MON0269	06/22/2004	46.3673	360
MON0269	07/07/2004	71.5955	190
MON0269	07/20/2004	73.9686	240
MON0269	08/10/2004	79.9562	130
MON0269	08/24/2004	52.1723	150
MON0269	09/08/2004	87.4589	110
MON0269	09/21/2004	43.7203	560
MON0355	11/03/2003	30.0292	200
MON0355	11/17/2003	29.1165	230
MON0355	12/01/2003	19.4597	510
MON0355	12/15/2003	7.5758	2910
MON0355	01/06/2004	11.1355	930
MON0355	01/21/2004	69.2041	20
MON0355	02/04/2004	11.9022	1330
MON0355	02/18/2004	37.1303	4610
MON0355	03/02/2004	13.2713	10
MON0355	03/16/2004	37.9518	40
MON0355	04/06/2004	22.6725	130
MON0355	04/20/2004	29.6276	230
MON0355	05/11/2004	46.3673	200
MON0355	05/25/2004	50.3834	230
MON0355	06/08/2004	21.1391	1180
MON0355	06/22/2004	46.3673	270
MON0355	07/07/2004	71.5955	220
MON0355	07/20/2004	73.9686	160

Sampling Station Identifier	Date	Daily flow frequency	*E. Coli* MPN/100ml
MON0355	08/10/2004	79.9562	170
MON0355	08/24/2004	52.1723	100
MON0355	09/08/2004	87.4589	70
MON0355	09/21/2004	43.7203	300
MON0575	11/03/2003	30.0292	190
MON0575	11/17/2003	29.1165	130
MON0575	12/01/2003	19.4597	350
MON0575	12/15/2003	7.5758	650
MON0575	01/06/2004	11.1355	470
MON0575	01/21/2004	69.2041	10
MON0575	02/04/2004	11.9022	190
MON0575	02/18/2004	37.1303	30
MON0575	03/02/2004	13.2713	10
MON0575	03/16/2004	37.9518	30
MON0575	04/06/2004	22.6725	70
MON0575	04/20/2004	29.6276	40
MON0575	05/11/2004	46.3673	110
MON0575	05/25/2004	50.3834	130
MON0575	06/08/2004	21.1391	410
MON0575	06/22/2004	46.3673	110
MON0575	07/07/2004	71.5955	130
MON0575	07/20/2004	73.9686	30
MON0575	08/10/2004	79.9562	360
MON0575	08/24/2004	52.1723	350
MON0575	09/08/2004	87.4589	120
MON0575	09/21/2004	43.7203	250
OWN0007	11/03/2003	30.0292	200
OWN0007	11/17/2003	29.1165	150
OWN0007	12/01/2003	19.4597	200

Sampling Station Identifier	Date	Daily flow frequency	*E. Coli* MPN/100ml
OWN0007	12/15/2003	7.5758	480
OWN0007	01/06/2004	11.1355	120
OWN0007	01/21/2004	69.2041	10
OWN0007	02/04/2004	11.9022	400
OWN0007	02/18/2004	37.1303	60
OWN0007	03/02/2004	13.2713	60
OWN0007	03/16/2004	37.9518	70
OWN0007	04/06/2004	22.6725	110
OWN0007	04/20/2004	29.6276	150
OWN0007	05/11/2004	46.3673	730
OWN0007	05/25/2004	50.3834	320
OWN0007	06/08/2004	21.1391	580
OWN0007	06/22/2004	46.3673	460
OWN0007	07/07/2004	71.5955	250
OWN0007	07/20/2004	73.9686	320
OWN0007	08/10/2004	79.9562	240
OWN0007	08/24/2004	52.1723	220
OWN0007	09/08/2004	87.4589	1190
OWN0007	09/21/2004	43.7203	400
PIN0000	11/03/2003	30.0292	150
PIN0000	11/17/2003	29.1165	180
PIN0000	12/01/2003	19.4597	260
PIN0000	12/15/2003	7.5758	1660
PIN0000	01/06/2004	11.1355	390
PIN0000	01/21/2004	69.2041	20
PIN0000	02/04/2004	11.9022	470
PIN0000	02/18/2004	37.1303	10
PIN0000	03/02/2004	13.2713	10
PIN0000	03/16/2004	37.9518	70

Sampling Station Identifier	Date	Daily flow frequency	*E. Coli* MPN/100ml
PIN0000	04/06/2004	22.6725	110
PIN0000	04/20/2004	29.6276	110
PIN0000	05/11/2004	46.3673	150
PIN0000	05/25/2004	50.3834	280
PIN0000	06/08/2004	21.1391	390
PIN0000	06/22/2004	46.3673	610
PIN0000	07/07/2004	71.5955	130
PIN0000	07/20/2004	73.9686	290
PIN0000	08/10/2004	79.9562	240
PIN0000	08/24/2004	52.1723	200
PIN0000	09/08/2004	87.4589	1040
PIN0000	09/21/2004	43.7203	910
TOM0011	11/03/2003	30.0292	170
TOM0011	11/17/2003	29.1165	100
TOM0011	12/01/2003	19.4597	220
TOM0011	12/15/2003	7.5758	89
TOM0011	01/06/2004	11.1355	310
TOM0011	01/21/2004	69.2041	10
TOM0011	02/04/2004	11.9022	130
TOM0011	02/18/2004	37.1303	40
TOM0011	03/02/2004	13.2713	30
TOM0011	03/16/2004	37.9518	40
TOM0011	04/06/2004	22.6725	90
TOM0011	04/20/2004	29.6276	110
TOM0011	05/11/2004	46.3673	230
TOM0011	05/25/2004	50.3834	370
TOM0011	06/08/2004	21.1391	750
TOM0011	06/22/2004	46.3673	270
TOM0011	07/07/2004	71.5955	5200

Sampling Station Identifier	Date	Daily flow frequency	*E. Coli* MPN/100ml
TOM0011	07/20/2004	73.9686	3870
TOM0011	08/10/2004	79.9562	179
TOM0011	08/24/2004	52.1723	7700
TOM0011	09/08/2004	87.4589	1570
TOM0011	09/21/2004	43.7203	810
TUS0007	11/03/2003	17.8897	120
TUS0007	11/17/2003	23.6948	20
TUS0007	12/01/2003	12.6506	180
TUS0007	12/15/2003	3.5414	320
TUS0007	01/06/2004	18.9303	190
TUS0007	01/21/2004	43.0814	120
TUS0007	02/04/2004	9.9124	330
TUS0007	02/18/2004	39.9598	60
TUS0007	03/02/2004	23.2749	60
TUS0007	03/16/2004	29.4085	60
TUS0007	04/06/2004	18.7660	50
TUS0007	04/20/2004	22.3622	320
TUS0007	05/11/2004	39.4670	330
TUS0007	05/25/2004	41.4385	310
TUS0007	06/08/2004	26.9441	880
TUS0007	06/22/2004	36.4367	730
TUS0007	07/07/2004	38.5360	990
TUS0007	07/20/2004	58.4885	540
TUS0007	08/10/2004	61.3363	480
TUS0007	08/24/2004	64.2753	430
TUS0007	09/08/2004	77.3092	1470
TUS0007	09/21/2004	63.6911	500

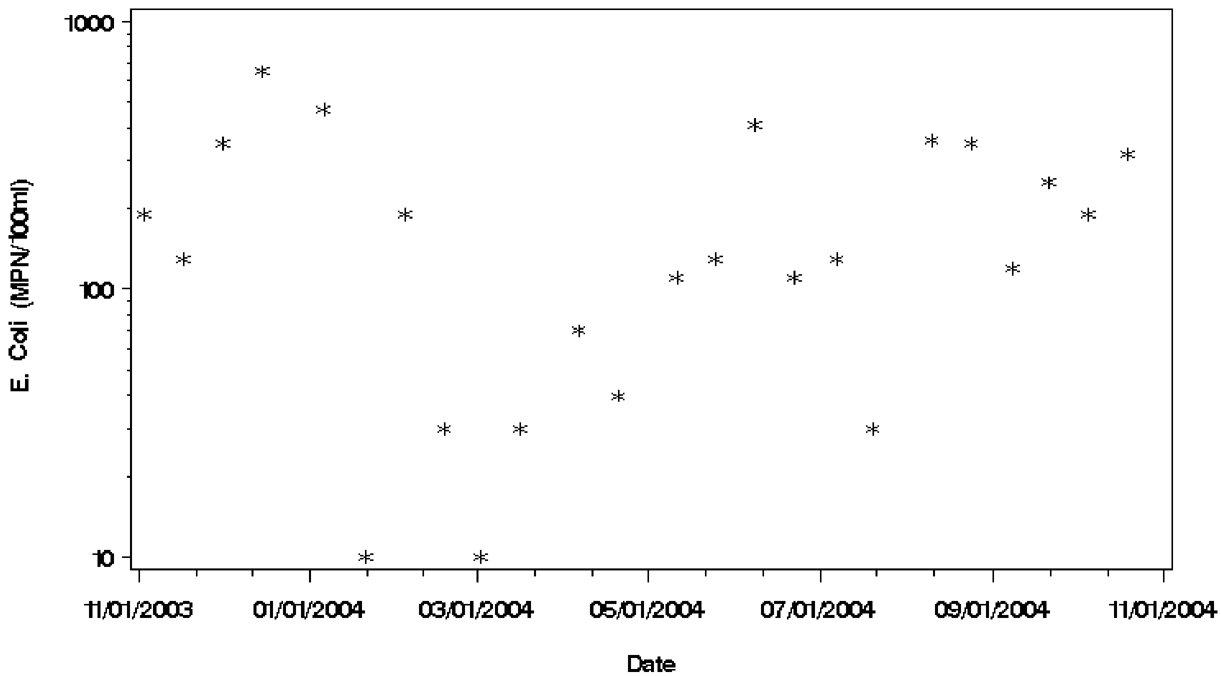

Figure A-1: *E. coli* Concentration vs. Time for the Upper Monocacy River Monitoring Station MON0575

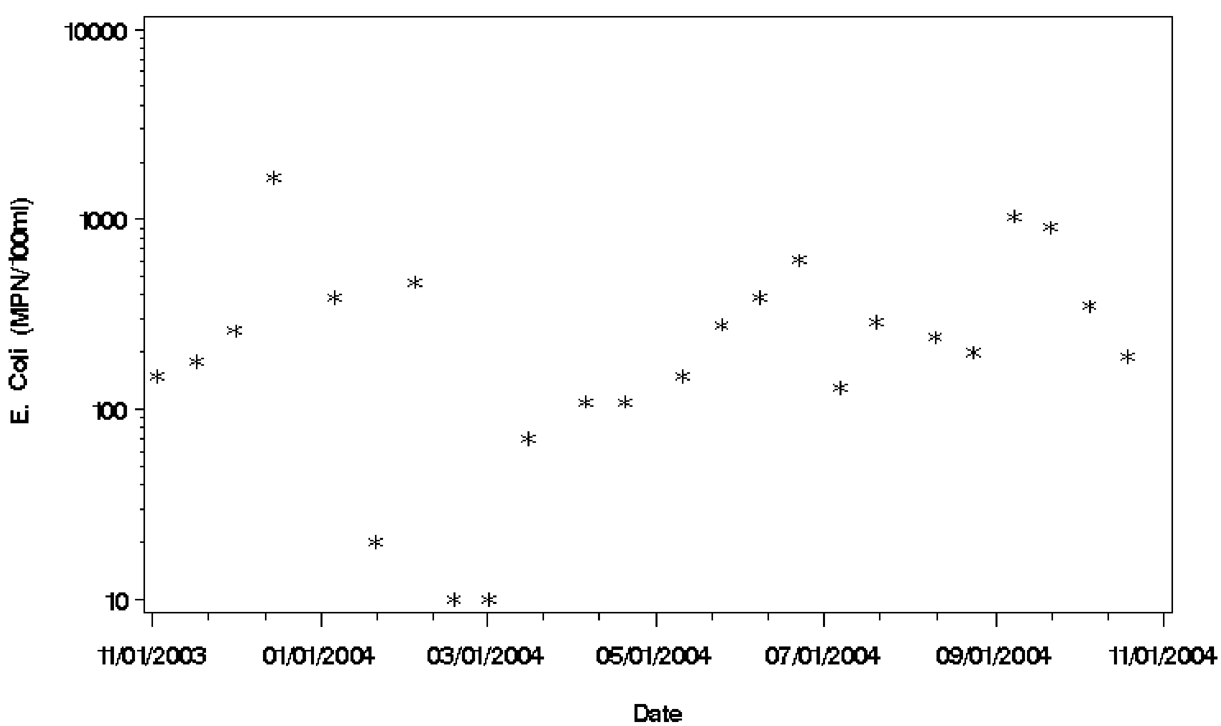

Figure A-2: *E. coli* Concentration vs. Time for the Upper Monocacy River Monitoring Station PIN0000

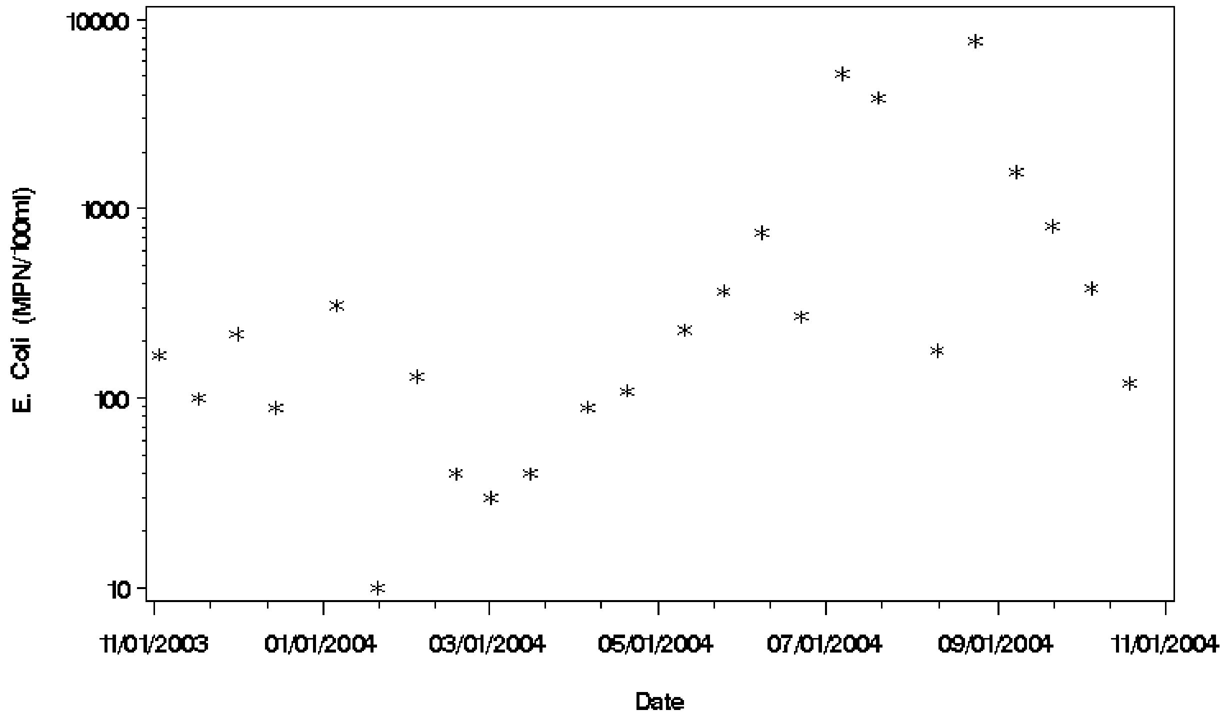

Figure A-3: *E. coli* Concentration vs. Time for the Upper Monocacy River Monitoring Station TOM0011

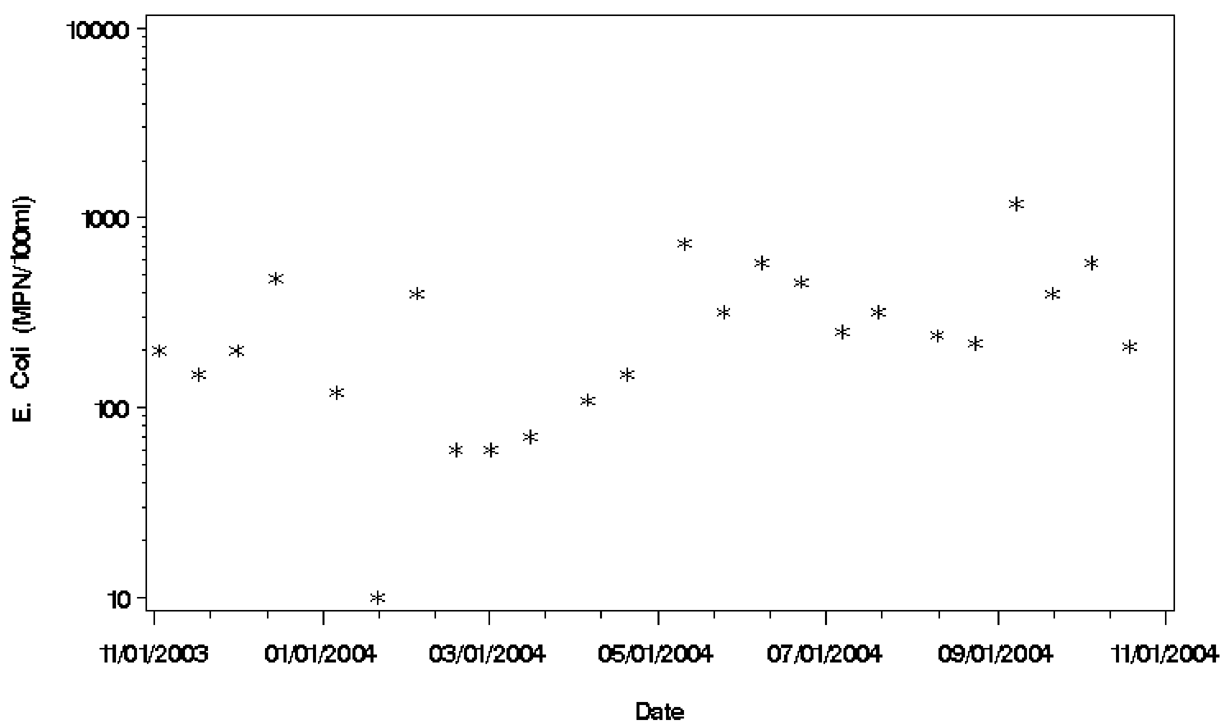

Figure A-4: *E. coli* Concentration vs. Time for the Upper Monocacy River Monitoring Station OWN0007

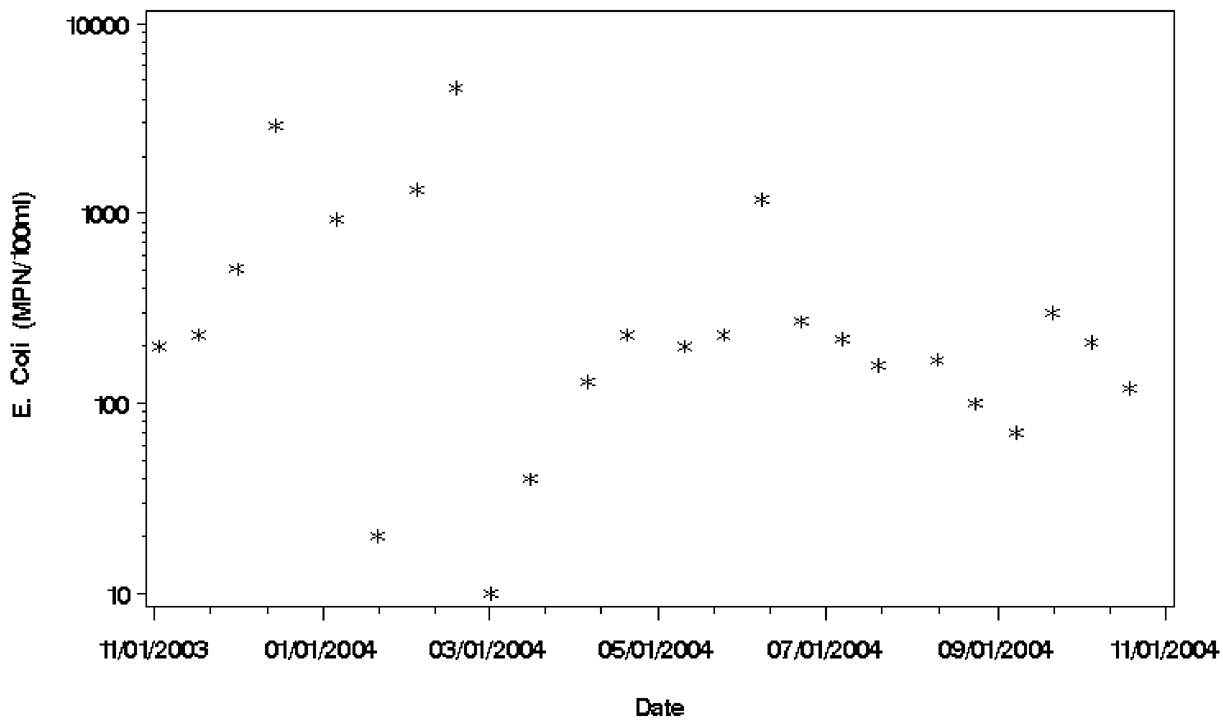

Figure A-5: *E. coli* Concentration vs. Time for the Upper Monocacy River Monitoring Station MON0355

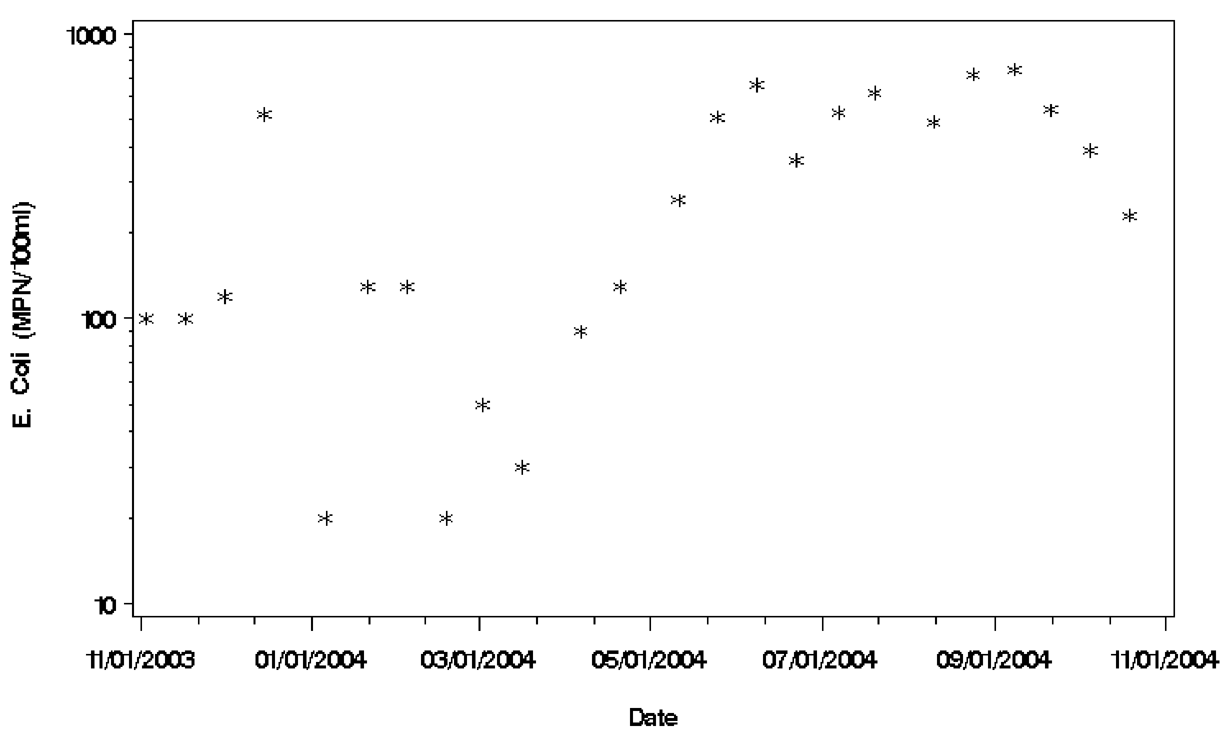

Figure A-6: *E. coli* Concentration vs. Time for the Upper Monocacy River Monitoring Station HUN0009

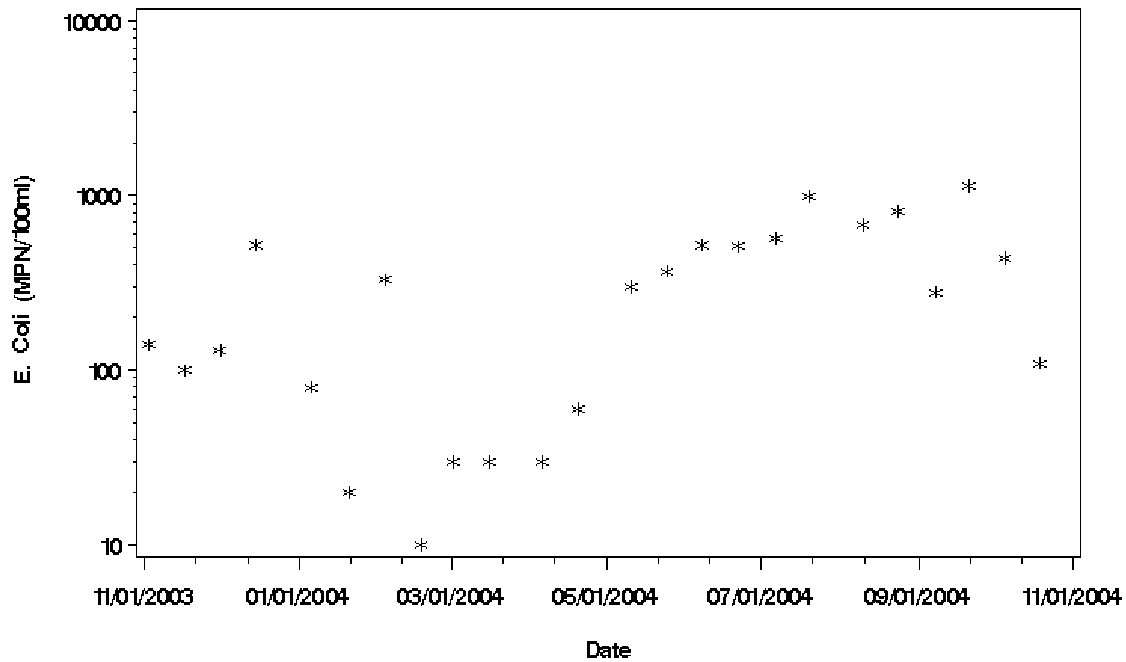

Figure A-7: *E. coli* Concentration vs. Time for the Upper Monocacy River Monitoring Station FIS0012

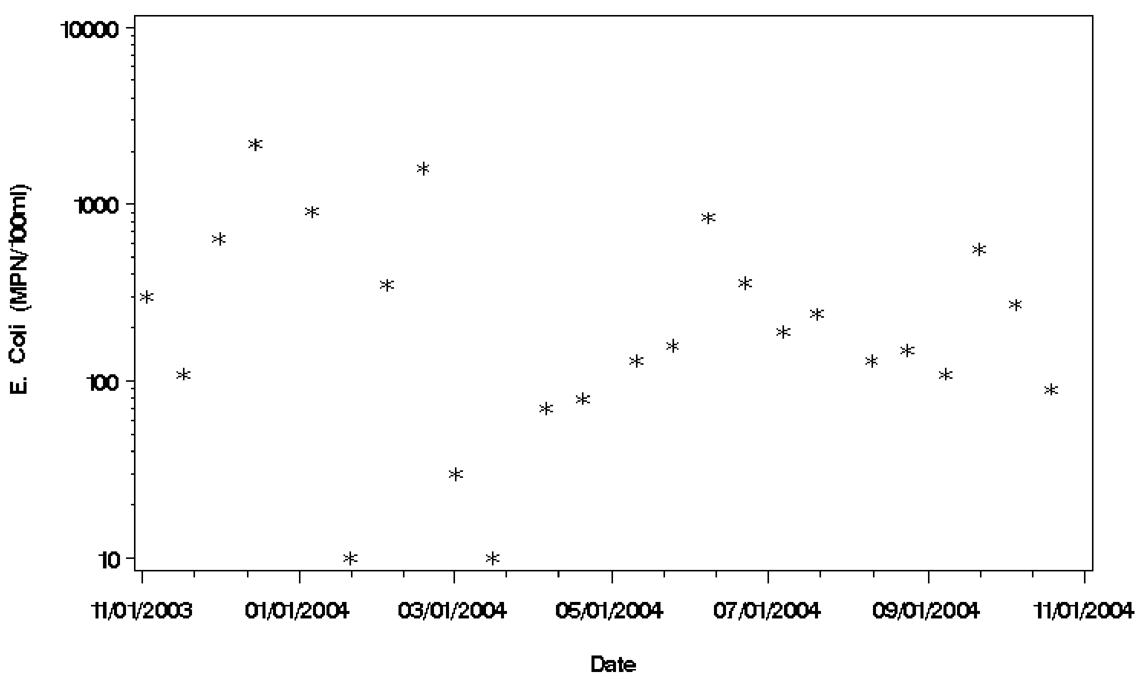

Figure A-8: *E. coli* Concentration vs. Time for the Upper Monocacy River Monitoring Station MON0269

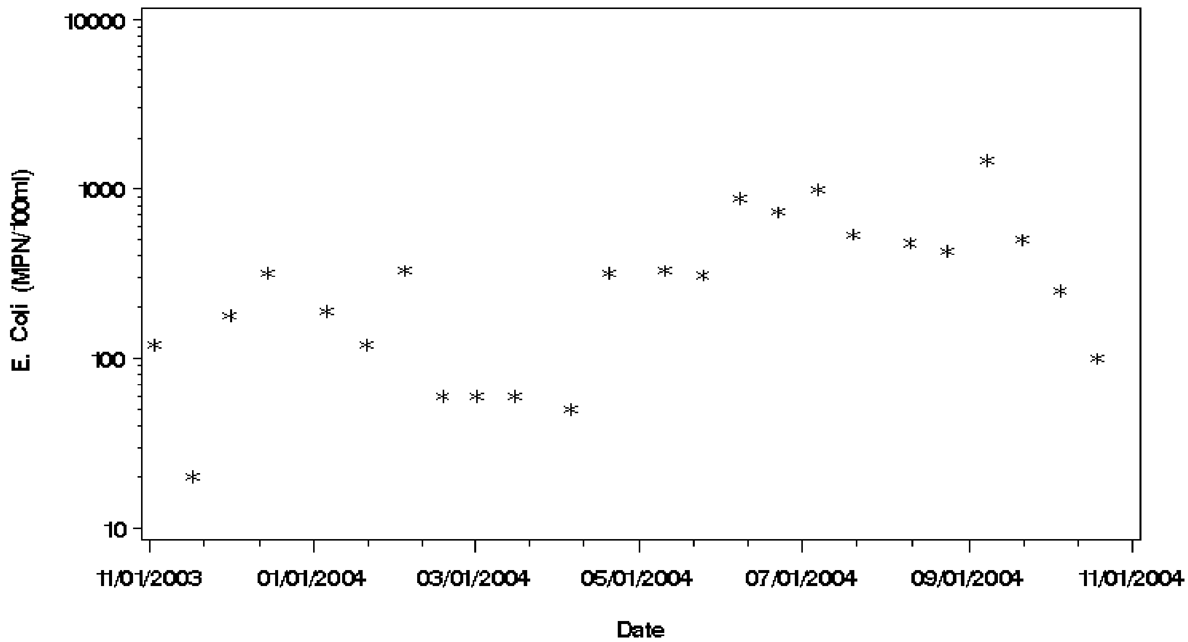

Figure A-9: *E. coli* Concentration vs. Time for the Upper Monocacy River Monitoring Station TUS0007

Appendix B – Flow Duration Curve Analysis to Define Strata

The Upper Monocacy River watershed was assessed to determine hydrologically significant strata. The purpose of these strata is to apply weights to monitoring data and thus (1) reduce bias associated with the monitoring design and (2) approximate a critical condition for TMDL development. The strata group hydrologically similar water quality samples and provide a better estimate of the mean concentration at the monitoring station.

The flow duration curve for a watershed is a plot of all possible daily flows, ranked from highest to lowest, versus their probability of exceedance. In general, the higher flows will tend to be dominated by excess runoff from rain events and the lower flows will result from drought type conditions. The mid-range flows are a combination of high base flow with limited runoff and lower base flow with excess runoff. The range of these mid-level flows will vary with soil antecedent conditions. The purpose of the following analysis is to identify hydrologically significant groups, based on the previously described flow regimes, within the flow duration curve.

Flow Analysis

The Upper Monocacy River watershed has one active USGS flow gauge (01639000). The gauge and dates of information used are as follows:

Table B-1: USGS Gauges in the Upper Monocacy River Watershed

USGS Gage #	Dates used	Description
01639000	October 1, 1989 to September 30, 2004	Monocacy River at Bridgeport, MD

A flow duration curve for this gauge is presented in Figure B-1.

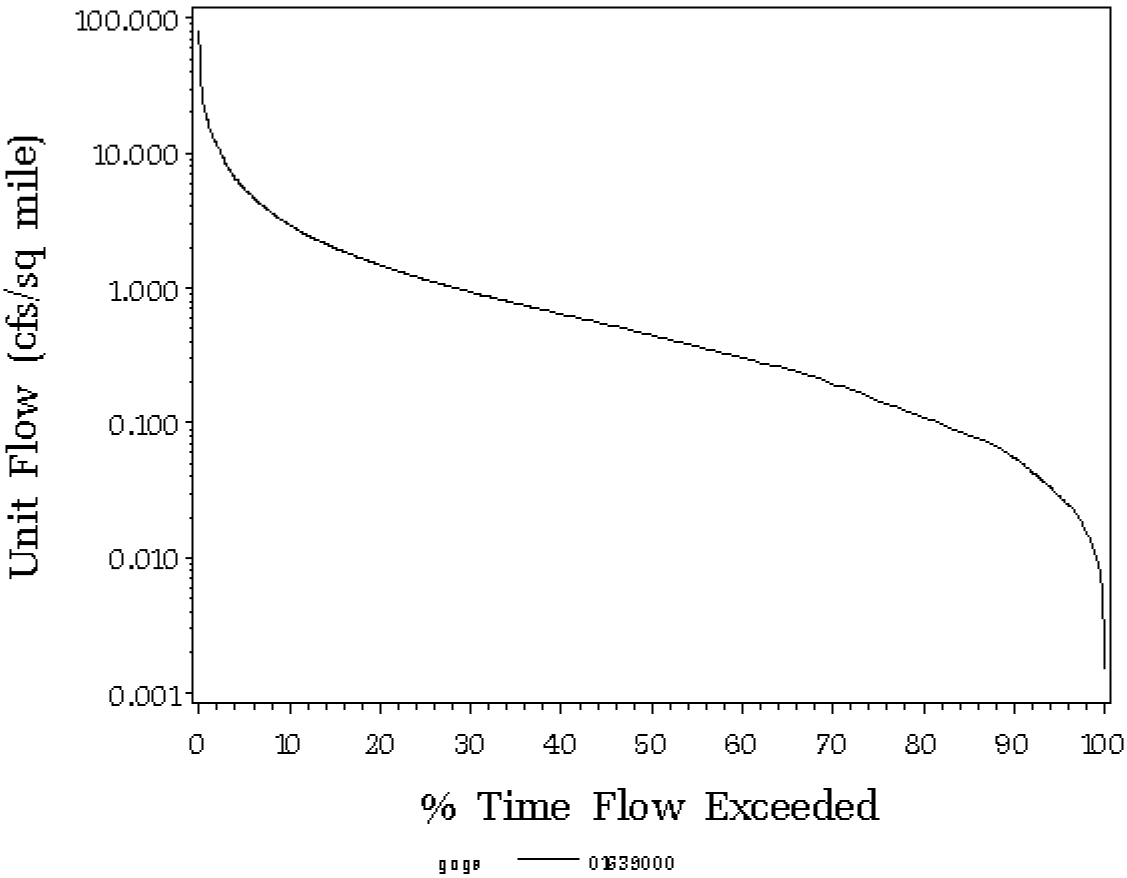

Figure B-1: Upper Monocacy River Flow Duration Curves

Based on the long-term flow data for the Upper Monocacy River watershed and other watersheds in the region (*i.e.* Double Pipe Creek and Lower Monocacy River), the long term average daily unit flows range between 1.2 to 1.4 cfs/sq. mile, which corresponds to a range of 21th to 28th flow frequency based on the flow duration curves of these watersheds. Using the definition of a high flow condition as occurring when flows are higher than the long-term average flow and a low flow condition as occurring when flows are lower than the long-term average flow, the 25th percentile threshold was selected to define the limits between high flows and low flows in this watershed. Therefore, a high flow condition will be defined as occurring when the daily flow duration percentile is less than 25% and a low flow condition will be defined as occurring when the daily flow duration percentile is greater than 25%. Definitions of high and low range flows are presented in Table B-2.

Table B-2: Definition of Flow Regimes

High flow	Represents conditions where stream flow tends to be dominated by surface runoff.
Low flow	Represents conditions where stream flow tends to be more dominated by groundwater flow.

Flow-Data Analysis

The final analysis to define the daily flow duration intervals (flow regions, strata) includes the bacteria monitoring data. Bacteria (*E. coli*) monitoring data are "placed" within the regions (strata) based on the daily flow duration percentile of the date of sampling. Figures B-2 to B-10 show the Upper Monocacy River *E. coli* monitoring data with corresponding flow frequency for the average annual condition.

Maryland's water quality standards for bacteria state that, when available, the geometric mean indicator should be based on at least five samples taken representatively over 30 days. Therefore, in situations in which fewer than five samples "fall" within a particular flow regime interval, the interval and the adjacent interval will be joined. In the Upper Monocacy River, for the annual average flow condition, there are sufficient samples in both the high flow and low flow strata to estimate the geometric means. However, in the seasonal (May 1st – September 30th) flow condition, there are no sufficient samples within the high flow strata to estimate geometric means; therefore, for this condition an average seasonal geometric mean will be calculated.

Weighting factors for estimating a weighted geometric mean are based on the frequency of each flow stratum during the averaging period. The weighting factors for the averaging periods and hydrological conditions are presented in Table B-3. Averaging periods are defined in this report as:

(1) Average Annual Hydrological Condition
(2) Annual High Flow Condition
(3) Annual Low Flow Condition
(4) Seasonal (May 1st – September 30th) Average Flow Condition

Weighted geometric means for the average annual condition are plotted with the monitoring data on Figures B-2 to B-10.

Table B-3: Weighting Factors for Estimation of Geometric Mean

USGS Gage	Hydrological Condition		Subwatershed	Weighting Factor High Flow	Weighting Factor Low Flow
01639000	Annual	Average	All	0.25	0.75
		High Flow	All	0.48	0.52
		Low Flow	All	0.03	0.97
	Seasonal	Average	All	N/A	N/A

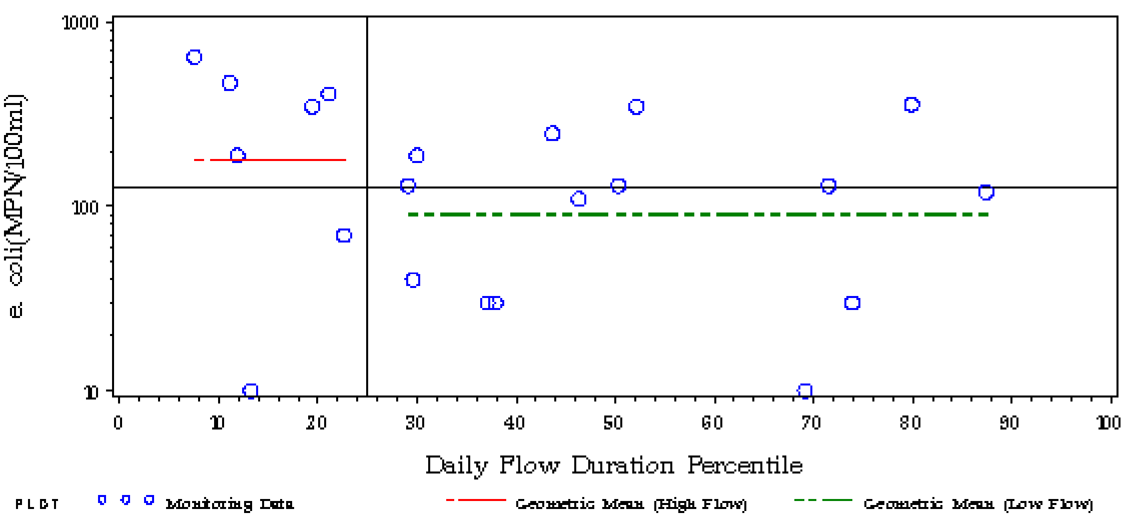

Figure B-2: *E. coli* Concentration vs. Flow Duration for the Upper Monocacy River Monitoring Station MON0575

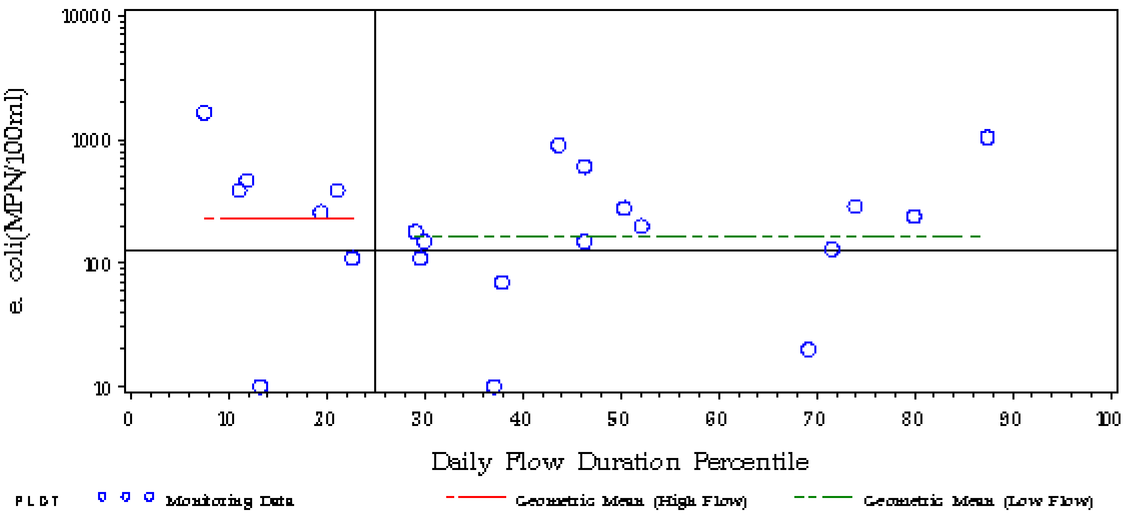

Figure B-3: *E. coli* Concentration vs. Flow Duration for the Upper Monocacy River Monitoring Station PIN0000

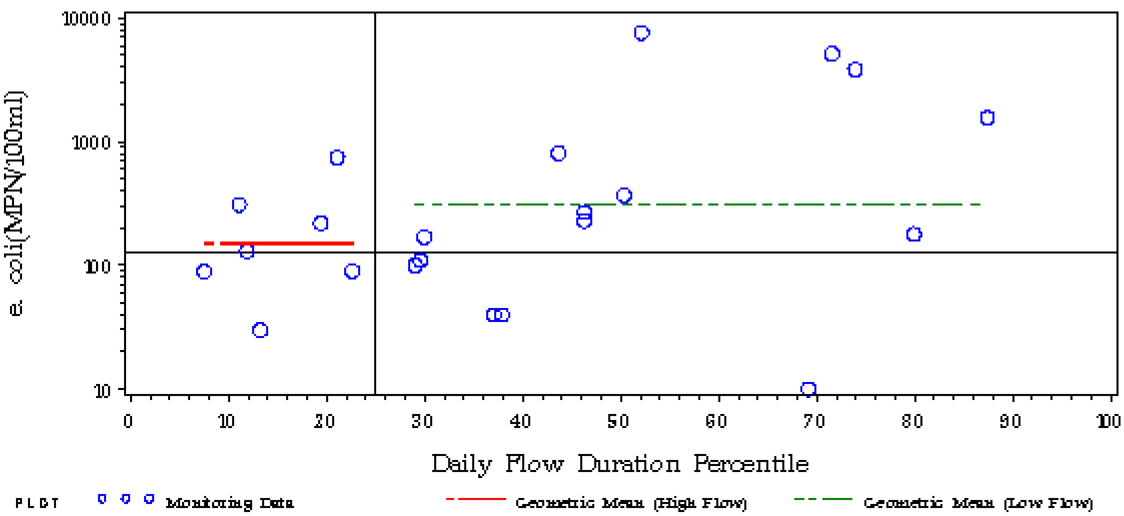

Figure B-4: *E. coli* Concentration vs. Flow Duration for the Upper Monocacy River Monitoring Station TOM0011

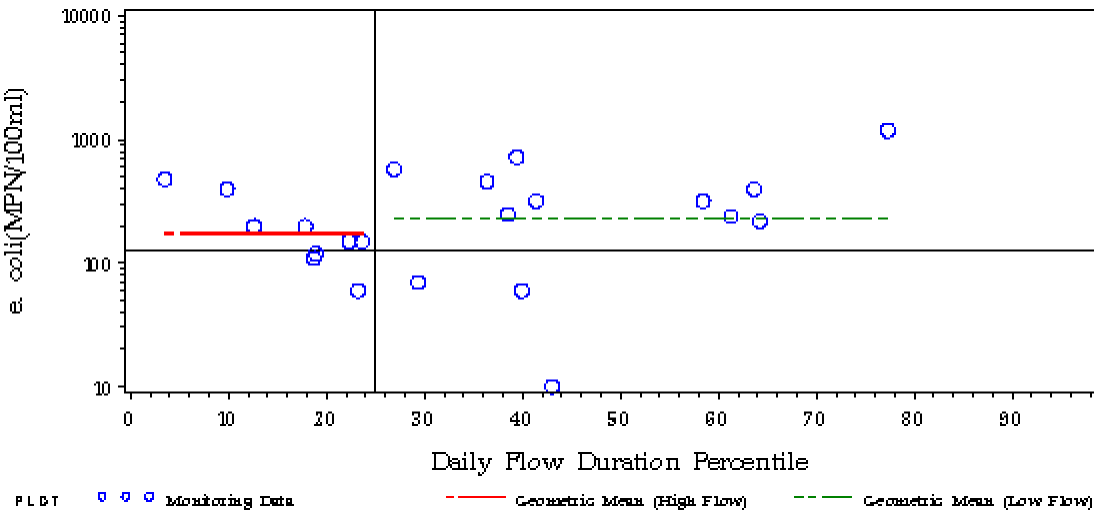

Figure B-5: *E. coli* Concentration vs. Flow Duration for the Upper Monocacy River Monitoring Station OWN0007

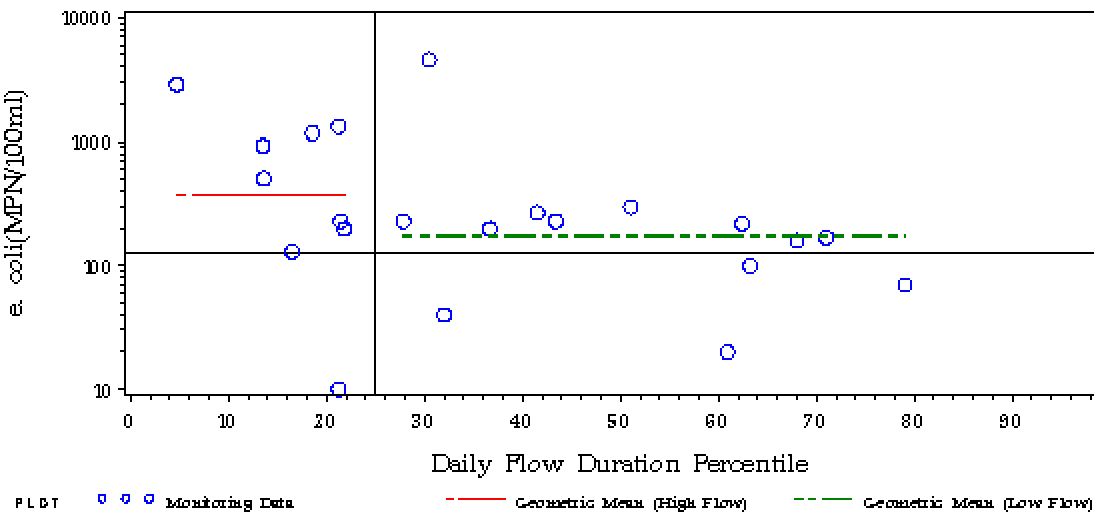

Figure B-6: *E. coli* Concentration vs. Flow Duration for the Upper Monocacy River Monitoring Station MON0355

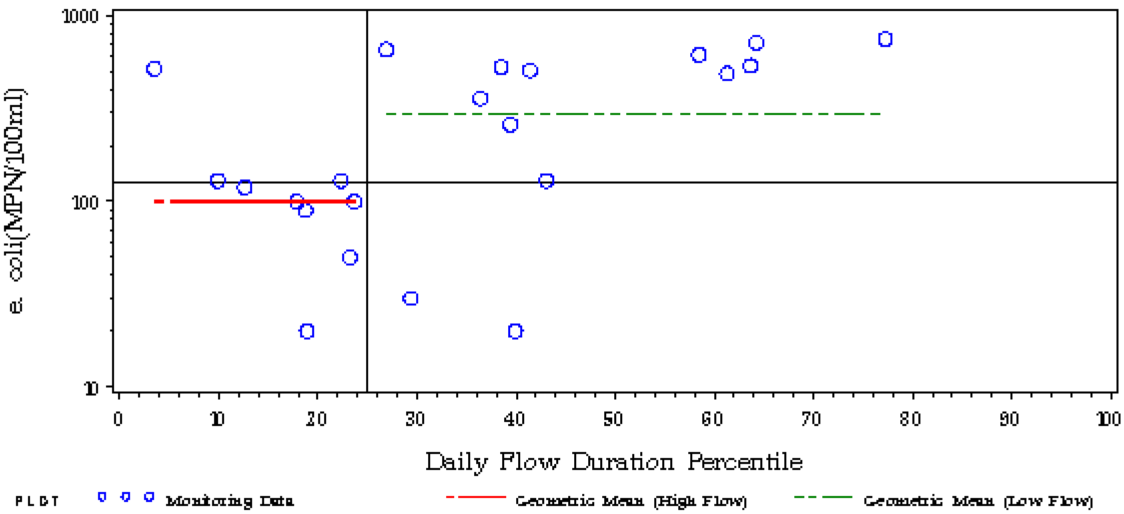

Figure B-7: *E. coli* Concentration vs. Flow Duration for the Upper Monocacy River Monitoring Station HUN0009

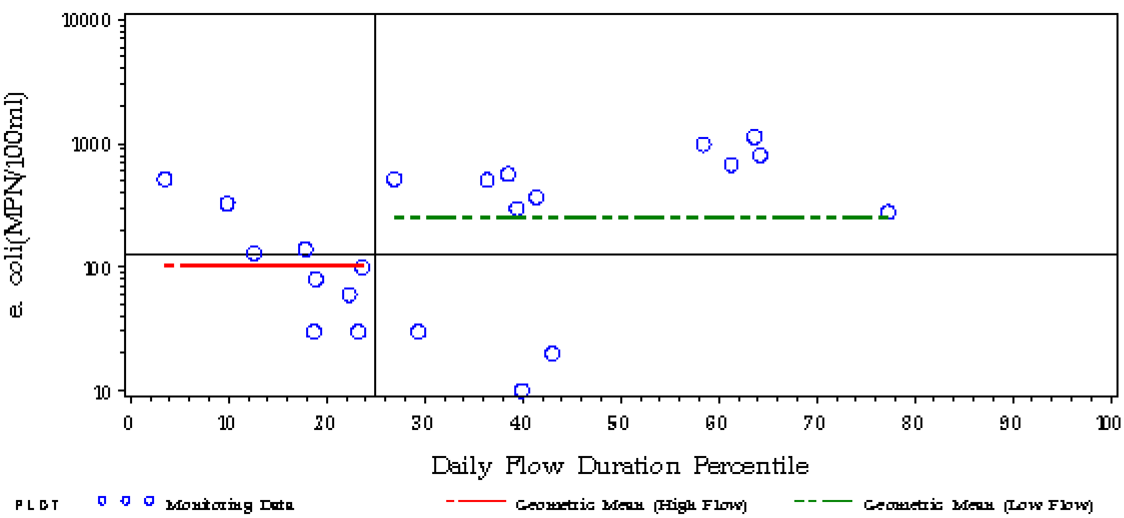

Figure B-8: *E. coli* Concentration vs. Flow Duration for the Upper Monocacy River Monitoring Station FIS0012

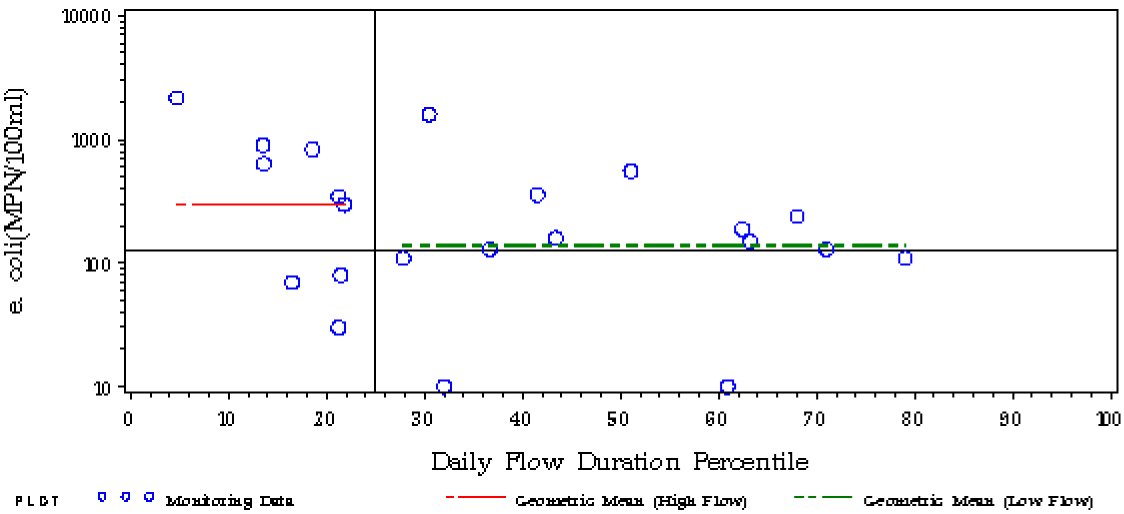

Figure B-9: *E. coli* Concentration vs. Flow Duration for the Upper Monocacy River Monitoring Station MON0269

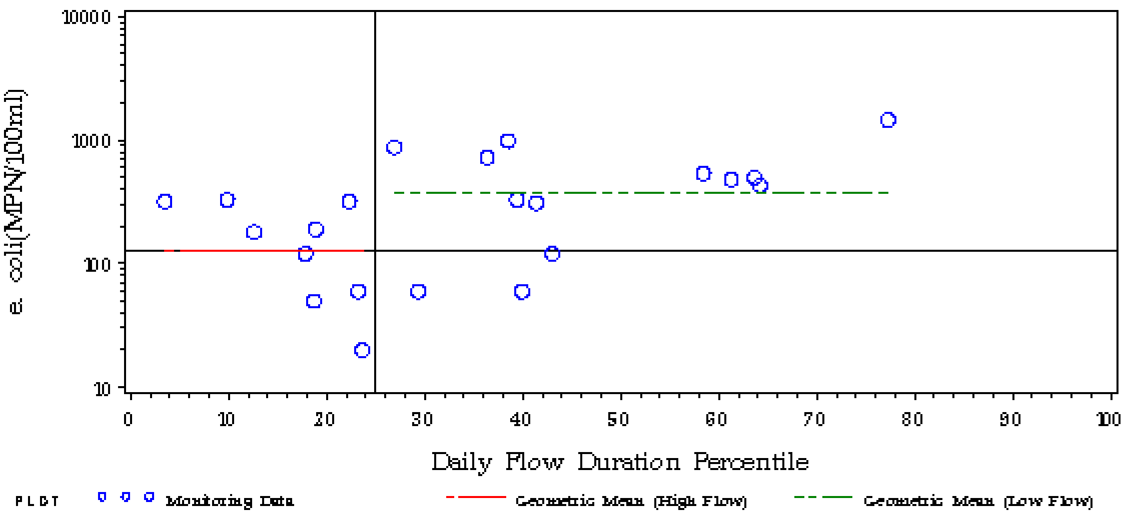

Figure B-10: *E. coli* Concentration vs. Flow Duration for the Upper Monocacy River Monitoring Station TUS0007

Appendix C – BST Report

Identifying Sources of Fecal Pollution in Upper Monocacy River Watershed, Maryland

June 2004 – October 2006

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Department of Biological Sciences and Environmental Health Science
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October 31, 2006

Table of Contents

INTRODUCTION

Microbial Source Tracking. Microbial Source Tracking (MST) is a relatively recent scientific and technological innovation designed to distinguish the origins of enteric microorganisms found in environmental waters. Several different methods and a variety of different indicator organisms (both bacteria and viruses) have successfully been used for MST, as described in recent reviews (Scott et al. 2002; Simpson et al. 2002). When the indicator organism is bacteria, the term Bacterial Source Tracking (BST) is often used. Some common bacterial indicators for BST analysis include: *E. coli, Enterococcus* spp., *Bacteroides-Prevotella,* and *Bifidobacterium* spp.

Techniques for MST can be grouped into one of the following three categories: molecular (genotypic) methods, biochemical (phenotypic) methods, or chemical methods. Ribotyping, Pulsed-Field Gel Electrophoresis (PFGE), and Randomly-Amplified Polymorphic DNA (RAPD) are examples of molecular techniques. Biochemical methods include Antibiotic Resistance Analysis (ARA), F-specific coliphage typing, and Carbon Source Utilization (CSU) analysis. Chemical techniques detect chemical compounds associated with human activities, but do not provide any information regarding nonhuman sources. Examples of this type of technology include detection of optical brighteners from laundry detergents or caffeine (Simpson et al., 2002).

Many of the molecular and biochemical methods of MST are “library-based,” requiring the collection of a database of fingerprints or patterns obtained from indicator organisms isolated from known sources. Statistical analysis determines fingerprints/patterns of known sources species or categories of species (i.e., human, livestock, pets, wildlife). Indicator isolates collected from water samples are analyzed using the same MST method to obtain their fingerprints or patterns, which are then statistically compared to those in the library. Based upon this comparison, the final results are expressed in terms of the “statistical probability” that the water isolates came from a given source (Simpson et al. 2002).

In this BST project, we studied the following Maryland nontidal watersheds: Antietam Creek, Concoheague Creek, Double Pipe Creek, Lower Monocacy River, and Upper Monocacy River. Also included in the study was the Potomac River Watershed shellfish harvesting area. The methodology used was the ARA with *Enterococcus* spp. as the indicator organism. Previous BST publications have demonstrated the predictive value of using this particular technique and indicator organism (Hagedorn 1999; Wiggins 1999). A pilot study using PFGE, a genotypic BST method, was used on a subset of known-source isolates collected from the Potomac River Watershed.

Antibiotic Resistance Analysis. A variety of different host species can potentially contribute to the fecal contamination found in natural waters. Many years ago, scientists speculated on the possibility of using resistance to antibiotics as a way of determining the sources of this fecal contamination (Bell et al. 1983; Krumperman 1983). In ARA, the premise is that bacteria isolated from different hosts can be discriminated based upon differences in the selective pressure of microbial populations found in the gastrointestinal tract of those hosts (humans, livestock, pets, wildlife) (Wiggins 1996). 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.

In ARA, isolates from known sources are tested for resistance or sensitivity against a panel of antibiotics and antibiotic concentrations. This information is then used to construct a library of antibiotic resistance patterns from known-source bacterial isolates. Microbial isolates collected from water samples are then tested and their resistance results are recorded. Based upon a comparison of resistance patterns of water and library isolates, a statistical analysis can predict the likely host source of the water isolates. (Hagedorn 1999; Wiggins 1999).

LABORATORY METHODS

Isolation of *Enterococcus* from Known-Source Samples. Fecal samples, identified to source, were delivered to the Salisbury University (SU) BST lab by Maryland Department of the Environment (MDE) personnel. Fecal material suspended in phosphate buffered saline was plated onto selective m-Enterococcus agar. After incubation at 37^{o} C, up to eight (8) *Enterococcus* isolates were randomly selected from each fecal sample for ARA testing.

Isolation of Enterococcus from Water Samples. Water samples were collected by MDE staff and shipped overnight to MapTech Inc, Blacksburg, Va. Bacterial isolates were collected by membrane filtration. Up to 24 randomly selected *Enterococcus* isolates were collected from each water sample and all isolates were then shipped to the SU BST lab.

Antibiotic Resistance Analysis. Each bacterial isolate from both water and scat were grown in Enterococcosel® broth (Becton Dickinson, Sparks, MD) prior to ARA testing. *Enterococci* are capable of hydrolyzing esculin, turning this broth black. Only esculin-positive isolates were tested for antibiotic resistance.

Bacterial isolates were plated onto tryptic soy agar plates, each containing a different concentration of a given antibiotic. Plates were incubated overnight at 37^{o} C and isolates then scored for growth (resistance) or no growth (sensitivity). Data consisting of a “1” for resistance or “0” for sensitivity for each isolate at each concentration of each antibiotic was then entered into a spread-sheet for statistical analysis.

The following table includes the antibiotics and concentrations used for isolates in analyses for all the study watersheds.

Table C-1. Antibiotics and concentrations used for ARA.

Antibiotic	Concentration (µg/ml)
Amoxicillin	0.625
Cephalothin	10, 15, 30, 50
Chloramphenicol	10
Chlortetracycline	60, 80, 100
Erythromycin	10
Gentamycin	5, 10, 15
Neomycin	40, 60, 80
Oxytetracycline	20, 40, 60, 80, 100
Salinomycin	10
Streptomycin	40, 60, 80, 100
Tetracycline	10, 30, 50, 100
Vancomycin	2.5

KNOWN-SOURCE LIBRARY

Construction and Use. Fecal samples (scat) from known sources in each watershed were collected during the study period by MDE personnel and delivered to the BST Laboratory at SU. *Enterococcus* isolates were obtained from known sources (e.g., human, dog, cow, horse, deer, fox, rabbit, and goose). For each watershed, a library of patterns of *Enterococcus* isolate responses to the panel of antibiotics was analyzed using the statistical software CART® (Salford Systems, San Diego, CA). *Enterococcus* isolate response patterns were also obtained from bacteria in water samples collected at the monitoring stations in each basin. Using statistical techniques, these patterns were then compared to those in the appropriate library to identify the probable source of each water isolate. A combined library of known sources was used for Antietam Creek and Concocheaque Creek Watersheds using patterns from scat obtained from both watersheds, and the water isolate patterns of each were compared to the combined library. A combined known-source library was also used for Double Pipe Creek, Lower Monocacy River, and Upper Monocacy River, with water isolate patterns of each compared to this combined library.

STATISTICAL ANALYSIS

We applied a tree classification method, [1]CART®, to build a model that classifies isolates into source categories based on ARA data. CART® builds a classification tree by recursively splitting the library of isolates into two nodes. Each split is determined by the antibiotic

variables (antibiotic resistance measured for a collection of antibiotics at varying concentrations). The first step in the tree-building process splits the library into two nodes by considering every binary split associated with every variable. The split is chosen that maximizes a specified index of homogeneity for isolate sources within each of the nodes. In subsequent steps, the same process is applied to each resulting node until a *stopping* criterion is satisfied. Nodes where an additional split would lead to only an insignificant increase in the *homogeneity index* relative to the *stopping* criterion are referred to as *terminal* nodes.[2] The collection of *terminal* nodes defines the classification model. Each *terminal* node is associated with one source, the source isolate with an unknown source), based that is most populous among the library isolates in the node. Each water sample isolate (i.e., an on its antibiotic resistance pattern, is identified with one specific *terminal* node and is assigned the source of the majority of library isolates in that *terminal* node.[3]

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1 The Elements of Statistical Learning: Data Mining, Inference, and Prediction. Hastie T, Tibshirani R, and Friedman J. Springer 2001.

2 An ideal split, i.e., a split that achieves the theoretical maximum for homogeneity, would produce two nodes each containing library isolates from only one source.

3 The CART® tree-classification method we employed includes various features to ensure the development of an optimal classification model. For brevity in exposition, we have chosen not to present details of those features, but suggest the following sources: Breiman L, et al. *Classification and Regression Trees*. Pacific Grove: Wadsworth, 1984; and Steinberg D and Colla P. *CART—Classification and Regression Trees.* San Diego, CA: Salford Systems, 1997.

Upper Monocacy River Watershed ARA Results

Known-Source Library. A 1,684 known-source isolate library was constructed that included 559 isolates from the Upper Monocacy River Watershed (UMO), combined with 571 isolates from sources in the Double Pipe Creek Watershed (DOP), and 554 isolates from the Lower Monocacy River Watershed (LMO). The known sources in the combined library were grouped into four categories: humans, livestock (cows and horses), pets (specifically dogs), and wildlife (deer, fox, goose, muskrat, and raccoon) (see Table C-2 UMO). The library was analyzed for its ability to take a subset of the library isolates and correctly predict the identity of their host sources when they were treated as unknowns. Average rates of correct classification (ARCC) for the library were found by repeating this analysis using several probability cutoff points, as described above. The number-not-classified for each probability was determined. From these results, the percent unknown and percent correct classification (RCCs) was calculated (Table C-3 UMO).

Table C-2: UMO: Upper Monocacy River. Category, total number, and number of unique patterns in the Upper Monocacy portion and in the combined DOP-LMO-UMO known-source library.

Category	Potential Sources	Total Isolates	Unique Patterns
Upper Monocacy River Library:			
human	human	135	92
livestock	horse, cow	175	70
pet	dog	86	52
wildlife	deer, fox, goose, muskrat, raccoon	163	47
Total		559	261
Double Pipe Creek Library:			
human	human	96	69
livestock	horse, cow	156	53
pet	dog	80	41
wildlife	deer, fox, goose, raccoon	239	78
Total		571	241
Lower Monocacy River Library:			
human	human	126	103
livestock	horse, cow	179	57
pet	dog	56	37
wildlife	deer, fox, goose, raccoon	193	44
Total		554	241

Combined DOP-LMO-UMO Library:

human	human	357	264
livestock	cow, horse	510	180
pet	dog	222	130
wildlife	deer, fox, goose, muskrat, raccoon	595	169
Total		1684	743

Table C-3: UMO: Upper Monocacy River. Number of isolates not classified, percent unknown, and percent correct for eight (8) threshold probabilities for UMO known-source isolates using the combined DOP-LMO- UMO known-source library.

Threshold	0	0.25	0.375	0.5	0.6	0.7	0.8	0.9
% correct	66.0%	66.0%	66.3%	70.9%	75.1%	81.5%	85.1%	86.0%
% unknown	0.0%	0.0%	3.9%	17.5%	48.3%	66.2%	78.4%	84.6%
# not classified	0	0	22	98	270	370	438	473

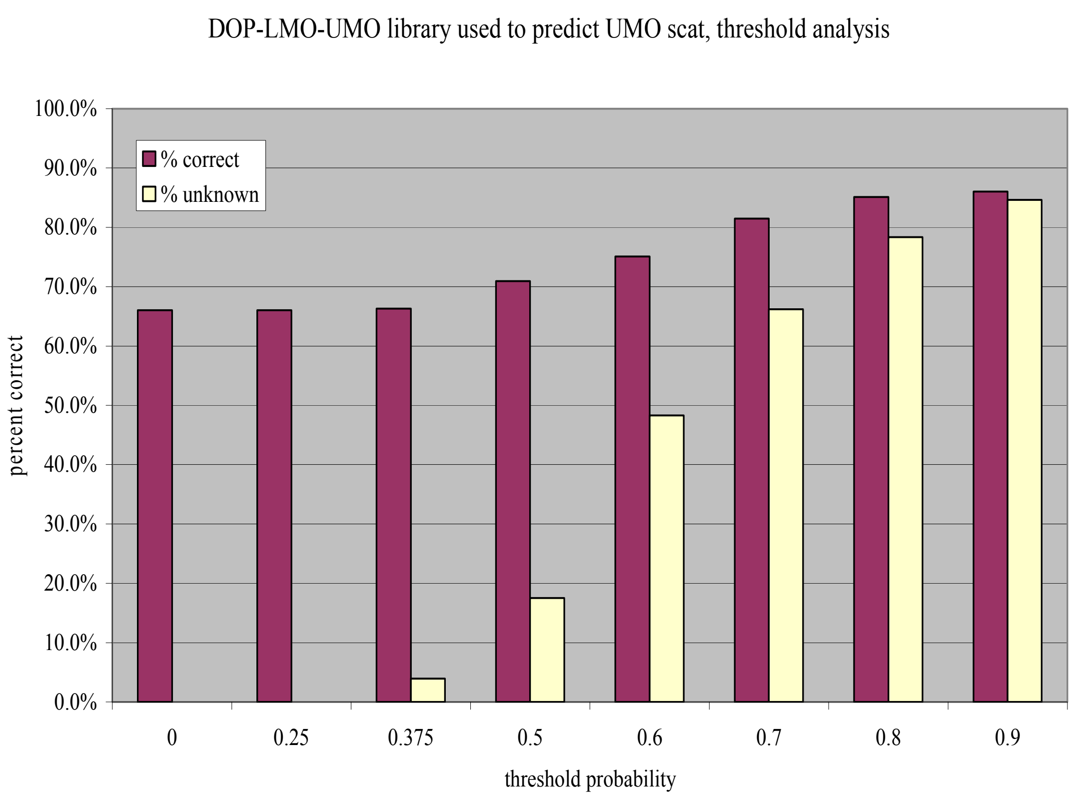


Figure C-2: UMO. Upper Monocacy Classification Model: Percent Correct versus Percent Unknown using a combined DOP-LMO-UMO library.

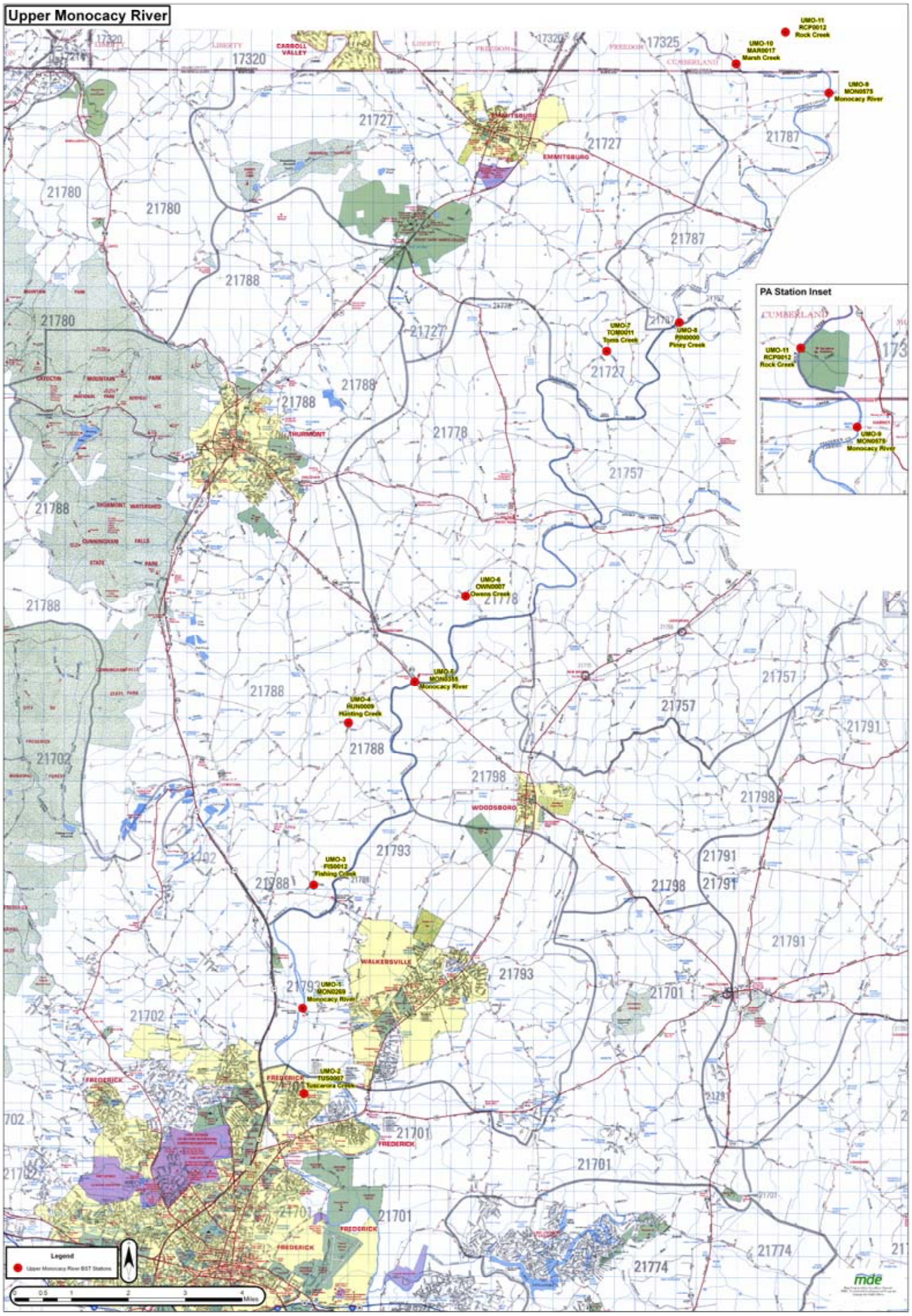
For the Upper Monocacy River Watershed, a cutoff probability of 0.50 (50%) was shown to yield an ARCC of 71% (Table C-3 UMO). The rates of correct classification for the four categories of sources in the Upper Monocacy River portion of the library, using the cutoff probability of 0.50 (50%), are shown in Table C-4 UMO below. The RCCs for human and pet are 88% and 87%, respectively, with 73% for wildlife, and 46% for livestock.

Table C-4: UMO: Upper Monocacy River. Actual species categories versus predicted categories, at 50% probability cutoff, with rates of correct classification (RCC) for each category.

	Predicted						
Actual	human	livestock	pet	wildlife	Unknown	Total	RCC*
human	101	6	6	2	20	135	87.8%
livestock	8	61	12	52	42	175	45.9%
pet	8	0	60	1	17	86	87.0%
wildlife	8	16	15	105	19	163	72.9%
Total	125	83	93	160	98	559	

*RCC = Actual number of predicted species category / Total number predicted.
Example: 163 pet correctly predicted / 175 total number predicted for pet = 163/175 = 93%.

Upper Monocacy River Water Samples. Monthly monitoring from 12 monitoring stations on Upper Monocacy River was the source of water samples (Figure C-2: UMO). The maximum number of *Enterococcus* isolates per water sample was 24, although the number of isolates that actually grew was sometimes fewer than 24. A total of 2,442 *Enterococcus* isolates were analyzed by statistical analysis. The BST results by species category, shown in Table C-5: UMO indicates that 69% of the water isolates were assigned to a probable host source when using a 0.50 (60%) probability cutoff.



Note: Red dots indicate water monitoring sites.

Figure C-2: UMO. Map of the Upper Monocacy River Watershed.

Table C-5: UMO: Probable host source distribution of water isolates by species category, based on DOP-LMO-UMO combination library model with a 50% threshold probability.

Category	Number	% assigned to category 50% Prob.	% assigned to category (excluding unknowns)
human	243	10.0%	14.3%
livestock	458	18.8%	27.0%
pet	617	25.3%	36.4%
wildlife	376	15.4%	22.2%
unknown	748	30.6%	
Total	2442	100.0%	100.0%
% classified	**69%**		

The seasonal distribution of water isolates from samples collected at each sampling station is shown below in Table C-6: UMO.

Table C-6: UMO: Upper Monocacy River. *Enterococcus* isolates obtained from water collected during the spring, summer, fall, and winter seasons, by monitoring station.

	Season				
Station	Spring	Summer	Fall	Winter	Total
FIS0012	54	70	62	42	228
HUN0009	60	62	64	39	225
MAR0017	51	46	51	57	205
MAR0018	0	0	1	0	1
MON0269	41	52	65	48	206
MON0355	49	37	72	54	212
MON0575	58	59	59	45	221
OWN0007	57	72	67	45	241
PIN0000	54	55	66	47	222
RCP0012	51	49	55	58	213
TOM0011	55	68	69	47	239
TUS0007	65	72	57	35	229
Total	595	642	688	517	2442

Tables C-7: UMO and C-8: UMO (below) show the number and percent of the probable sources for each monitoring station by month.

Table C-7: UMO: Upper Monocacy River. BST Analysis: Number of Isolates per Station per Date.

		Predicted Source					
Station	Date	Human	Livestock	Pet	Wildlife	Unknown	Total
FIS0012	11/17/03	0	2	0	12	1	15
FIS0012	12/01/03	6	4	6	1	6	23
FIS0012	01/06/04	4	3	4	5	2	18
FIS0012	02/04/04	6	7	8	0	3	24
FIS0012	04/06/04	1	0	0	4	1	6
FIS0012	05/11/04	1	9	5	4	5	24
FIS0012	06/08/04	0	0	2	0	22	24
FIS0012	07/07/04	0	4	0	0	18	22
FIS0012	08/10/04	2	1	1	8	12	24
FIS0012	09/08/04	1	3	14	4	2	24
FIS0012	10/05/04	2	2	9	0	11	24
HUN0009	11/17/03	0	4	7	6	3	20
HUN0009	12/01/03	2	3	10	2	4	21
HUN0009	01/06/04	4	1	2	3	7	17
HUN0009	02/04/04	8	3	5	2	0	18
HUN0009	03/02/04	0	2	1	0	1	4
HUN0009	04/06/04	1	2	3	1	5	12
HUN0009	05/11/04	1	7	3	7	6	24
HUN0009	06/08/04	0	0	3	0	21	24
HUN0009	07/07/04	4	2	3	2	3	14
HUN0009	08/10/04	4	4	5	5	6	24
HUN0009	09/08/04	1	2	14	1	6	24
HUN0009	10/05/04	1	2	10	2	8	23
MAR0017	11/17/03	2	5	0	6	1	14
MAR0017	12/01/03	0	5	1	6	3	15
MAR0017	01/06/04	2	2	2	4	8	18
MAR0017	02/04/04	2	5	11	0	6	24
MAR0017	03/02/04	0	3	1	0	11	15
MAR0017	04/06/04	0	1	3	2	3	9
MAR0017	05/11/04	0	2	0	6	10	18
MAR0017	06/08/04	2	2	13	3	4	24
MAR0017	07/07/04	0	1	2	1	8	12
MAR0017	08/10/04	0	0	1	0	9	10
MAR0017	09/08/04	3	1	11	1	8	24
MAR0017	10/05/04	2	2	6	5	7	22
MON0269	11/17/03	1	3	2	5	6	17
MON0269	12/01/03	4	10	7	1	2	24
MON0269	01/06/04	4	3	7	4	4	22
MON0269	02/04/04	2	3	10	5	2	22
MON0269	03/02/04	0	2	0	0	2	4
MON0269	04/06/04	1	1	5	0	1	8
MON0269	05/11/04	0	3	1	3	2	9

		Predicted Source					
Station	Date	Human	Livestock	Pet	Wildlife	Unknown	Total
MON0269	06/08/04	1	0	5	2	16	24
MON0269	07/07/04	0	0	1	0	4	5
MON0269	08/10/04	1	11	1	5	6	24
MON0269	09/08/04	0	1	4	5	13	23
MON0269	10/05/04	0	3	8	4	9	24
MON0355	11/17/03	0	1	8	4	11	24
MON0355	12/01/03	8	6	4	3	3	24
MON0355	01/06/04	6	7	6	2	0	21
MON0355	02/04/04	4	7	9	0	3	23
MON0355	03/02/04	1	4	2	1	2	10
MON0355	04/06/04	1	2	2	3	2	10
MON0355	05/11/04	0	5	1	7	2	15
MON0355	06/08/04	0	5	7	2	10	24
MON0355	07/07/04	2	0	0	0	1	3
MON0355	08/10/04	1	0	0	9	2	12
MON0355	09/08/04	0	0	18	0	4	22
MON0355	10/05/04	0	3	4	3	14	24
MON0575	11/17/03	2	1	3	6	6	18
MON0575	12/01/03	1	6	0	10	3	20
MON0575	01/06/04	2	4	2	7	2	17
MON0575	02/04/04	5	6	2	1	10	24
MON0575	03/02/04	0	1	3	0	0	4
MON0575	04/06/04	0	0	1	7	2	10
MON0575	05/11/04	8	3	8	0	5	24
MON0575	06/08/04	2	0	16	3	3	24
MON0575	07/07/04	0	5	5	0	1	11
MON0575	08/10/04	4	3	3	5	9	24
MON0575	09/08/04	0	5	7	2	10	24
MON0575	10/05/04	0	4	4	3	10	21
OWN0007	11/17/03	2	2	7	6	5	22
OWN0007	12/01/03	1	5	12	1	2	21
OWN0007	01/06/04	0	1	4	5	7	17
OWN0007	02/04/04	8	1	7	2	4	22
OWN0007	03/02/04	0	0	0	3	3	6
OWN0007	04/06/04	1	7	0	1	1	10
OWN0007	05/11/04	5	1	6	0	11	23
OWN0007	06/08/04	6	5	5	1	7	24
OWN0007	07/07/04	1	4	8	6	5	24
OWN0007	08/10/04	1	4	6	5	8	24
OWN0007	09/08/04	1	0	16	3	4	24
OWN0007	10/05/04	1	2	11	1	9	24
PIN0000	11/17/03	0	3	7	6	2	18
PIN0000	12/01/03	0	16	2	3	3	24

		Predicted Source					
Station	**Date**	**Human**	**Livestock**	**Pet**	**Wildlife**	**Unknown**	**Total**
PIN0000	01/06/04	4	6	5	2	3	20
PIN0000	02/04/04	14	2	7	1	0	24
PIN0000	03/02/04	0	0	0	1	2	3
PIN0000	04/06/04	0	4	0	2	3	9
PIN0000	05/11/04	0	2	1	2	16	21
PIN0000	06/08/04	3	2	9	3	7	24
PIN0000	07/07/04	0	1	6	1	2	10
PIN0000	08/10/04	0	4	1	4	12	21
PIN0000	09/08/04	1	1	15	1	6	24
PIN0000	10/05/04	3	2	7	1	11	24
RCP0012	11/17/03	4	0	1	10	3	18
RCP0012	12/01/03	0	2	1	8	3	14
RCP0012	01/06/04	8	6	3	3	3	23
RCP0012	02/04/04	2	1	4	2	11	20
RCP0012	03/02/04	1	5	2	1	6	15
RCP0012	04/06/04	1	0	3	1	0	5
RCP0012	05/11/04	4	0	8	3	7	22
RCP0012	06/08/04	4	2	3	2	13	24
RCP0012	07/07/04	1	2	2	0	10	15
RCP0012	08/10/04	0	2	1	4	3	10
RCP0012	09/08/04	3	19	0	0	2	24
RCP0012	10/05/04	0	4	8	4	7	23
TOM0011	11/17/03	6	7	4	3	4	24
TOM0011	12/01/03	6	4	5	4	2	21
TOM0011	01/06/04	2	3	8	1	4	18
TOM0011	02/04/04	4	7	3	3	5	22
TOM0011	03/02/04	1	1	0	2	3	7
TOM0011	04/06/04	3	3	0	1	0	7
TOM0011	05/11/04	2	10	2	3	7	24
TOM0011	06/08/04	1	1	11	0	11	24
TOM0011	07/07/04	0	8	0	2	10	20
TOM0011	08/10/04	1	7	3	2	11	24
TOM0011	09/08/04	4	4	10	0	6	24
TOM0011	10/05/04	0	3	3	9	9	24
TUS0007	11/17/03	0	1	5	3	1	10
TUS0007	12/01/03	3	2	13	3	2	23
TUS0007	01/06/04	2	3	1	4	2	12
TUS0007	02/04/04	0	13	6	0	1	20
TUS0007	03/02/04	0	1	0	1	1	3
TUS0007	04/06/04	2	3	8	1	10	24
TUS0007	05/11/04	0	11	1	4	7	23
TUS0007	06/08/04	1	2	4	0	11	18
TUS0007	07/07/04	0	8	1	6	9	24

		Predicted Source					
Station	**Date**	**Human**	**Livestock**	**Pet**	**Wildlife**	**Unknown**	**Total**
TUS0007	08/10/04	2	14	2	6	0	24
TUS0007	09/08/04	0	7	4	3	10	24
TUS0007	10/05/04	0	3	12	1	8	24
Total		243	458	617	376	748	2442

Table C-8: UMO. Upper Monocacy River. BST Analysis: Percentage of Sources per Station per Date.

		Predicted Source					
Station	**Date**	**Human**	**Livestock**	**Pet**	**Wildlife**	**Unknown**	**Total**
FIS0012	11/17/03	0%	13%	0%	80%	7%	100%
FIS0012	12/01/03	26%	17%	26%	4%	26%	100%
FIS0012	01/06/04	22%	17%	22%	28%	11%	100%
FIS0012	02/04/04	25%	29%	33%	0%	13%	100%
FIS0012	04/06/04	17%	0%	0%	67%	17%	100%
FIS0012	05/11/04	4%	38%	21%	17%	21%	100%
FIS0012	06/08/04	0%	0%	8%	0%	92%	100%
FIS0012	07/07/04	0%	18%	0%	0%	82%	100%
FIS0012	08/10/04	8%	4%	4%	33%	50%	100%
FIS0012	09/08/04	4%	13%	58%	17%	8%	100%
FIS0012	10/05/04	8%	8%	38%	0%	46%	100%
HUN0009	11/17/03	0%	20%	35%	30%	15%	100%
HUN0009	12/01/03	10%	14%	48%	10%	19%	100%
HUN0009	01/06/04	24%	6%	12%	18%	41%	100%
HUN0009	02/04/04	44%	17%	28%	11%	0%	100%
HUN0009	03/02/04	0%	50%	25%	0%	25%	100%
HUN0009	04/06/04	8%	17%	25%	8%	42%	100%
HUN0009	05/11/04	4%	29%	13%	29%	25%	100%
HUN0009	06/08/04	0%	0%	13%	0%	88%	100%
HUN0009	07/07/04	29%	14%	21%	14%	21%	100%
HUN0009	08/10/04	17%	17%	21%	21%	25%	100%
HUN0009	09/08/04	4%	8%	58%	4%	25%	100%
HUN0009	10/05/04	4%	9%	43%	9%	35%	100%
MAR0017	11/17/03	14%	36%	0%	43%	7%	100%
MAR0017	12/01/03	0%	33%	7%	40%	20%	100%
MAR0017	01/06/04	11%	11%	11%	22%	44%	100%
MAR0017	02/04/04	8%	21%	46%	0%	25%	100%
MAR0017	03/02/04	0%	20%	7%	0%	73%	100%
MAR0017	04/06/04	0%	11%	33%	22%	33%	100%
MAR0017	05/11/04	0%	11%	0%	33%	56%	100%
MAR0017	06/08/04	8%	8%	54%	13%	17%	100%
MAR0017	07/07/04	0%	8%	17%	8%	67%	100%

		Predicted Source					
Station	**Date**	**Human**	**Livestock**	**Pet**	**Wildlife**	**Unknown**	**Total**
MAR0017	08/10/04	0%	0%	10%	0%	90%	100%
MAR0017	09/08/04	13%	4%	46%	4%	33%	100%
MAR0017	10/05/04	9%	9%	27%	23%	32%	100%
MON0269	11/17/03	6%	18%	12%	29%	35%	100%
MON0269	12/01/03	17%	42%	29%	4%	8%	100%
MON0269	01/06/04	18%	14%	32%	18%	18%	100%
MON0269	02/04/04	9%	14%	45%	23%	9%	100%
MON0269	03/02/04	0%	50%	0%	0%	50%	100%
MON0269	04/06/04	13%	13%	63%	0%	13%	100%
MON0269	05/11/04	0%	33%	11%	33%	22%	100%
MON0269	06/08/04	4%	0%	21%	8%	67%	100%
MON0269	07/07/04	0%	0%	20%	0%	80%	100%
MON0269	08/10/04	4%	46%	4%	21%	25%	100%
MON0269	09/08/04	0%	4%	17%	22%	57%	100%
MON0269	10/05/04	0%	13%	33%	17%	38%	100%
MON0355	11/17/03	0%	4%	33%	17%	46%	100%
MON0355	12/01/03	33%	25%	17%	13%	13%	100%
MON0355	01/06/04	29%	33%	29%	10%	0%	100%
MON0355	02/04/04	17%	30%	39%	0%	13%	100%
MON0355	03/02/04	10%	40%	20%	10%	20%	100%
MON0355	04/06/04	10%	20%	20%	30%	20%	100%
MON0355	05/11/04	0%	33%	7%	47%	13%	100%
MON0355	06/08/04	0%	21%	29%	8%	42%	100%
MON0355	07/07/04	67%	0%	0%	0%	33%	100%
MON0355	08/10/04	8%	0%	0%	75%	17%	100%
MON0355	09/08/04	0%	0%	82%	0%	18%	100%
MON0355	10/05/04	0%	13%	17%	13%	58%	100%
MON0575	11/17/03	11%	6%	17%	33%	33%	100%
MON0575	12/01/03	5%	30%	0%	50%	15%	100%
MON0575	01/06/04	12%	24%	12%	41%	12%	100%
MON0575	02/04/04	21%	25%	8%	4%	42%	100%
MON0575	03/02/04	0%	25%	75%	0%	0%	100%
MON0575	04/06/04	0%	0%	10%	70%	20%	100%
MON0575	05/11/04	33%	13%	33%	0%	21%	100%
MON0575	06/08/04	8%	0%	67%	13%	13%	100%
MON0575	07/07/04	0%	45%	45%	0%	9%	100%
MON0575	08/10/04	17%	13%	13%	21%	38%	100%
MON0575	09/08/04	0%	21%	29%	8%	42%	100%
MON0575	10/05/04	0%	19%	19%	14%	48%	100%
OWN0007	11/17/03	9%	9%	32%	27%	23%	100%
OWN0007	12/01/03	5%	24%	57%	5%	10%	100%
OWN0007	01/06/04	0%	6%	24%	29%	41%	100%
OWN0007	02/04/04	36%	5%	32%	9%	18%	100%

		Predicted Source					
Station	**Date**	**Human**	**Livestock**	**Pet**	**Wildlife**	**Unknown**	**Total**
OWN0007	03/02/04	0%	0%	0%	50%	50%	100%
OWN0007	04/06/04	10%	70%	0%	10%	10%	100%
OWN0007	05/11/04	22%	4%	26%	0%	48%	100%
OWN0007	06/08/04	25%	21%	21%	4%	29%	100%
OWN0007	07/07/04	4%	17%	33%	25%	21%	100%
OWN0007	08/10/04	4%	17%	25%	21%	33%	100%
OWN0007	09/08/04	4%	0%	67%	13%	17%	100%
OWN0007	10/05/04	4%	8%	46%	4%	38%	100%
PIN0000	11/17/03	0%	17%	39%	33%	11%	100%
PIN0000	12/01/03	0%	67%	8%	13%	13%	100%
PIN0000	01/06/04	20%	30%	25%	10%	15%	100%
PIN0000	02/04/04	58%	8%	29%	4%	0%	100%
PIN0000	03/02/04	0%	0%	0%	33%	67%	100%
PIN0000	04/06/04	0%	44%	0%	22%	33%	100%
PIN0000	05/11/04	0%	10%	5%	10%	76%	100%
PIN0000	06/08/04	13%	8%	38%	13%	29%	100%
PIN0000	07/07/04	0%	10%	60%	10%	20%	100%
PIN0000	08/10/04	0%	19%	5%	19%	57%	100%
PIN0000	09/08/04	4%	4%	63%	4%	25%	100%
PIN0000	10/05/04	13%	8%	29%	4%	46%	100%
RCP0012	11/17/03	22%	0%	6%	56%	17%	100%
RCP0012	12/01/03	0%	14%	7%	57%	21%	100%
RCP0012	01/06/04	35%	26%	13%	13%	13%	100%
RCP0012	02/04/04	10%	5%	20%	10%	55%	100%
RCP0012	03/02/04	7%	33%	13%	7%	40%	100%
RCP0012	04/06/04	20%	0%	60%	20%	0%	100%
RCP0012	05/11/04	18%	0%	36%	14%	32%	100%
RCP0012	06/08/04	17%	8%	13%	8%	54%	100%
RCP0012	07/07/04	7%	13%	13%	0%	67%	100%
RCP0012	08/10/04	0%	20%	10%	40%	30%	100%
RCP0012	09/08/04	13%	79%	0%	0%	8%	100%
RCP0012	10/05/04	0%	17%	35%	17%	30%	100%
TOM0011	11/17/03	25%	29%	17%	13%	17%	100%
TOM0011	12/01/03	29%	19%	24%	19%	10%	100%
TOM0011	01/06/04	11%	17%	44%	6%	22%	100%
TOM0011	02/04/04	18%	32%	14%	14%	23%	100%
TOM0011	03/02/04	14%	14%	0%	29%	43%	100%
TOM0011	04/06/04	43%	43%	0%	14%	0%	100%
TOM0011	05/11/04	8%	42%	8%	13%	29%	100%
TOM0011	06/08/04	4%	4%	46%	0%	46%	100%
TOM0011	07/07/04	0%	40%	0%	10%	50%	100%
TOM0011	08/10/04	4%	29%	13%	8%	46%	100%
TOM0011	09/08/04	17%	17%	42%	0%	25%	100%
TOM0011	10/05/04	0%	13%	13%	38%	38%	100%

			Predicted Source				
Station	**Date**	**Human**	**Livestock**	**Pet**	**Wildlife**	**Unknown**	**Total**
TUS0007	11/17/03	0%	10%	50%	30%	10%	100%
TUS0007	12/01/03	13%	9%	57%	13%	9%	100%
TUS0007	01/06/04	17%	25%	8%	33%	17%	100%
TUS0007	02/04/04	0%	65%	30%	0%	5%	100%
TUS0007	03/02/98	0%	0%	0%	0%	100%	100%
TUS0007	03/02/99	0%	100%	0%	0%	0%	100%
TUS0007	03/02/00	0%	0%	0%	100%	0%	100%
TUS0007	04/06/04	8%	13%	33%	4%	42%	100%
TUS0007	05/11/04	0%	48%	4%	17%	30%	100%
TUS0007	06/08/04	6%	11%	22%	0%	61%	100%
TUS0007	07/07/04	0%	33%	4%	25%	38%	100%
TUS0007	08/10/04	8%	58%	8%	25%	0%	100%
TUS0007	09/08/04	0%	29%	17%	13%	42%	100%
TUS0007	10/05/04	0%	13%	50%	4%	33%	100%

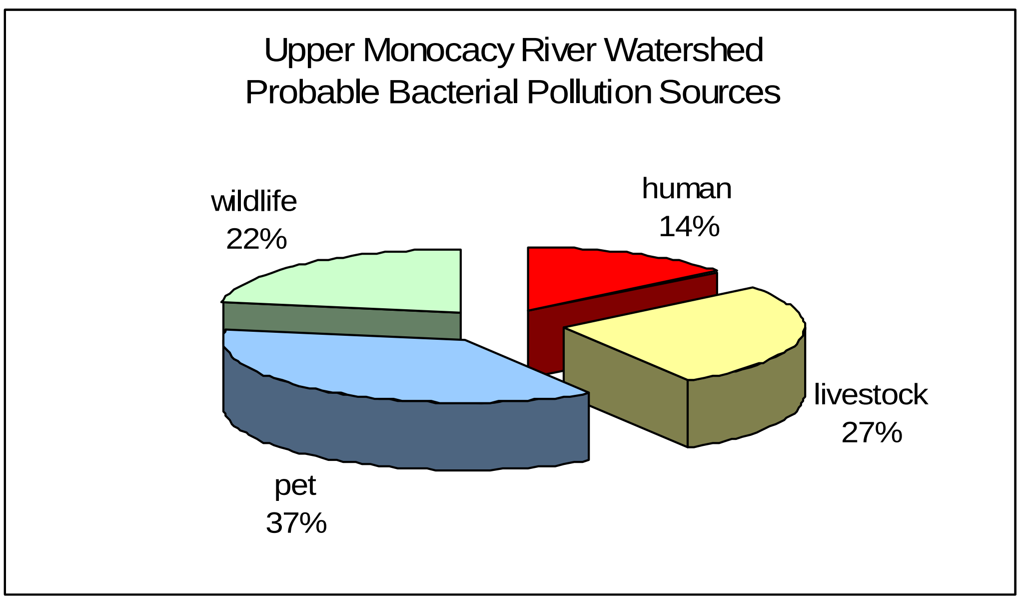


Figure C-3: Upper Monocacy River Watershed relative contributions by probable sources of *Enterococcus* contamination.

Upper Monocacy River Summary

The use of ARA allowed the identification of probable bacterial sources in the Upper Monocacy River Watershed for source categories in the library. When water isolates were compared to the library and potential sources predicted, 69% of the isolates were classified by statistical analysis. The largest category of potential sources in the watershed as a whole was pet (37%), followed by livestock (27%), human (14%), and wildlife (22%).

REFERENCES

Bell, J.B., Elliott, G.E. & Smith, D.W. 1983. Influence of Sewage Treatment an Urbanization on Selection of Multiple Resistance in Fecal Coliform Populations. *Appl. Environ. Microbiol.* 46, 227-32.

Department of Health and Human Services. Centers for Disease Control and Prevention. Pulsenet. 2006. "National Molecular Subtyping Network for Foodborne Disease Surveillance" http://www.cdc.gov/pulsenet [Available 01.26.06].

Hagedorn, C., Robinson, S.L., Filtz, J.R., Grubbs, S.M., Angier, T.A. & Beneau, R.B. 1999. Determining Sources of Fecal Pollution in a Rural Virginia Watershed with Antibiotic Resistance Patterns in Fecal Streptococci. *Appl. Environ. Microbiol.* 65, 5522-5531.

Krumperman, P.H. 1983. Multiple Antibiotic Resistance Indexing of *Escherichia coli* to Identify High-Risk Sources of Fecal Contamination of Foods. *Appl. Environ. Microbiol.* 46, 165-70.

Scott, T.M., Rose, J.B., Jenkins, T.M., Farrah, S.R. & Lukasik, J. 2002 Microbial Source Tracking: Current Methodology and Future Directions. *Appl. Environ. Microbiol.* 68(12), 3373-3385.

Simpson, J.M., Santo Domingo, J.W. & Reasoner, D.J. 2002 Microbial Source Tracking: State of the Science. *Environ. Sci. Technol.* 36(24), 5279-5288.

Wiggins, B.A. 1996. Discriminant Analysis of Antibiotic Resistance Patterns in Fecal Streptococci, a Method to Differentiate Human and Animal Sources of Fecal Pollution in Natural Waters. *Appl. Environ. Microbiol.* 62, 3997-4002.

Wiggins, B.A., Andrews, R.W., Conway, R.A., Corr, C.L., Dobratz, E. J., Dougherty, D.P., Eppard, J.R., Knupp, S.R., Limjoco, M.C., Mettenburg, J.M., Rinehardt, J.M., Sonsino, J., Torrijos, R.L. & Zimmerman, M.E. 1999. Use of Antibiotic Resistance Analysis to Identify Nonpoint Sources of Fecal Pollution. *Appl. Environ. Microbiol.* 65, 3483-3486.

ACKNOWLEDGEMENTS

We wish to thank the Richard A. Henson School of Science and Technology of Salisbury University, Salisbury, MD for its support. We also want to acknowledge Dr. Bertram Price and Joshua Greenberg of Price Associates, Inc., for their contributions to the statistical analysis in this project.

Appendix D – Estimating Maximum Daily Loads

This appendix documents the technical approach used to define maximum daily loads of fecal bacteria consistent with the annual average TMDL which, when met, are protective of water quality standards in Upper Monocacy River. The approach builds upon the TMDL analysis that was conducted to ensure that compliance with the annual average target will result in compliance with the applicable water quality standards. The annual average loading target was converted into allowable *daily* values by using the loadings developed from the TMDL analysis. The approach is consistent with available EPA guidance on generating daily loads for TMDLs.

The available guidance for developing daily loads does not specify a single allowable approach; it contains a range of options. Selection of a specific method for translating a time-series of allowable loads into expression of a TMDL requires decisions regarding both the level of resolution (e.g., single daily load for all conditions vs. loads that vary with environmental conditions) and level of probability associated with the TMDL.

Level of Resolution

The level of resolution pertains to the amount of detail used in specifying the maximum daily load. The draft EPA guidance on daily loads provides three categories of options for level of resolution.

1. **Representative daily load:** In this option, a single daily load (or multiple representative daily loads) is specified that covers all time periods and environmental conditions.
2. **Flow-variable daily load:** This option allows the maximum daily load to vary based upon the observed flow condition.
3. **Temporally-variable daily load:** This option allows the maximum daily load to vary based upon seasons or times of varying source or water body behavior.

Probability Level

Essentially all TMDLs have some probability of being exceeded, with the specific probability being either explicitly specified or implicitly assumed. This level of probability reflects, directly or indirectly, two separate phenomena:

1. Water quality criteria consist of components describing acceptable magnitude, duration, and frequency. The frequency component addresses how often conditions can allowably surpass the combined magnitude and duration components.
2. Pollutant loads, especially from wet weather sources, typically exhibit a large degree of variability over time. It is rarely practical to specify a "never to be exceeded value" for a daily load, as essentially any loading value has some finite probability of being exceeded.

The draft daily load guidance states that the probability component of the maximum daily load should be "based on a representative statistical measure" that is dependent upon the specific TMDL and best professional judgment of the developers. This statistical measure represents how often the maximum daily load is expected/allowed to be exceeded. The primary options for selecting this level of protection would be:

1. **The maximum daily load reflects some central tendency:** In this option, the maximum daily load is based upon the mean or median value of the range of loads expected to occur. The variability in the actual loads is not addressed.
2. **The maximum daily load reflects a level of protection implicitly provided by the selection of some "critical" period**: In this option, the maximum daily load is based upon the allowable load that is predicted to occur during some critical period examined during the analysis. The developer does not explicitly specify the probability of occurrence.
3. **The maximum daily load is a value that will be exceeded with a pre-defined probability:** In this option, a "reasonable" upper bound percentile is selected for the maximum daily load based upon a characterization of the variability of daily loads. For example, selection of the 95th percentile value would result in a maximum daily load that would be exceeded 5% of the time.

Selected Approach for Defining Maximum Daily Loads for Nonpoint Sources and MS4

Four of the nine subwatersheds of the Upper Monocacy River are located within both MD and PA. Bacteria concentrations and loads for the entire subwatershed are measured at the outlet of each subwatershed. Therefore, for computational purposes the parameters needed to estimate maximum daily loads will be calculated for each subwatershed regardless of whether it is totally or partially located in MD. Calculations of maximun daily loads for all nine subwatersheds are presented below; however, only the MDLs for the subwatershed portions located in MD are presented in the MDL table (Table D-5). MDLs for the MD portion of the watershed in those subwatersheds partially located in PA were calculated using the ratios of the areas of the subwatershed in MD and in PA to the total area of the subwatershed.

To calculate the Upper Monocacy River MDL for nonpoint sources and MS4, a "representative daily load" option was selected as the level of resolution, and a value "that will be exceeded with a pre-defined probability" was selected as the level of protection. In these options, the maximum daily load is one single daily load that covers to the two flow strata, with an upper bound percentile that accounts for the variability of daily loads. The upper bound percentile and the maximum daily loads were estimated following EPA's "*Technical Support Document for Water Quality-Based Toxics Control*" (1991 TSD) (EPA 1991); and "*Approaches For Developing a Daily Load Expression for TMDLs Computed for Longer Term Averages*" (EPA 2006).

The 1991 TSD illustrates a way to identify a target maximum daily concentration from a long-term average concentration (LTA) based on a coefficient of variation (CV) and the assumption of a log-normal distribution of the data. The equations for determining both the upper boundary percentile and corresponding maximum daily load described in the TSD are as follows:

$$MDLC = LTA * e^{[Z\sigma - 0.5\sigma^2]} \qquad \text{(D1)}$$

and $$MDL = MDLC*Q*F \qquad \text{(D2)}$$

where

MDLC = Maximum daily load concentration (MPN/100ml)

LTAC = Long-term average TMDL concentration (MPN/100ml)

MDL = Maximum Daily Load (MPN/day)

Z = z-score associated with upper bound percentile (unitless)

$\sigma^2 = \ln(CV^2 + 1)$

CV = Coefficient of variation

Q = Flow (cfs)

F = conversion factor

The first step is to use the bacteria monitoring data to estimate the upper bound percentile as the percentile of the highest observed bacteria concentration in each of the three monitoring stations of the Upper Monocacy River. Using the maximum value of *E. coli* observed in each monitoring station, and solving for the z-score using the above formula, the value of "z" and its corresponding percentile is found as shown below. The percentile associated with the particular value of z can be found in tables in statistics books or using the function NORMSINV(%) in EXCEL©.

$$Z = [\log_{10}(MOC) - \log(AM) + 0.5\sigma^2]/\sigma$$

Where

Z = z-score associated with upper bound percentile

MOC = Maximum observed bacteria concentration (MPN/100ml)

AM = Arithmetic mean observed bacteria concentrations (MPN/100ml)

$\sigma^2 = \ln(CV^2 + 1)$

CV = Coefficient of variation (arithmetic)

Note that these equations use arithmetic parameters, not geometric parameters as used in the calculations of the long-term annual average TMDL. Therefore, bias correction factors are not necessary to estimate the loads as will be explained below.

The highest percentile of all the stations analyzed by stratum will define the upper bound percentile to be used in estimating the maximum daily limits. As explained in Section 4.6, the value with the highest percentile by stratum was observed at the MON0355 station. In the case of Upper Monocacy River, a value measured during low-flow conditions at the MON0355 station resulted in the highest percentile of all three stations and strata. This value translates to the 99.7^{th} percentile, which is the upper boundary percentile to be used in the computation of the maximum daily limits (MDLs) throughout this analysis. Results of the analysis to estimate the recurrence or upper boundary percentile for all subwatersheds, including those partially located in Pennsylvania, are shown in Table D-1.

Table D-1: Percentiles of Maximum Observed Bacteria Concentrations in the Upper Monocacy River Subwatersheds

Station	Strata	Maximum Observed *E. coli* Concentration (MPN/100ml)	Percentile
MON0575[1]	High Flow	650	81.0%
	Low Flow	360	90.9%
PIN0000[1]	High Flow	1,660	89.2%
	Low Flow	1,040	92.9%
TOM0011[1]	High Flow	750	94.1%
	Low Flow	7,700	95.3%
OWN0007	High Flow	580	88.2%
	Low Flow	1,190	93.9%
MON0355sub[1]	High Flow	2,910	83.9%
	Low Flow	4,610	99.7%
HUN0009	High Flow	660	91.1%
	Low Flow	750	84.9%
FIS0012	High Flow	520	86.1%
	Low Flow	1,140	87.8%
MON0269sub	High Flow	2,180	88.1%
	Low Flow	1,600	96.8%
TUS0007	High Flow	330	83.5%
	Low Flow	1,470	91.4%

[1]Subwatersheds partially located in Pennsylvania

As seen in Table D-1, the highest percentile value obtained from all nine stations and strata is 99.7%, therefore, the upper boundary percentile to be used to estimate MDLs in this analysis will equal 99.7%. This 99.7th percentile value results in a maximum daily load that would not be exceeded 99.7% of the time, as, in a similar manner, a TMDL that represents the long term average condition would be expected to be exceeded half the time even after all required controls were implemented.

The MDLCs are estimated based on a statistical methodology referred to as "Statistical Theory of Rollback (STR)". This method predicts concentrations of a pollutant after its sources have been controlled (post-control concentrations), in this case after annual average TMDL implementation. Using STR, the daily TMDLs are calculated as presented below.

First, the long-term average TMDL concentrations (C_{LTA}) by stratum are estimated by applying the required percent reduction to the baseline (monitoring data) concentrations (C_b) by stratum as follows:

From Section 4.3, equations (8) and (9):

$L_b = L_{b\text{-}H} + L_{b\text{-}L}$

$L_b = Q_H * C_{bH} * F_{1H} * W_H + Q_L * C_{bL} * F_{1L} * W_L$

And from equation (10)

$Annual\ Average\ TMDL = L_b * (1 - R)$

Therefore, $L_b*(1\text{-}R) = Q_H*C_H*F_{1H}*W_H*(1\text{-}R) + Q_L*C_L*F_{1L}*W_L*(1\text{-}R)$

As explained before, a reduction in concentration is proportional to a reduction in load, thus the bacteria concentrations expected after reductions are applied are equal to the baseline concentrations multiplied by one minus the required reduction:

$$C_{LTA\text{-}H} = C_{b\text{-}H}*(1\text{-}R_H)$$

$$C_{LTA\text{-}L} = C_{b\text{-}L}*(1\text{-}R_L)$$

The TMDL concentrations estimated as explained above for all subwatersheds, including those partially located in PA, are shown in Table D-2.

Table D-2: Long-term Annual Average (LTA) TMDL Bacteria Concentrations

Station	Strata	LTA Geometric Mean Concentrations (MPN/100ml)	LTA Arithmetic Mean[1] Concentrations (MPN/100ml)
MON0575[2]	High Flow	98	233
	Low Flow	73	136
PIN0000[2]	High Flow	75	271
	Low Flow	54	119
TOM0011[2]	High Flow	24	40
	Low Flow	49	311
OWN0007	High Flow	72	104
	Low Flow	70	134
MON0355sub[2]	High Flow	177	1,118
	Low Flow	89	179
HUN0009	High Flow	29	63
	Low Flow	53	104
FIS0012	High Flow	38	82
	Low Flow	56	172
MON0269sub	High Flow	22	64
	Low Flow	32	53
TUS0007	High Flow	4	7
	Low Flow	13	21

[1]Only arithmetic parameters are used in the daily loads analysis.
[2]Subwatersheds partially located in Pennsylvania

The next step is to calculate the 99.7th percentile (the MDL concentrations) of these expected concentrations (LTA concentrations) using the coefficient of variation of the baseline concentrations. Based on a general rule for coefficient of variations, the coefficient of variation of the distribution of the concentrations of a pollutant does not change after these concentrations have been reduced or controlled by a fixed proportion (Ott and Wayne 1995).

Therefore, the coefficient of variation estimated using the monitoring data concentrations does not change, and it can be used to estimate the 99.7th percentile of the long-term average TMDL concentrations (LTAC) using equation (D1). These values are presented for all subwatersheds, including those partially located in Pennsylvania, in Table D-3.

Table D-3: Maximum Daily Load (MDL) Concentrations

Station	Strata	CV	MDL Concentrations (MPN/100ml)
MON0575[1]	High Flow	2.764	3,664
	Low Flow	1.389	1,570
PIN0000[1]	High Flow	3.457	6,147
	Low Flow	1.960	1,710
TOM0011[1]	High Flow	1.382	406
	Low Flow	6.219	9,699
OWN0007	High Flow	1.046	765
	Low Flow	1.638	1,612
MON0355sub[1]	High Flow	6.255	34,936
	Low Flow	1.742	2,293
HUN0009	High Flow	1.888	870
	Low Flow	1.673	1,279
FIS0012	High Flow	1.913	1,157
	Low Flow	2.925	3,477
MON0269sub	High Flow	2.778	1,245
	Low Flow	1.323	506
TUS0007	High Flow	1.279	53
	Low Flow	1.340	204

[1] Subwatersheds partially located in Pennsylvania

With the 99.7th percentiles of LTA TMDL bacteria concentrations estimated for both high flow and low flow strata as explained above, the maximum daily load for MS4 and nonpoint sources for each subwatershed can be now estimated as:

$$Daily\ TMDL\ (MPN/day) = Q_H*(99.5^{th}C_{LTA\text{-}H})*F_{1H}*W_H + Q_L*(99.5^{th}C_{LTA\text{-}L})*F_{1L}*W_L$$

<u>Selected Approach for Defining Maximum Daily Loads for Other Point Sources</u>

The TMDL also considers contributions from other point sources (i.e., municipal and industrial WWTP) in watersheds that have NPDES permits with fecal bacteria limits. The TMDL analysis that defined the average annual TMDL held each of these sources constant at their existing NPDES permit limit (daily or monthly) for the entire year. The approach used to determine maximum daily loads was dependent upon whether a maximum daily load was specified within the permit. If a maximum daily load was specified within the permit, then the maximum design flow is multiplied by the maximum daily limit to obtain a maximum daily load. If a maximum daily limit was not specified in the permit, then the maximum daily loads are calculated from guidance in the TSD for Water Quality-based Toxics Control (EPA 1991). The long-term average annual TMDL was converted to maximum daily limits using Table 5-2 of the TSD assuming a coefficient of variation of 0.6 and a 99th percentile probability. This results in a dimensionless multiplication factor of 3.11. The average annual bacteria loads for WWTPs are reported in billion MPN/year. In the Upper Monocacy River, to estimate the maximum daily loads for WWTPs, the annual average loads are multiplied by the multiplication factor as follows:

WWTP-WLA MDL (billion MPN/day) = [WWTP-WLA billion MPN/year)]*(3.11/365)

The Maximum Daily Loads for the Upper Monocacy River subwatersheds, including those partially located in PA, are presented in Table D-4 below.

Table D-4: Maximum Daily Loads (MDL)

Station	Strata	Maximum Daily Load by Stratum (Billion *E. coli* MPN/day)	Maximum Daily Load Weighted (Billion *E. coli* MPN/day)
MON0575[1]	High Flow	56,119	15,517
	Low Flow	1,983	
PIN0000[1]	High Flow	22,861	6,108
	Low Flow	523	
TOM0011[1]	High Flow	3,851	6,640
	Low Flow	7,570	
OWN0007	High Flow	3,238	1,232
	Low Flow	564	
MON0355sub[1]	High Flow	257,189	65,341
	Low Flow	1,391	
HUN0009	High Flow	3,963	1,343
	Low Flow	469	
FIS0012	High Flow	2,275	990
	Low Flow	569	
MON0269sub	High Flow	1,798	495
	Low Flow	61	
TUS0007	High Flow	101	49
	Low Flow	32	

[1]Subwatersheds partially located in Pennsylvania

Maximum Daily Load Allocations

Using the MDLs estimated as explained above, loads are allocated following the same methodology as the annual average TMDL (See section 4.8). A summary of maximum daily loads for the Upper Monocacy River watershed in Maryland, is presented in Table D-5.

Table D-5: Upper Monocacy River Watershed Maximum Daily Loads

Subwatersheds	Maryland			
	MDL	LA	SW-WLA	WWTP-WLA
	Billion MPN *E. coli*/day			
Upper Monocacy River (MON0575)[1]	**155**	78	77	N/A
Piney Creek (PIN0000)[1]	**4,886**	4,456	414	16.3
Toms Creek (TOM0011)[1]	**2,191**	1,841	336	14.2
Owens Creek (OWN0007)	**1,232**	808	423	0.8
Upper Monocacy River (MON0355sub)[1]	**46,392**	43,610	2,782	N/A
Hunting Creek (HUN0009)	**1,343**	1,121	207	15.2
Fishing Creek (FIS0012)	**990**	910	79	0.5
Upper Monocacy River (MON0269sub)	**496**	366	129	0.5
Tuscarora Creek (TUS0007)	**49**	35	13	0.7
TOTAL*	**57,734**	53,225	4,461	48.3

[1]MDL only for the portion of the subwatershed located in Maryland

REFERENCES

Limno-Tech, Inc. 2007. Draft Memorandum: Technical Approach for Four Alternative Options to Define Maximum Daily Loads for the Anacostia TMDL. Washington, DC. January 23, 2007.

EPA (U.S. Environmental Protection Agency). 2006. Approaches For Developing a Daily Load Expression for TMDLs Computed for Longer Term Averages. Draft guidance document. Washington, DC. October 2006.

EPA (U.S. Environmental Protection Agency). 1991. Technical Support Document for Water Quality-Based Toxics Control (1991 TSD). Washington, DC.

Appendix E – Relationship of Fecal Bacteria TMDLs for the Double Pipe Creek, Upper Monocacy River, and Lower Monocacy River Watersheds

The purpose of this appendix is to explain the hydrologic relationship between the Double Pipe Creek, Upper Monocacy River, and Lower Monocacy River watersheds and how this affects the fecal bacteria TMDLs for each of the respective watersheds. As illustrated in Figure E-1, the three watersheds are hydrologically connected, beginning with the Double Pipe Creek watershed to the east. The Double Pipe Creek watershed flows into the Upper Monocacy River watershed, near the small town of Rocky Ridge. It is also shown in Figure E-1 that the Upper Monocacy River watershed includes land in Pennsylvania and Maryland. The combined flow from the Upper Monocacy River watershed and the Double Pipe Creek watershed flows into the Lower Monocacy River watershed. The hydrologic connectivity of the watersheds is illustrated in Figure E-2.

The baseline fecal bacteria loads for the watersheds are shown in Table E-1. The TMDL calculations are shown in Tables E-2 through E-4. Further information can be found in the individual TMDL documents for each watershed.

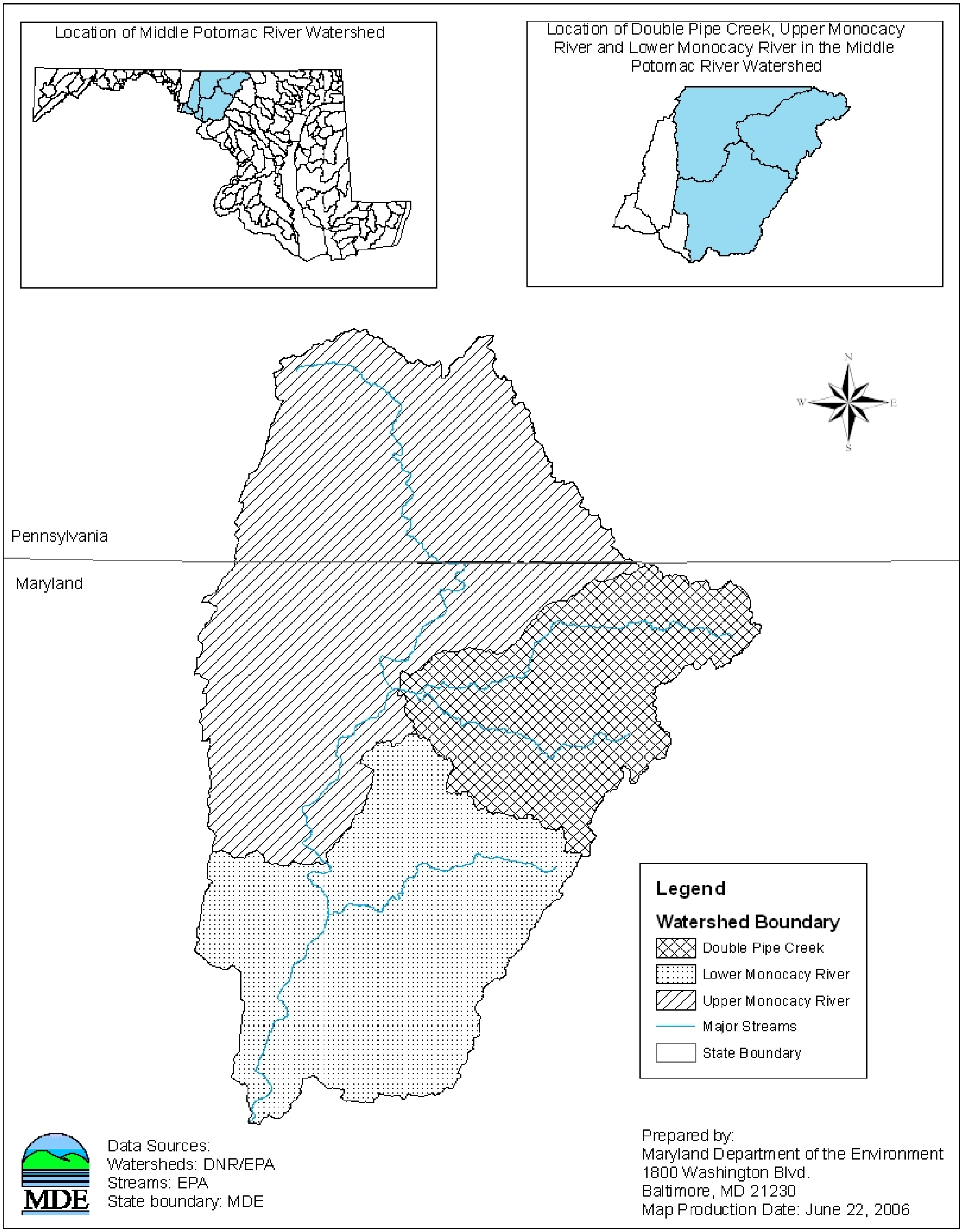


Figure E-1: Location of the Double Pipe Creek, Upper Monocacy River, and Lower Monocacy River Watersheds

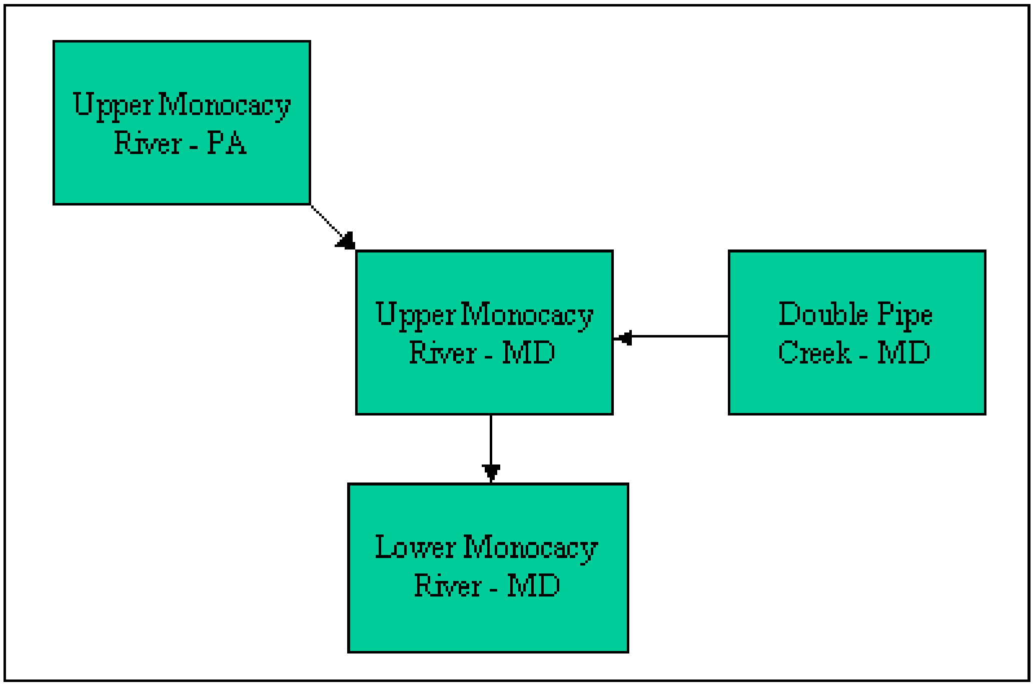


Figure E-2: Flow Schematic of the Double Pipe Creek, Upper Monocacy River, and Lower Monocacy River Watersheds

Table E-1: Fecal Bacteria Baseline Loads

Watershed	Total Baseline Load	=	MD 8-digit Basin Load	+	Upstream Load
	Billion MPN *E. coli*/year				
Double Pipe Creek	11,614,269	=	11,614,269	+	N/A
Upper Monocacy River	15,073,485	=	1,985,054	+	13,088,431[1]
Lower Monocacy River	20,856,810	=	5,783,325	+	15,073,485[2]

[1]The upstream load is equivalent to the Double Pipe Creek baseline load (11,614,269 billion MPN *E. coli*/year) plus the PA baseline load (1,474,162 billion MPN *E. coli*/year).
[2]The upstream load is equivalent to the Upper Monocacy River baseline load.

Table E-2: Double Pipe Creek TMDL

TMDL Billion MPN *E. coli*/year	=	LA	+	Stormwater WLA	+	WWTP WLA	+	MOS
		Billion MPN *E. coli*/year						
282,168	=	181,528	+	91,249	+	9,391	+	Incorporated

Table E-3: Upper Monocacy River TMDL Summary

TMDL Billion MPN *E. coli*/year	=	LA_{UM}	+	WLA_{UM}	+	LA_{DP}	+	LA_{PA}	+	MOS
		Billion MPN *E. coli*/year								
1,353,850	=	438,751	+	57,483	+	282,168[1]	+	575,448[2]	+	Incorporated

[1] This upstream load allocation is equivalent to the Double Pipe Creek TMDL.
[2] This upstream PA load allocation is determined to be necessary in order to meet MD water quality standards in the MD portion of the Upper Monocacy River watershed.

Table E-4: Lower Monocacy River TMDL Summary

TMDL Billion MPN *E. coli*/year	=	LA_{LM}	+	WLA_{LM}	+	LA_{UM}	+	MOS
		Billion MPN *E. coli*/year						
2,033,379	=	426,161	+	253,368	+	1,353,850[1]	+	Incorporated

[1]This upstream load allocation is equivalent to the Upper Monocacy River TMDL.