Total Maximum Daily Loads of Fecal Bacteria for the Double Pipe Creek Basin in Carroll and Frederick Counties, Maryland

FINAL

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Submitted to:

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List of Abbreviations

ARCC	Average rates of correct classification
ARA	Antibiotic Resistance Analysis
BMP	Best Management Practice
BST	Bacteria Source Tracking
CAFO	Confined Animal Feeding Operations
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
CWP	Center for Watershed Protection
DNR	Department of Natural Resources
EPA	United States 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
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
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 Double Pipe Creek watershed (basin number 02-14-03-04). 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 Double Pipe Creek and its tributaries Little Pipe Creek, Big Pipe Creek, Sam's Creek, Meadow Branch, and Bear Branch in the State of Maryland's 303(d) List as impaired by the following (years listed in parentheses): nutrients (1996), sediments (1996) and impacts to biological communities (2002). Double Pipe Creek was also listed for fecal bacteria in 2002 as category 3(a) (waters that have insufficient data and information to determine waterbody attainment status). In 2003 and 2004, MDE monitored Double Pipe Creek for fecal bacteria and the monitoring data analysis confirmed a fecal bacteria impairment in the watershed. Double Pipe Creek and its tributaries Big Pipe Creek, Little Pipe Creek, Meadow Branch and Sam's Creek have been designated as Use IV-P waterbodies (Recreational Trout Waters and Public Water Supply). Bear Branch is designated as a Use III-P waterbody (Nontidal 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 Double Pipe Creek that will allow for attainment of the beneficial use designation of primary contact recreation. The listings for nutrients, suspended 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.

For this TMDL analysis, the Double Pipe Creek watershed has been divided into seven subwatersheds, which include the tributaries Little Pipe Creek and Big Pipe Creek (with two subwatersheds each), as well as Sam's Creek, Meadow Branch and Bear Branch. The pollutant loads set forth in this document are for these seven subwatersheds. 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 seven representative stations in the Double Pipe Creek watershed where samples were collected for one year. Multiple antibiotic resistance analysis (ARA) source tracking was used to determine the relative proportion of domestic (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 Double Pipe Creek 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 all seven subwatersheds, 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 Double Pipe Creek watershed is 282,168 billion MPN *E. coli*/year, with a maximum daily load of 8,082 MPN/day. These total loads represent the sum of individual TMDLs for the seven Double Pipe Creek subwatersheds. The long-term annual average TMDL represents a reduction of approximately 97.6 % from the baseline load of 11,614,269 billion MPN/year. The TMDL is distributed between a load allocation (LA) for nonpoint sources and waste load allocations (WLAs) for point sources, including National Pollutant Discharge Elimination System (NPDES) wastewater treatment plants (WWTPs) and NPDES regulated stormwater discharges, including municipal separate storm sewer systems (MS4s).

The long-term annual average allocations are as follows: the LA is 181,528 billion MPN *E. coli*/year. The WWTP WLA is 9,391 billion MPN *E. coli*/year. The Stormwater WLA is 91,249 billion MPN *E. coli*/year. 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/100ml to 119.7 MPN/100ml.

The maximum daily loads, estimated using predicted long-term annual average TMDL concentrations (after source controls), are allocated as follows: the LA is 6,148 billion MPN *E. coli*/day. The WWTP WLA is 80 billion MPN *E. coli*/day. The Stormwater WLA is 1,854 billion MPN *E. coli*/day.

Since Double Pipe Creek is a major tributary of the Upper Monocacy River, which also receives an upstream load from Pennsylvania and in turn flows into the Lower Monocacy River, an appendix is included that explains the hydrologic relationship of the three watersheds, along with a comprehensive TMDL summary for the entire Monocacy River basin (Appendix E).

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 any of the seven Double Pipe Creek 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 Double Pipe Creek (basin number 02-14-03-04). 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.

Double Pipe Creek and its tributaries, Little Pipe Creek, Big Pipe Creek, Sam's Creek, Meadow Branch and Bear Branch, have been identified in the State of Maryland's 303(d) List as impaired by the following (years listed in parentheses): nutrients (1996), sediments (1996) and impacts to biological communities (2002). It was also listed for fecal bacteria in 2002 as category 3(a) (waters that have insufficient data and information to determine waterbody attainment status). In 2003 and 2004, MDE monitored Double Pipe Creek for fecal bacteria and the monitoring data analysis confirmed a fecal bacteria impairment in the watershed. Therefore, this report documents a TMDL of fecal bacteria for the watershed. Double Pipe Creek and its tributaries Big Pipe Creek, Little Pipe Creek, Meadow Branch and Sam's Creek have been designated as Use IV-P waterbodies (Recreational Trout Waters and Public Water Supply). Bear Branch is designated as a Use III-P waterbody (Nontidal 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 Double Pipe Creek that will allow for attainment of the beneficial use designation of primary contact recreation. The listings for nutrients, suspended 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.

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 Maryland's current bacteria water quality criteria, either *E. coli* or enterococci. The indicator organism used in the Double Pipe Creek TMDL analysis was *E. coli*.

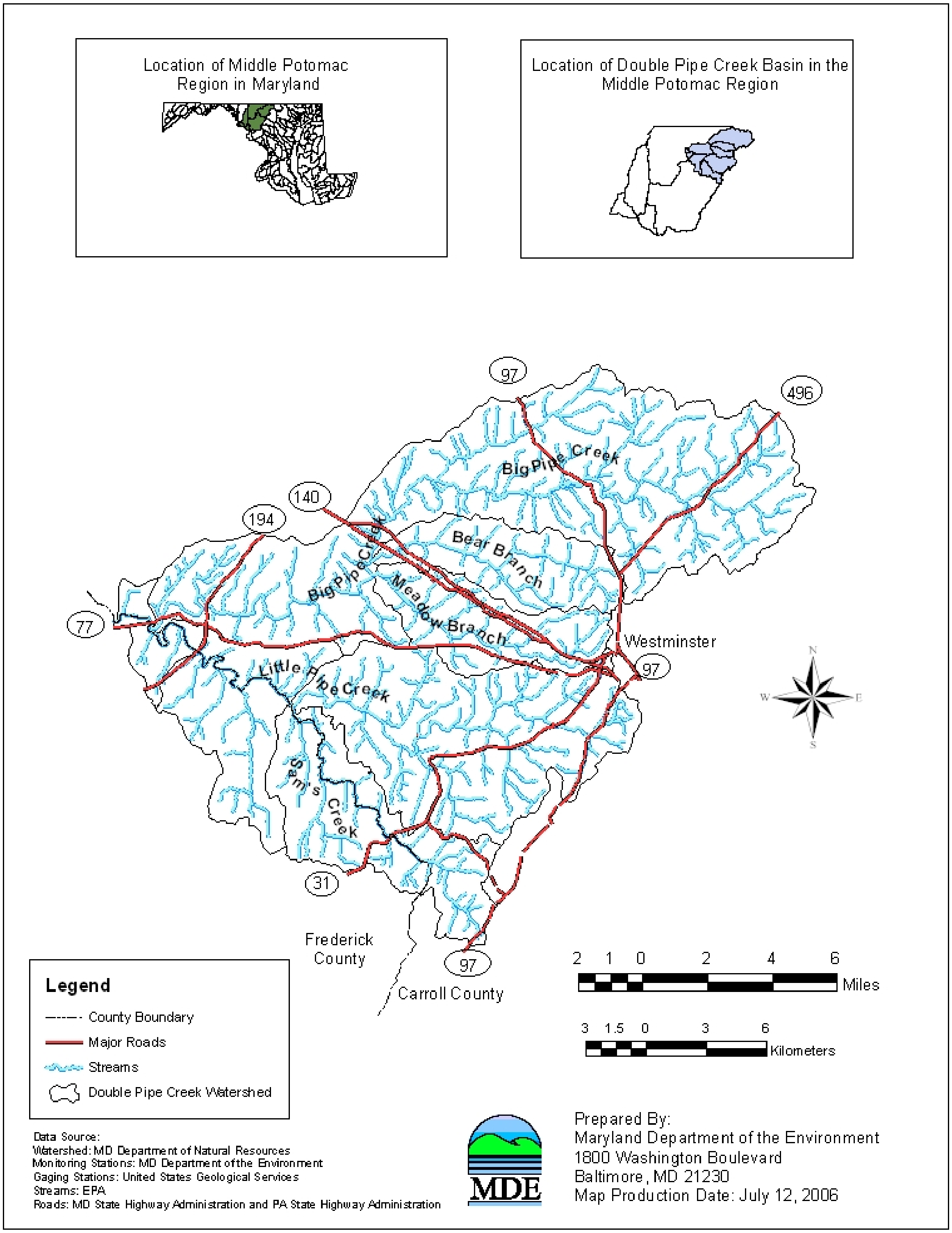
2.0 SETTING AND WATER QUALITY DESCRIPTION

2.1 General Setting

Location

The Double Pipe Creek watershed is located in Carroll and Frederick Counties in Maryland (MD) (Figure 2.1.1). The total drainage area of Double Pipe Creek is approximately 192.6 square miles (123,232 acres), and lies north, west, and southwest of the Westminster metropolitian area. Double Pipe Creek and its tributaries flow through several small towns that include Manchester, Union Bridge, Taneytown, New Windsor, and Westminster. The headwaters of Double Pipe Creek originate in Westminster and Manchester, flowing west toward the city of Rocky Ridge, entering the Monocacy River and eventually emptying into the Middle Potomac River near the town of Dickerson.

There are two major drainage areas comprising the Double Pipe Creek watershed: Big Pipe Creek and Little Pipe Creek. These branches are free-flowing (non-tidal) streams, and flow into Double Pipe Creek at Detour and Keymar, MD before discharging into the Monocacy River at Rocky Ridge.



Data Source:
Watershed: MD Department of Natural Resources
Monitoring Stations: MD Department of the Environment
Gaging Stations: United States Geological Services
Streams: EPA
Roads: MD State Highway Administration and PA State Highway Administration

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Map Production Date: July 12, 2006

Figure 2.1.1: Location Map of the Double Pipe Creek Basin

Land Use

The 2002 Maryland Department of Planning (MDP) land use/land cover data show that the watershed can be characterized as primarily crops/pasture. The watershed is very rural with a large area of the watershed dominated by cropland and livestock/feeding operations. There are four minor urban areas and one major urban area in respect to their largely rural surroundings. The four minor urban areas are Taneytown, Manchester, Union Bridge, and New Windsor. The one major urban area is Westminster (MDE 2002).

The land use percentage distribution for the Double Pipe Creek Basin is shown in Table 2.1.1, and spatial distributions for each land use are shown in Figure 2.1.2.

Table 2.1.1: Land Use Percentage Distribution for Double Pipe Creek Basin

Land Type	Maryland Acreage	Maryland Percentage
Forest	23,405	19.4 %
Urban	14,742	12.2 %
Crops	68,612	57 %
Pasture	13,562	11.3 %
Water	31	0.1 %
Totals	**120,352**	**100.0%**

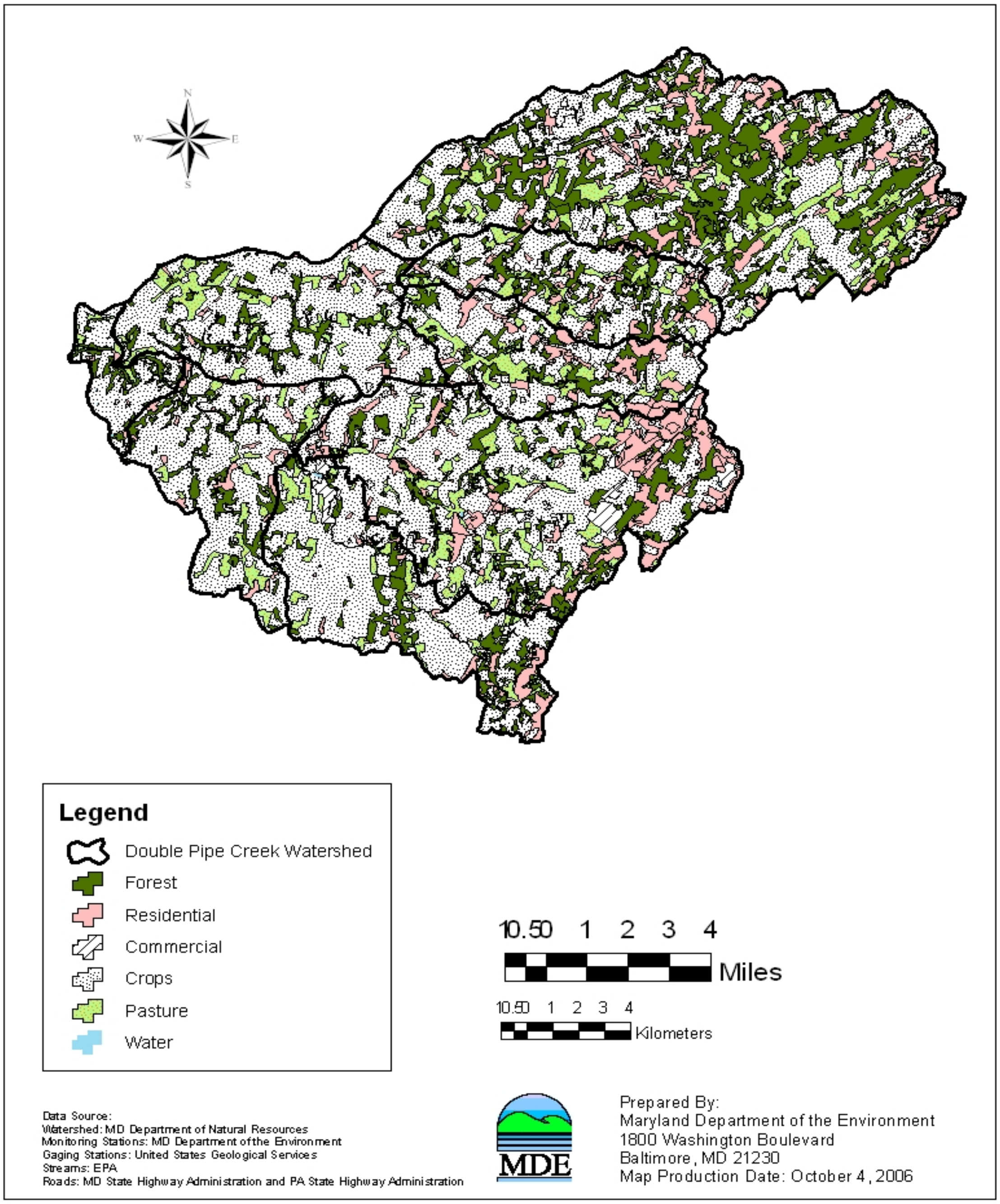


Figure 2.1.2: Land Use of the Double Pipe Creek Watershed

Population

The total population in the Double Pipe Creek watershed is estimated to be 39,191. Figure 2.1.3 illustrates the population density in the watershed. The population and the number of households were estimated based on a weighted average from the Geographic Information Systems (GIS) 2000 U. S. Census Block and the MDP Land Use 2002 Cover. Since the Double Pipe Creek 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 Double Pipe Creek watershed. The number of dwellings per acre was derived from information for residential density (low, medium, high) from the MDP land use cover and the Mid-Atlantic Regional Earth Science Applications Center (RESAC) land use cover.

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).

Table 2.1.3: Total Population Per Subwatershed in Double Pipe Creek Watershed

Subwatershed	Station	Population
Bear Branch	BEB0009	2,645
Big Pipe Creek	BPC0120	7,689
Meadow Branch	MEB0000	6,092
Big Pipe Creek	BPC0006	1,344
Little Pipe Creek	LPC0091	17,789
Sam's Creek	SAM0001	1,906
Little Pipe Creek	LPC0032	1,726
	TOTAL	**39,191**

Note: Monitoring stations are listed by flow, from upstream to downstream, for the two main branches, Big Pipe Creek (first four stations) and Little Pipe Creek (last three stations), including their respective tributaries.

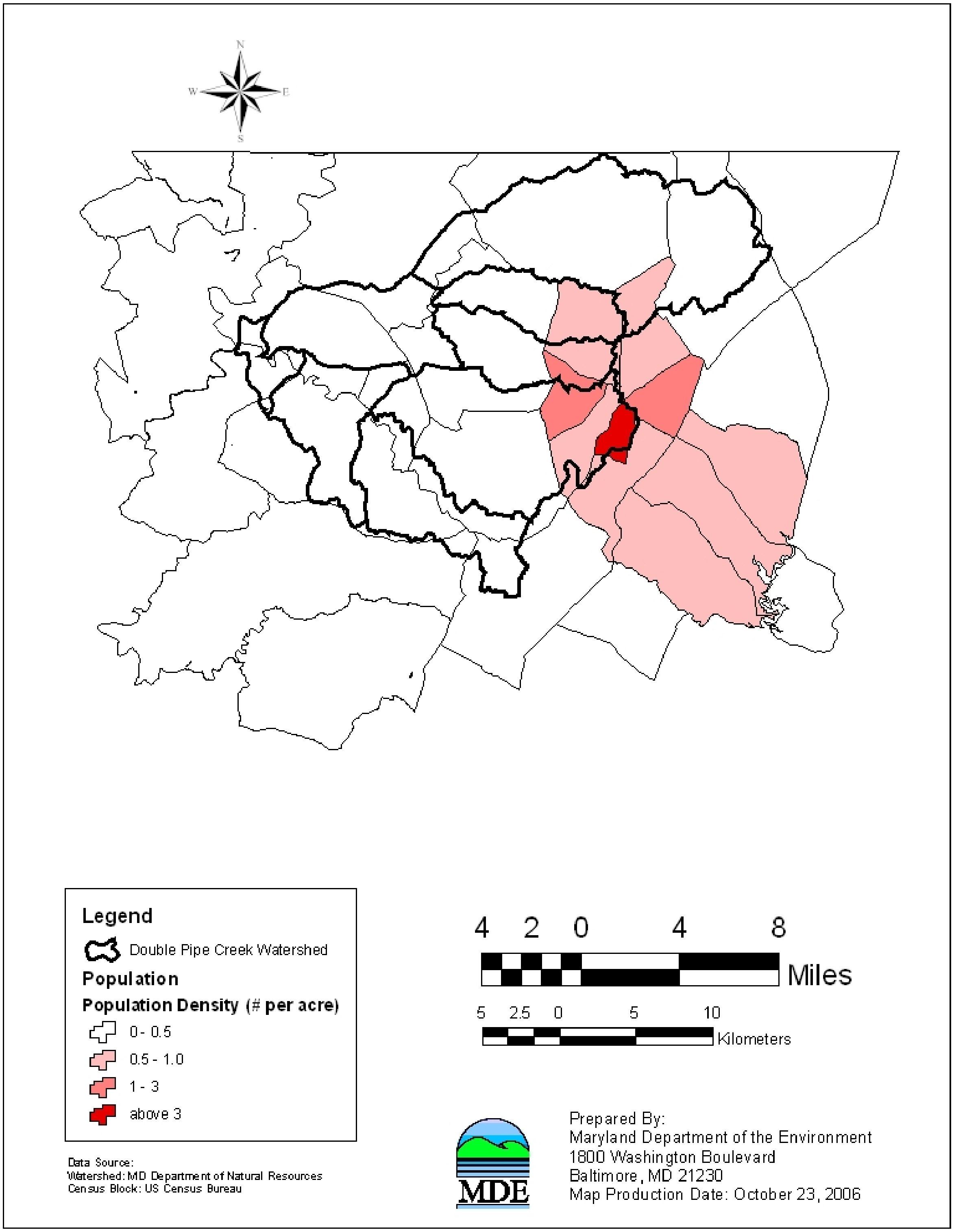


Figure 2.1.3: Population Density in Double Pipe Creek Basin

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. These geometric mean results were compared to the current water quality standard at the time, which required concentrations 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 Double Pipe Creek watershed. MDE conducted monitoring sampling from November 2003 through November 2004. There are seven MDE monitoring stations in the Double Pipe Creek 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 Double Pipe Creek. 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 two main branches: Big Pipe Creek, including Bear Branch and Meadow Branch (four stations), followed by Little Pipe Creek, including Sam's Creek (three stations). Observations recorded during the period 2003-2004 from the seven MDE monitoring stations are shown in Appendix A. A table listing the monitoring results from the Double Pipe Creek watershed appears in Appendix A.

Bacteria counts are highly variable and results are presented on a log scale for the seven monitoring stations for data collected for November 2003 through November 2004. Bacteria counts ranged between 10 and 130,000 MPN/100 ml.

Table 2.2.1: Historical Monitoring Data in the Double Pipe Creek Watershed

Sponsor	Location	Date	Design	Summary
MDE	MD	11/03 to 10/04	*E. coli*	7 stations 2 samples per month
MDE	MD	11/03 to 10/04	BST(ARA) (enterococci)	7 stations 1 sample per month

Table 2.2.2: Locations of DNR (CORE) Monitoring Station in the Double Pipe Creek Watershed

Tributary	Monitoring Station	LATITUDE Dec-Deg	LONGITUDE Dec-Deg
Big Pipe Creek	BPC0035	39^{o} 36.733	77^{o} 14.216'

Table 2.2.3: Locations of MDE Monitoring Stations in the Double Pipe Creek Watershed

Tributary	Monitoring Station	Observation Period	Total Observations	LATITUDE Dec-Deg	LONGITUDE Dec-Deg
Bear Branch	BEB0009	2003 - 2004	22	39^{o} 38.130'	77 07.692
Big Pipe Creek	BPC0120	2003 - 2004	22	39^{o} 38.423'	77 08.304
Meadow Branch	MEB0000	2003 - 2004	22	39^{o} 37.522'	77 08.454
Big Pipe Creek	BPC0006	2003 - 2004	22	39^{o} 36.360'	77 15.789
Little Pipe Creek	LPC0091	2003 - 2004	22	39^{o} 34.130'	77 11.041
Sam's Creek	SAM0001	2003 - 2004	22	39^{o} 33.611'	77 10.884
Little Pipe Creek	LPC0032	2003 - 2004	22	39^{o} 35.464'	77 14.560

Table 2.2.4: Locations of USGS Gauging Stations in Double Pipe Creek Watershed

Monitoring Station	Observation Period Used in TMDL Analysis	Total Observations	LATITUDE Dec-deg	LONGITUDE Dec-deg
01639500	1989 – 2004	5,477	39^{o} 36.742'	77^{o} 14.247'

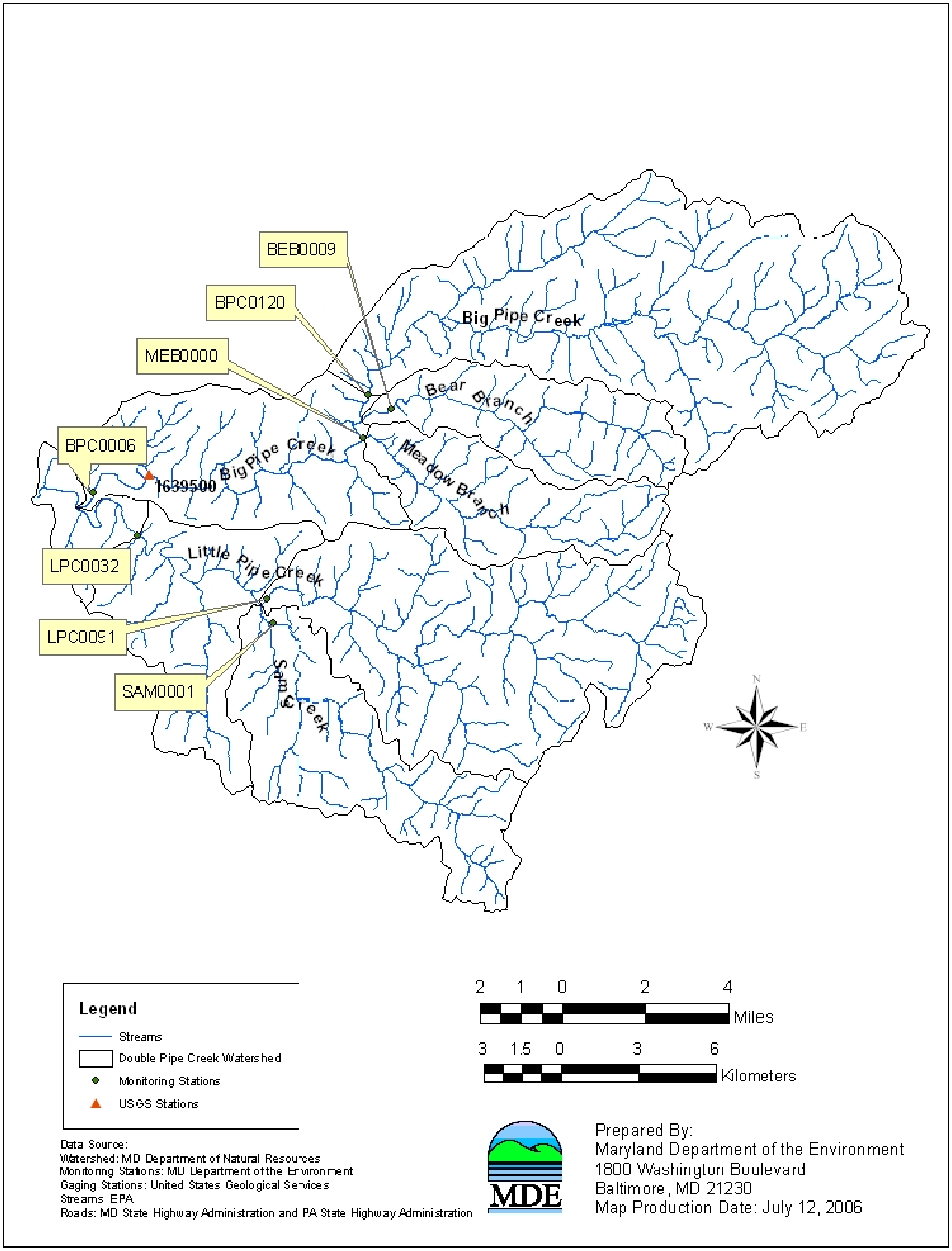


Figure 2.2.1: Monitoring Stations and Subwatersheds in the Double Pipe Creek Basin

2.3 Water Quality Impairment

Designated Uses and Water Quality Standard

The Maryland water quality standards Surface Water Use Designation for the Double Pipe Creek mainstem and its tributaries Big Pipe Creek, Little Pipe Creek, Meadow Branch and Sam's Creek, is Use IV-P (Water Contact Recreation, Protection of Aquatic Life, Recreational Trout Waters and Public Water Supply); its tributary Bear Branch is designated as Use III-P (Water Contact Recreation, Protection of Aquatic Life, Non-tidal Cold Water and Public Water Supply) (COMAR 26.08.02.08P). The Double Pipe Creek watershed was listed for fecal bacteria in 2002 as category 3(a) (waters that have insufficient data and information to determine waterbody attainment status). Data collected by MDE in 2003-2004 showed high levels of fecal bacteria in seven monitoring stations throughout the watershed, confirming the fecal bacteria impairment and resulting in the development of this fecal bacteria TMDL.

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 COMAR 26.08.02.03-3 Water Quality Criteria Specific to Designated Uses: Table 1

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 Double Pipe Creek was assessed by comparing both the annual and the seasonal (May 1st –September 30th) 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 Double Pipe Creek 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.

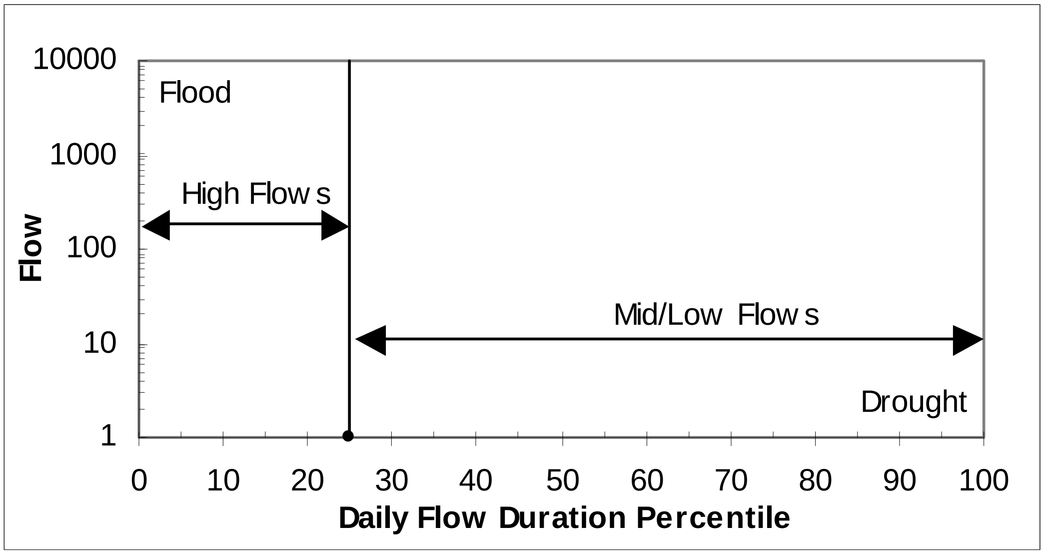


Figure 2.3.1: Conceptual Diagram of Flow Duration Zones

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 25th to 30th daily flow duration percentiles were representative of average daily flows. It is assumed for this analysis that flows higher than the 25th percentile flow represent high flows, and flows lower than the 25th percentile 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 Double Pipe Creek 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 Double Pipe Creek 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

Table 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 Double Pipe Creek subwatersheds for the annual and the seasonal (May 1st –September 30th) periods. Monitoring stations are listed by flow from upstream to downstream.

Table 2.3.3: Double Pipe Creek Annual Steady-State Geometric Means by Stratum per Subwatersheds

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)
Bear Branch BEB0009	High	11	60	14,200	593	734
	Low	11	100	4,880	789	
Big Pipe Creek BPC0120	High	11	30	29,100	446	416
	Low	11	110	9,210	406	
Meadow Branch MEB0000	High	11	20	8,800	570	800
	Low	11	100	17,330	895	
Big Pipe Creek BPC0006	High	11	130	24,190	748	267
	Low	11	10	540	189	
Little Pipe Creek LPC0091	High	11	210	24,190	2,041	1,153
	Low	11	250	2,480	954	
Sam’s Creek SAM0001	High	11	50	68,700	1,018	1,069
	Low	11	50	7,700	1,086	
Little Pipe Creek LPC0032	High	11	220	130,000	2,346.5	1,290
	Low	11	180	2,910	1,057	

Table 2.3.4: Double Pipe Creek Seasonal (May 1st-September 30th) Period Steady-State Geometric Means by Stratum per Subwatersheds

Tributary Station	Flow Stratum	# of Samples	*E. coli* Minimum Concentration (MPN/100ml)	*E. coli* Maximum Concentration (MPN/100ml)	Seasonal Steady-State Geometric Mean (MPN/100ml)	Seasonal Weighted Geometric Mean (MPN/100ml)
Bear Branch BEB0009	High	2	13,000	14,200	13,587	2,282
	Low	8	660	4,880	1,259	
Big Pipe Creek BPC0120	High	2	24,190	29,100	26,532	1,512
	Low	8	240	9210	582	
Meadow Branch MEB0000	High	2	7,700	8,800	8,232	2,602
	Low	8	730	17,330	1,773	
Big Pipe Creek BPC0006	High	2	17,800	24,190	20,750	876
	Low	8	180	540	305	
Little Pipe Creek LPC0091	High	2	15,530	24,190	19,382	2,520
	Low	8	860	2,480	1,277	
Sam’s Creek SAM0001	High	2	24,190	68,700	40,766	4,699
	Low	8	990	7,700	2,287	
Little Pipe Creek LPC0032	High	2	24,190	130,000	56,078	4,186
	Low	8	930	2,910	1,763	

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 activities generally arise from failing septic systems and their associated drain fields or leaking infrastructure (i.e., sewer systems). The entire Double Pipe Creek watershed is covered by two National Pollutant Discharge Elimination System (NPDES) Municipal Separate Storm Sewer System (MS4) individual permits, which are technically point sources subject to waste load allocation (WLA); therefore, nonpoint source contributions from domestic animal and human sources will be categorized as point sources and assigned to the Stormwater WLA. 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) 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

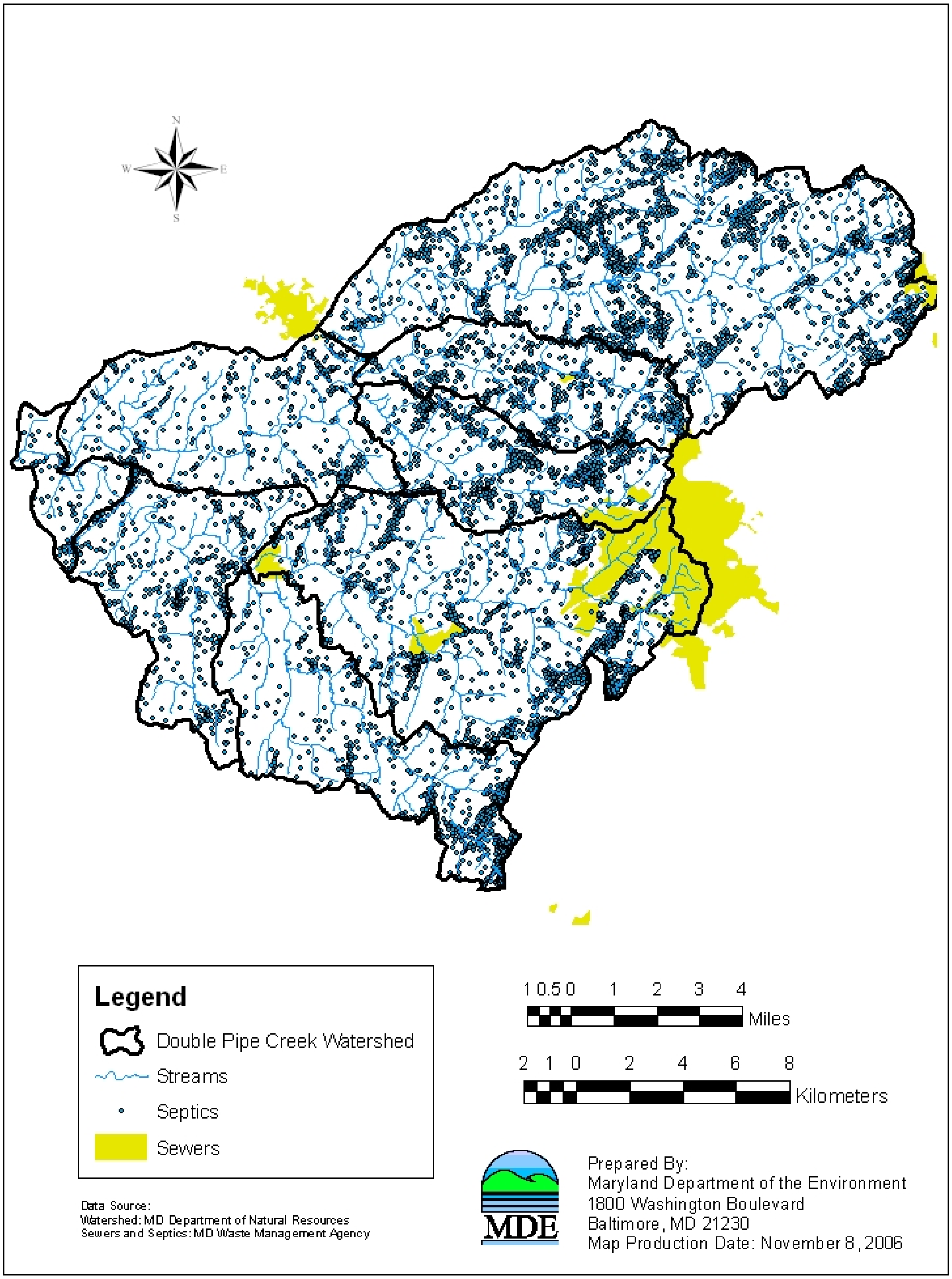
The Double Pipe Creek watershed is serviced by both sewer systems and septic systems. Sewer systems are present in the towns of Westminster, New Winsdor and Union Bridge. Wastewater collected by these systems is treated at the Westminster Wastewater Treatment Plant (WWTP), the New Windsor WWTP, and the Union Bridge WWTP, all of which discharge into Little Pipe Creek.

Septic Systems

On-site disposal (septic) systems are located throughout the Double Pipe Creek watershed. Table 2.4.1 presents the total households and the number of septic systems per subwatershed. Figure 2.4.1 depicts the areas that are serviced by sewers and septic systems.

Table 2.4.1: Septic Systems and Households Per Subwatershed in Double Pipe Creek Watershed

Tributary	Station	Households per Subwatershed	Septic Systems (units)
Bear Branch	BEB0009	1,218	761
Big Pipe Creek	BPC0120	4,843	2,456
Meadow Branch	MEB0000	3,125	898
Big Pipe Creek	BPC0006	551	501
Little Pipe Creek	LPC0091	10,595	1,636
Sam’s Creek	SAM0001	1,085	741
Little Pipe Creek	LPC0032	756	590
	TOTAL	22,173	7,583



Data Source:
Watershed: MD Department of Natural Resources
Sewers and Septics: MD Waste Management Agency

Prepared By:
Maryland Department of the Environment
1800 Washington Boulevard
Baltimore, MD 21230
Map Production Date: November 8, 2006

Figure 2.4.1: Sanitary Sewer Service and Septics Areas in Double Pipe Creek 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 can include industrial and municipal WWTPs and Phase I municipal separate storm sewer systems (MS4s). MDE general permits have been established for surface water discharges that include the following: Phase II and other MS4 permits, 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 and other NPDES regulated stormwater entities 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. MS4s programs are designed to reduce the amount of pollution that enters a waterbody from storm sewer systems to the maximum extent practicable.

The Double Pipe Creek watershed is located in Carroll and Frederick Counties, which are both individual Phase I National Pollutant Discharge Elimination System (NPDES) MS4 permit jurisdictions. Stormwater in the watershed is primarily conveyed through storm sewers covered by NPDES MS4 permits. Bacteria loads associated with these MS4s are therefore included in the Stormwater WLA of this TMDL, which also encompasses any other NPDES regulated Phase I and Phase II stormwater entities in the watershed, including State and federal permittees.

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 five SSOs reported to MDE between September 2003 and November 2004 in the Carroll County portion of the Double Pipe Creek watershed. Approximately 73,000 gallons of SSOs were discharged through various waterways (surface water, groundwater, sanitary sewers, etc.) in the Carroll County portion of the watershed. No SSOs were reported in the Frederick County portion of the watershed. Figure 2.4.2 depicts the locations where SSOs occurred in the watershed between September 2003 and November 2004.

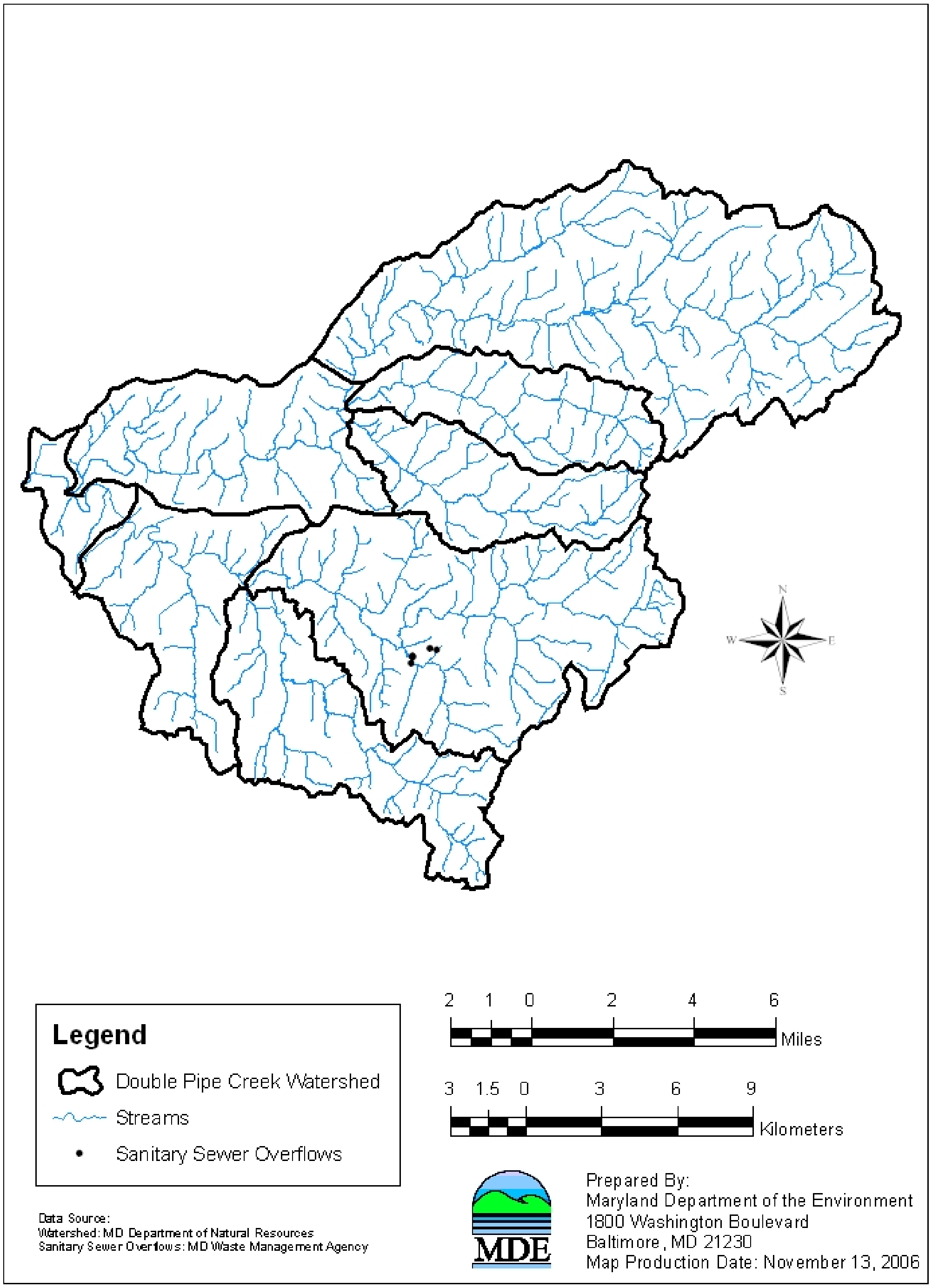


Figure 2.4.2: Sanitary Sewer Overflows Areas in Double Pipe Creek Watershed

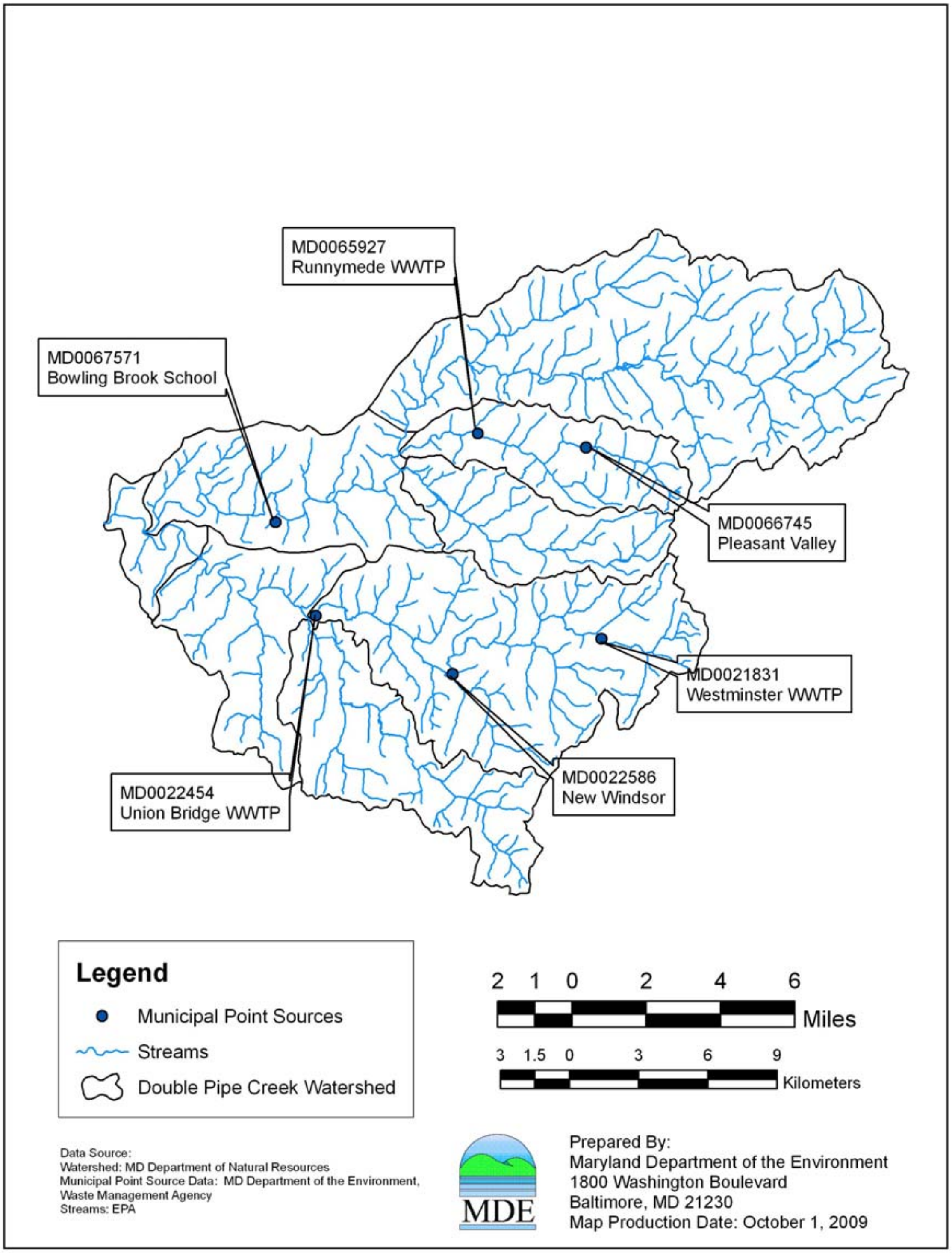
Municipal and Industrial Wastewater Treatment Plants (WWTPs)

Wastewater treatment plants are designed to treat wastewater before it can be 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 six NPDES permitted point source facilities with permits regulating the discharge of fecal bacteria directly into the Double Pipe Creek watershed (Table 2.4.2 and Figure 2.4.3). These six WWTPs combined use an activated sludge process to treat approximately 4,800,000 gallons per day (4.8 MGD). Table 2.4.2 lists the active WWTPs in the Carroll County portion of the watershed. There are no WWTPs in the Frederick County portion of the watershed.

Table 2.4.2: NPDES Permit Holders with Permits Regulating Fecal Bacteria Discharge in the Double Pipe Creek Watershed

Permittee	NPDES Permit No.	County	Average Annual Flow (MGD)	Fecal Coliform Concentrations Annual AVG (MPN/100ml)	Fecal Coliform Load Per Day (Billion MPN/day)
Westminster WWTP	MD0021831	Carroll	4.55	37.75	6.51
New Windsor WWTP	MD0022586	Carroll	0.09	4.62	0.02
Union Bridge WWTP	MD0022454	Carroll	0.14	3.49	0.02
Bowling Brook School	MD0067571	Carroll	0.005	1.81	0.0003
Runnymede WWTP	MD0065927	Carroll	0.001	3.00	0.0001
Pleasant Valley WWTP	MD0066745	Carroll	0.006	2.25	0.0005



Data Source:
Watershed: MD Department of Natural Resources
Municipal Point Source Data: MD Department of the Environment, Waste Management Agency
Streams: EPA

Prepared By:
Maryland Department of the Environment
1800 Washington Boulevard
Baltimore, MD 21230
Map Production Date: October 1, 2009

Figure 2.4.3: Permitted Point Sources Discharging Fecal Bacteria in Double Pipe Creek 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 Double Pipe Creek 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=0.3, low flow=0.7).

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.

Table 2.4.3: Distribution of Fecal Bacteria Source Loads in the Double Pipe Creek Basin for the Annual Period

STATION	Flow Stratum	% Domestic Animals	% Human	% Livestock	% Wildlife	% Unknown
BEB0009	High Flow	24.4	17.2	21.5	9.3	27.6
	Low Flow	25.2	10.4	24.3	8.7	31.4
	Weighted	25.0	12.1	23.6	8.8	30.4
BPC0120	High Flow	20.8	28.2	15.6	9.2	26.1
	Low Flow	34.2	22.2	14.4	6.4	22.8
	Weighted	30.8	23.7	14.7	7.1	23.6
MEB0000	High Flow	19.9	16.5	22.1	15.4	25.9
	Low Flow	27.0	11.4	23.1	9.9	28.5
	Weighted	25.2	12.7	22.9	11.3	27.9
BPC0006	High Flow	30.9	23.3	13.7	13.3	18.7
	Low Flow	19.2	9.2	17.5	12.1	41.8
	Weighted	22.1	12.7	16.6	12.4	36.0
LPC0091	High Flow	32.9	12.4	28.6	10.0	16.3
	Low Flow	23.6	14.5	21.9	8.5	31.5
	Weighted	25.9	14.0	23.5	8.8	27.7
SAM0001	High Flow	48.7	14.4	14.1	13.7	9.0
	Low Flow	23.3	9.4	20.8	11.3	35.2
	Weighted	29.6	10.6	19.1	11.9	28.7
LPC0032	High Flow	29.6	17.7	14.2	17.7	20.8
	Low Flow	18.5	16.5	36.2	5.4	23.4
	Weighted	21.2	16.8	30.7	8.4	22.8

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

STATION	Flow Stratum	% Domestic Animals	% Human	% Livestock	% Wildlife	% Unknown
BEB0009	**High Flow**	37.5	25.0	4.2	0	33.3
	Low Flow	28.9	8.2	24.2	6.6	32.0
	Weighted	31.0	12.4	19.2	4.9	32.4
BPC0006	**High Flow**	16.7	41.7	4.2	0	37.5
	Low Flow	37.5	19.7	14.7	3.0	25.0
	Weighted	32.3	25.2	12.1	2.3	28.1
MEB0000	**High Flow**	8.3	25.0	33.3	4.2	29.2
	Low Flow	30.2	11.5	20.4	11.2	26.6
	Weighted	24.7	14.9	23.7	9.4	27.3
BPC0006	**High Flow**	50.0	20.8	0	4.2	25.0
	Low Flow	26.1	7.7	15.1	7.7	43.3
	Weighted	32.1	11.0	11.3	6.8	38.7
LPC0091	**High Flow**	50.0	12.5	12.5	0	25.0
	Low Flow	28.0	13.9	24.7	8.1	25.2
	Weighted	33.5	13.5	21.7	6.1	25.1
SAM0001	**High Flow**	62.5	20.8	8.3	0	8.3
	Low Flow	24.2	5.1	21.0	5.1	44.4
	Weighted	33.8	9.0	17.9	3.8	35.4
LPC0032	**High Flow**	29.2	33.3	4.2	4.2	29.2
	Low Flow	15.6	18.8	31.6	7.5	26.4
	Weighted	19.0	22.4	24.7	6.6	27.1

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 Double Pipe Creek watershed area. 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, load allocations (LAs) for non point sources and natural background sources. A margin of safety (MOS) is also included and accounts for the uncertainty in the analytical procedures used for water quality modeling, and 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 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.

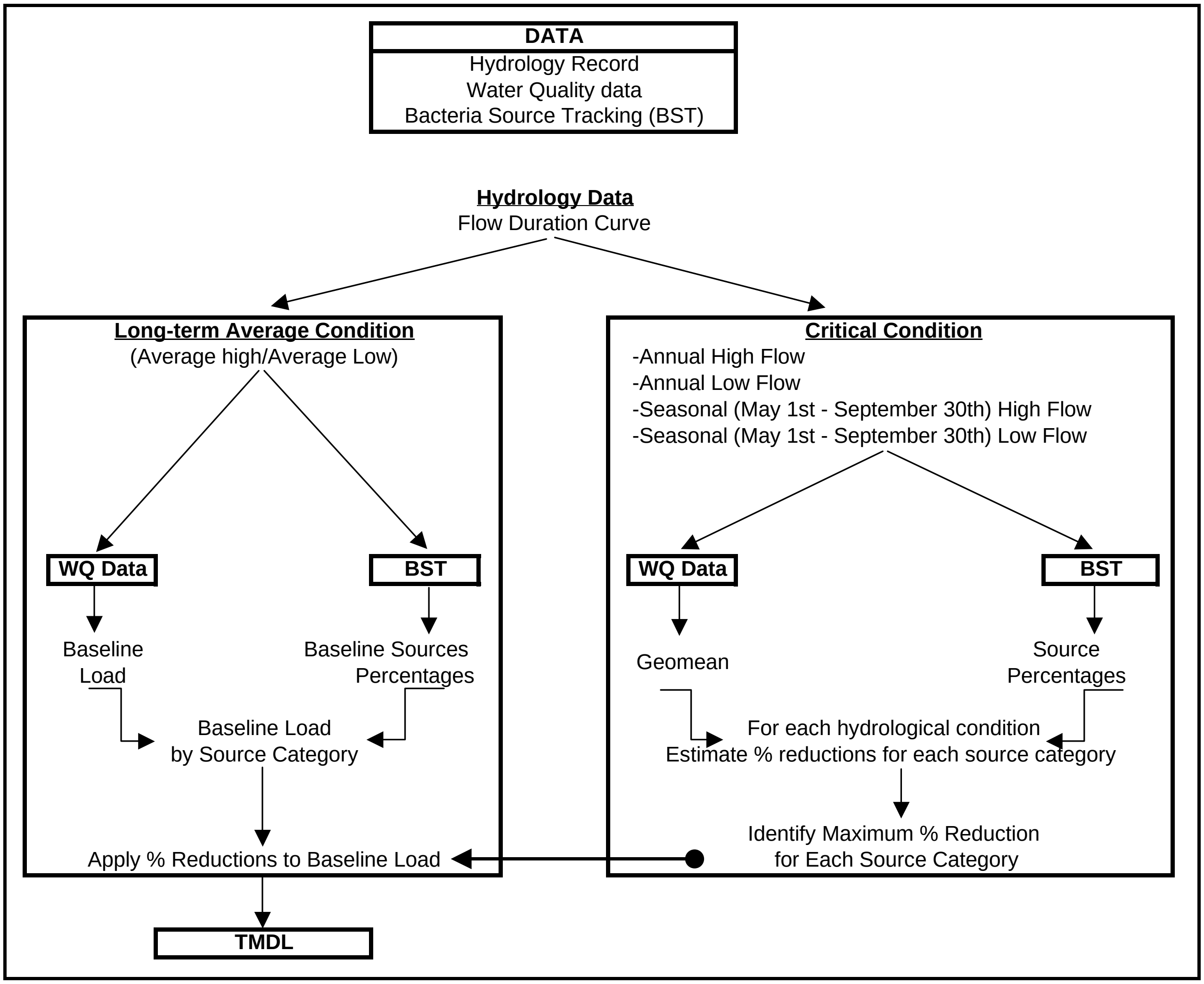


Figure 4.2.1: Diagram of Non-tidal Bacteria TMDL Analysis Framework

4.3 Estimating Baseline Loads

Baseline loads estimated in this TMDL analysis are reported in long-term average loads, using bacteria monitoring data and long-term flow data.

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.

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

The bias correction factor for each stratum is estimated as follows:

$$F1_i = A_i/C_i \tag{6}$$

where

$F1_i$ = 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:

$$L_i = Q_i * C_i * F_1 * F_2 \tag{7}$$

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_1 = Bias correction factor
F_2 = Unit conversion factor (0.0245)

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

$$L = \sum_{i=1}^{2} L_i * W_i \tag{8}$$

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

In the Double Pipe Creek 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 Subwatersheds 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. Of the five main tributaries in the Double Pipe Creek watershed, two have both upstream and downstream monitoring stations (Big Pipe Creek and Little Pipe Creek). The downstream segments of each are monitored at stations BPC0006 and LPC0032, respectively (see Figure 2.2.1), and identified as subwatersheds by adding the extension "sub" to their station names (BPC0006sub and LPC0032sub). Thus, there are a total of seven subwatersheds defined in this analysis.

The total baseline loads from the upstream watersheds, estimated from the monitoring data, were multiplied by a transport factor derived from first order decay. The decay factor 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 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:

$$\sum Q_{us} + Q_{sub} = Q_{ds} \tag{9}$$

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:

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

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 the ratio of high flow concentration to 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:

$$L = Q_{high} W_{high} C_{high} + Q_{low} W_{low} C_{low} \tag{11}$$

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 (10) 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:

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

where

$$R = \frac{C_{high}}{C_{low}} \tag{13}$$

and the final geometric mean concentration is estimated as follows:

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

To estimate the load from subwatershed BPC0006sub, the transported load from stations MEB0000, BPC0120 and BEB0009, estimated as explained above, is subtracted from the load measured at station BPC0006. The difference is assigned to subwatershed BPC0006sub. To estimate the load from subwatershed LPC0032sub, the transported load from stations LPC0091 and SAM0001 is subtracted from the load measured at station LPC0032. The difference is assigned to subwatershed LPC0032sub.

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 BPC0006sub and LPC0032sub were assigned from the analysis for BPC0006 and LPC0032, respectively.

Results of the baseline load calculations are presented in Table 4.3.1.

Table 4.3.1: Baseline Loads Calculations

Sub-watershed	Area (sq. miles)	Q (cfs)	*E. coli* Concentration (MPN/100ml)	Q (cfs)	*E. coli* Concentration (MPN/100ml)	Baseline Load (Billion MPN/year)	Weighted Geometric Mean Conc. MPN/100ml
BEB0009	14.7	48.1	592.9	8.9	788.6	369,052	734
BPC0120	58.0	190.2	445.7	35.1	406.3	1,143,443	416
MEB0000	15.2	49.8	570.5	9.2	895.3	376,282	800
BPC0006sub	22.4	73.5	1,184.7	13.5	1,281.6	1,262,413	1,257
LPC0091	41.7	136.6	2041.3	25.2	953.7	1,772,638	1,154
SAM0001	22.5	73.6	1017.6	13.6	1086.5	1,679,690	1,069
LPC0032sub	18.0	59.1	5,439.3	10.9	2,541.1	5,010,752	3,074

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 wet and dry periods. Seasonality is captured by assessing the time period when water contact recreation is expected (May 1st - September 30th). The average hydrological condition over a 15-year period is 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.

As stated above, Maryland’s proposed fecal bacteria TMDL for Double Pipe Creek has been determined by assessing various hydrological conditions to account for seasonal and annual averaging periods. The five conditions listed in Table 4.4.1were 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 Condition	365 days	All	All	0.25	0.75	Long Term Average
	High	365 days	All	All	0.74	0.26	April 3nd, 2002–April 2rd, 2003
	Low	365 days	All	All	0.0	1.0	Oct 5st, 1996 – Oct 4th, 1997
Seasonal	High	May 1st – Sept 30th	May 1st – Sept 30th	All	0.57	0.43	May 1st - Sept 30th, 1996
	Low	May 1st – Sept 30th	May 1st – Sept 30th	All	0.0	1.0	May 1st – Sept 30th, 2002

The critical condition requirement is met by determining by the maximum reduction per bacteria source that satisfies all hydrological conditions and meet 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 monitoring data for all stations located in the Double Pipe Creek watershed cover a sufficient temporal span (at least one year) to estimate annual and seasonal conditions.

Table 4.4.2 shows the reductions of fecal bacteria required in each subwatershed of Double Pipe Creek to meet water quality standards for designated uses.

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

Subwatershed	Hydrological Condition		Domestic Animals %	Human %	Livestock %	Wildlife %
BEB0009	Annual	Average	94.6%	98.0%	93.5%	6.9%
		High Flow	93.3%	98.0%	89.6%	0.0%
		Low Flow	98.0%	98.0%	95.8%	0.0%
	Seasonal	High Flow	98.0%	98.0%	98.0%	87.3%
		Low Flow	98.0%	98.0%	98.0%	21.4%
	Maximum Source Reduction		98.0%	98.0%	98.0%	87.3%
BPC0120	Annual	Average	70.9%	91.8%	73.0%	0.0%
		High Flow	70.2%	98.0%	72.0%	0.0%
		Low Flow	65.0%	98.0%	72.6%	0.0%
	Seasonal	High Flow	98.0%	98.0%	98.0%	78.9%
		Low Flow	77.3%	98.0%	76.2%	0.0%
	Maximum Source Reduction		98.0%	98.0%	98.0%	78.9%
MEB0000	Annual	Average	98.0%	98.0%	98.0%	14.9%
		High Flow	98.0%	98.0%	98.0%	10.5%
		Low Flow	98.0%	98.0%	98.0%	15.9%
	Seasonal	High Flow	98.0%	98.0%	98.0%	89.8%
		Low Flow	98.0%	98.0%	98.0%	66.8%
	Maximum Source Reduction		98.0%	98.0%	98.0%	89.8%
BPC0006sub	Annual	Average	99.0%	99.0%	99.0%	55.8%
		High Flow	99.0%	99.0%	99.0%	48.2%
		Low Flow	99.0%	99.0%	99.0%	59.1%
	Seasonal	High Flow	99.0%	99.0%	99.0%	95.2%
		Low Flow	99.0%	99.0%	99.0%	40.6%
	Maximum Source Reduction		99.0%	99.0%	99.0%	95.2%

Subwatershed	Hydrological Condition		Domestic Animals %	Human %	Livestock %	Wildlife %
LPC0091	Annual	Average	99.0%	98.5%	99.0%	23.2%
		High Flow	99.0%	98.5%	99.0%	48.6%
		Low Flow	99.0%	98.5%	99.0%	6.3%
	Seasonal	High Flow	99.0%	98.5%	99.0%	79.7%
		Low Flow	99.0%	98.5%	99.0%	22.7%
	Maximum Source Reduction		99.0%	98.5%	99.0%	79.7%
SAM0001	Annual	Average	98.0%	98.0%	98.0%	43.3%
		High Flow	99.0%	99.0%	99.0%	23.7%
		Low Flow	99.0%	99.0%	99.0%	41.4%
	Seasonal	High Flow	99.0%	99.0%	99.0%	98.7%
		Low Flow	99.0%	99.0%	99.0%	53.2%
	Maximum Source Reduction		99.0%	99.0%	99.0%	98.7%
LPC0032sub	Annual	Average	99.0%	99.0%	99.0%	22.8%
		High Flow	99.0%	99.0%	99.0%	70.3%
		Low Flow	85.0%	99.0%	99.0%	0.0%
	Seasonal	High Flow	99.0%	99.0%	99.0%	97.6%
		Low Flow	99.0%	99.0%	99.0%	11.7%
	Maximum Source Reduction		99.0%	99.0%	99.0%	97.6%

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, April 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" were removed and the known sources were then scaled up proportionally so that they totaled 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 BPC0006sub and LPC0032sub, were based on the sources identified at stations BPC0006 and LPC0032, respectively.

Table 4.6.1: Bacteria Source Distributions and Corresponding Baseline Loads Used in the 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	
BEB0009	36.0%	132,716	17.4%	64,063	34.0%	125,467	12.7%	46,806	369,052
BPC0120	40.4%	461,657	31.1%	355,137	19.3%	220,203	9.3%	106,446	1,143,443
MEB0000	35.0%	131,756	17.6%	66,329	31.7%	119,295	15.7%	58,901	376,282
BPC0006sub	34.6%	437,165	20.0%	252,107	26.0%	327,782	19.4%	245,359	1,262,413
LPC0091	21.5%	381,284	46.9%	831,690	3.9%	69,122	27.7%	490,541	1,772,638
SAM0001	41.5%	697,882	14.9%	250,686	26.9%	451,040	16.7%	280,083	1,679,690
LPC0032sub	27.5%	1,379,794	21.7%	1,089,258	39.8%	1,992,715	11.0%	548,984	5,010,752

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 all seven subwatersheds, 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 %	
BEB0009	75%	95%	75%	0%	No
BPC0120	75%	95%	75%	0%	No
MEB0000	75%	95%	75%	0%	No
BPC0006sub	75%	95%	75%	0%	No
LPC0091	75%	95%	75%	0%	No
SAM0001	75%	95%	75%	0%	No
LPC0032sub	75%	95%	75%	0%	No

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, none of the subwatersheds of Double Pipe Creek 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 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 %
BEB0009	98%	98%	98%	87.3%	96.6%
BPC0120	98%	98%	98%	78.9%	96.2%
MEB0000	98%	98%	98%	89.8%	96.7%
BPC0006sub	99%	99%	99%	95.3%	98.3%
LPC0091	99%	99%	99%	77.8%	93.4%
SAM0001	99%	99%	99%	98.7%	98.9%
LPC0032sub	99%	99%	99%	97.6%	98.8%

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/day. These loading caps are for the seven subwatersheds located upstream of their respective monitoring stations: BEB0009, BPC0120, MEB0000, and BPC0006sub; and LPC0091, SAM000, and LPC0032sub.

Annual Average TMDL

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 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 is required to meet water quality standards.

$$TMDL = L_b * (1 - R) \qquad (19)$$

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 TMDLs for the subwatersheds are shown in Tables 4.7.1 and 4.7.2.

Table 4.7.1: Double Pipe Creek Subwatersheds Annual Average TMDL Summary

Subwatershed ID	**Baseline Load *E. coli* (Billion MPN/year)**	**Long Term Average TMDL Load *E. coli* (Billion MPN/year)**	**% Target Reduction**
BEB0009	369,052	12,383	96.6%
BPC0120	1,143,443	43,194	96.2%
MEB0000	376,282	12,366	96.7%
BPC0006sub	1,262,413	21,948	98.3%
LPC0091	1,772,638	116,559	93.4%
SAM0001	1,679,690	17,734	98.9%
LPC0032sub	5,010,752	57,983	98.8%
Total	11,614,269	282,168	97.6 %

Table 4.7.2: TMDL Loads 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**	
BEB0009	21.4%	2,654	10.3%	1,281	20.3%	2,509	48.0%	5,938	12,383
BPC0120	21.4%	9,233	16.4%	7,103	10.2%	4,404	52.0%	22,455	43,194
MEB0000	21.3%	2,635	10.7%	1,327	19.3%	2,386	48.7%	6,019	12,366
BPC0006sub	19.9%	4,372	11.5%	2,521	14.9%	3,278	53.7%	11,777	21,948
LPC0091	3.3%	3,813	10.7%	12,475	0.6%	691	85.4%	99,580	116,559
SAM0001	39.4%	6,979	14.1%	2,507	25.4%	4,510	21.1%	3,737	17,734
LPC0032sub	23.8%	13,798	18.8%	10,893	34.4%	19,927	23.1%	13,366	57,983

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 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 Double Pipe Creek daily TMDL, 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 loads 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 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).

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

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 maximum daily load (MDL) for each flow stratum at each station is estimated using the upper boundary percentile computed in the first step above. Finally, maximum daily loads are computed from these MDL concentrations and their corresponding flows.

Results of the fecal bacteria MDL analysis for the Double Pipe Creek subwatersheds are shown in Table 4.7.3.

Table 4.7.3: Double Pipe Creek 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)
BEB0009	High Flow	743	221
	Low Flow	47	
BPC0120	High Flow	8,368	2,201
	Low Flow	147	
MEB0000	High Flow	1,012	350
	Low Flow	129	
BPC0006sub	High Flow	4,699	1,333
	Low Flow	211	
LPC0091	High Flow	9,063	2,370
	Low Flow	139	
SAM0001	High Flow	1,562	458
	Low Flow	90	
LPC0032sub	High Flow	4,412	1,149
	Low Flow	62	

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

4.8 TMDL Allocations

The TMDL allocations include the load allocation (LA) for certain nonpoint sources, and waste load allocations (WLAs) for WWTPs (if present in the watershed) and for NPDES-regulated stormwater entities (if present). The Stormwater WLA includes any nonpoint source loads deemed to be transported and discharged by regulated stormwater systems.). The margin of safety is explicit and is incorporated in the analysis using a conservative assumption; it is not specified as a separate term. The final loads are based on average hydrological conditions, with reductions estimated based on critical hydrological conditions. The load reduction scenario results in a load allocation 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.

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 (those nonpoint sources or portions thereof not transported and discharged by stormwater systems) and the WLA (point sources including

WWTPs, and NPDES regulated stormwater entities). Only the final LA or WLA is reported in this TMDL. Note that the assignment of a small allowable human load to the Stormwater WLA 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 Allocations

Allocation Category	LA	WLA	
		WWTPs	Stormwater
Human		X	X
Domestic			X
Livestock	X		
Wildlife	X		X

Load Allocation (LA)

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 stormwater entities, the nonpoint source contribution is estimated by subtracting any WWTP and CSO loads from the TMDL human load, and is then assigned to the LA. 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 stormwater WLA. There are six NPDES WWTPs with permits regulating the discharge of bacteria in the Double Pipe Creek watershed. There are no subwatersheds with assigned NPDES CSO WLA.

Livestock loads are all assigned to the LA. Domestic animals (pets) loads are assigned to the LA in watersheds with no MS4s or other NPDES-regulated stormwater systems. Since the entire Double Pipe Creek watershed is covered by NPDES MS4 permits, bacteria loads from domestic animal sources are assigned to the Stormwater WLA in all seven subwatersheds of Double Pipe Creek. However, wildlife sources will be distributed between the LA and the Stormwater WLA, based on a ratio of the amount of pervious non-urban and pervious urban land.

Waste Load Allocation (WLA)

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 existing NPDES-regulated stormwater permits, domestic animal bacteria loads are grouped together into a single Stormwater WLA, along with certain other nonpoint source loads. In watersheds with no existing NPDES-regulated stormwater permits, these loads will be included in the LA.

The jurisdictions within the Double Pipe Creek watershed, Carroll County and Frederick County, are covered by individual Phase I MS4 program regulations. Based on EPA's guidance, the Stormwater WLA 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. In addition to the counties' MS4s, the Stormwater WLA category encompasses any other NPDES regulated Phase I and Phase II stormwater entities in the watershed, including State and federal permittees. The Stormwater WLA distribution between Carroll County and Frederick County is presented in Table 4.8.2.

Table 4.8.2: Annual Average Stormwater Allocations

Station	**Stormwater WLA Loads (Billion MPN/year)**				
	Carroll County	%	Frederick County	%	Total
BEB0009	4,449	100%	0.0	0%	4,449
BPC0120	18,286	100%	0.0	0%	18,286
MEB0000	4,784	100%	0.0	0%	4,784
BPC0006sub	7,129	100%	0.0	0%	7,129
LPC0091	21,563	100%	0.0	0%	21,563
SAM0001	4,408	45%	5,332	55%	9,741
LPC0032sub	6,745	27%	18,552	73%	25,297
Total	67,365		23,884		91,249

Municipal and Industrial WWTPs

As explained in the source assessment section above, there are six municipal WWTPs with permits regulating the discharge of bacteria into Double Pipe Creek. There are no industrial WWTPs with a permit regulating the discharge of bacteria directly into the Creek. These six municipal WWTPs discharge bacteria into three subwatersheds: Little Pipe Creek (LPC0091), Bear Branch (BEB0009) and Big Pipe Creek (BPC0006). Bacteria loads assigned to these WWTPs are allocated as the WWTP WLA.

4.9 Summary

The long-term annual average TMDLs and the maximum daily loads for the Double Pipe Creek subwatersheds are presented in Tables 4.9.1 and 4.9.2.

Table 4.9.1: Double Pipe Creek Watershed TMDL

Subwatersheds	TMDL	LA	Stormwater WLA	WWTP WLA
	Billions MPN *E. coli*/year			
Bear Branch (BEB0009)	12,383	7,866	4,449	68
Big Pipe Creek (BPC0120)	43,194	24,909	18,286	N/A
Meadow Branch (MEB0000)	12,366	7,582	4,784	N/A
Big Pipe Creek (BPC0006sub)	21,948	14,775	7,129	44
Little Pipe Creek (LPC0091)	116,559	85,718	21,563	9,279
Sam's Creek (SAM0001)	17,734	7,993	9,741	N/A
Little Pipe Creek (LPC0032sub)	57,983	32,686	25,297	N/A
TOTAL*	282,168	181,528	91,249	9,391

*This total load represents the sum of the individual TMDLs of the subwatersheds presented above and not the TMDL for the Double Pipe Creek watershed as a whole.

Table 4.9.2: Double Pipe Creek Watershed Maximum Daily Loads

Subwatersheds	TMDL	LA	Stormwater WLA	WWTP WLA
	Billions MPN *E. coli*/day			
Bear Branch (BEB0009)	221	163	58	0.6
Big Pipe Creek (BPC0120)	2,201	1,631	570	0
Meadow Branch (MEB0000)	350	252	98	0
Big Pipe Creek (BPC0006sub)	1,333	1,050	283	0.4
Little Pipe Creek (LPC0091)	2,370	1,918	373	79
Sam's Creek (SAM0001)	458	271	187	0
Little Pipe Creek (LPC0032sub)	1,149	864	285	0
TOTAL*	8,082	6,148	1,854	80

*This total load represents the sum of the individual TMDLs of the subwatersheds presented above and not the TMDL for the Double Pipe Creek watershed as a whole.

See Appendix E for an explanation of the hydrologic relationship between the Double Pipe Creek, Upper Monocacy River, and Lower Monocacy River watersheds and how this relationship affects the fecal bacteria TMDLs for those watersheds.

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 Double Pipe Creek 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 wasteload allocations can and will be implemented. In the Double Pipe Creek watershed, the TMDL analysis indicates that, for all seven 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. Double Pipe Creek and its tributaries Big Pipe Creek, Little Pipe Creek, Bear Branch, Meadow Creek and Sam's Creek may not be able to attain water quality standards. The fecal bacteria load reductions required to meet water quality criteria in all seven subwatersheds of the Double Pipe Creek 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 wildlife controls 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.

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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
BEB0009	11/04/2003	20.4052	340
BEB0009	11/18/2003	25.7711	290
BEB0009	12/02/2003	16.0066	200
BEB0009	12/16/2003	6.0595	520
BEB0009	01/07/2004	25.4974	100
BEB0009	01/22/2004	45.0265	400
BEB0009	02/05/2004	22.1026	700
BEB0009	02/19/2004	7.6291	60
BEB0009	03/03/2004	23.2707	490
BEB0009	03/17/2004	21.5733	190
BEB0009	04/07/2004	21.1535	290
BEB0009	04/21/2004	24.2015	430
BEB0009	05/12/2004	41.4309	1080
BEB0009	05/26/2004	17.5032	14200
BEB0009	06/09/2004	33.5828	1850
BEB0009	06/23/2004	35.5539	660
BEB0009	07/08/2004	9.8011	13000
BEB0009	07/21/2004	62.9494	1310
BEB0009	08/11/2004	60.0475	4880
BEB0009	08/25/2004	65.4316	750
BEB0009	09/09/2004	65.4316	1220
BEB0009	09/22/2004	67.2203	820
BPC0006	11/04/2003	20.4052	200
BPC0006	11/18/2003	25.7711	150
BPC0006	12/02/2003	16.0066	250
BPC0006	12/16/2003	6.0595	1660
BPC0006	01/07/2004	25.4974	100
BPC0006	01/22/2004	45.0265	10
BPC0006	02/05/2004	22.1026	1120
BPC0006	02/19/2004	7.6291	530

Sampling Station Identifier	Date	Daily flow frequency	*E. coli* MPN/100ml
BPC0006	03/03/2004	23.2707	260
BPC0006	03/17/2004	21.5733	380
BPC0006	04/07/2004	21.1535	150
BPC0006	04/21/2004	24.2015	130
BPC0006	05/12/2004	41.4309	200
BPC0006	05/26/2004	17.5032	17800
BPC0006	06/09/2004	33.5828	540
BPC0006	06/23/2004	35.5539	460
BPC0006	07/08/2004	9.8011	24190
BPC0006	07/21/2004	62.9494	180
BPC0006	08/11/2004	60.0475	300
BPC0006	08/25/2004	65.4316	240
BPC0006	09/09/2004	65.4316	400
BPC0006	09/22/2004	67.2203	290
BPC0120	11/04/2003	20.4052	180
BPC0120	11/18/2003	25.7711	150
BPC0120	12/02/2003	16.0066	230
BPC0120	12/16/2003	6.0595	1550
BPC0120	01/07/2004	25.4974	110
BPC0120	01/22/2004	45.0265	230
BPC0120	02/05/2004	22.1026	560
BPC0120	02/19/2004	7.6291	50
BPC0120	03/03/2004	23.2707	30
BPC0120	03/17/2004	21.5733	150
BPC0120	04/07/2004	21.1535	110
BPC0120	04/21/2004	24.2015	220
BPC0120	05/12/2004	41.4309	240
BPC0120	05/26/2004	17.5032	29100
BPC0120	06/09/2004	33.5828	660
BPC0120	06/23/2004	35.5539	9210
BPC0120	07/08/2004	9.8011	24190
BPC0120	07/21/2004	62.9494	310
BPC0120	08/11/2004	60.0475	360
BPC0120	08/25/2004	65.4316	250

Sampling Station Identifier	Date	Daily flow frequency	*E. coli* MPN/100ml
BPC0120	09/09/2004	65.4316	620
BPC0120	09/22/2004	67.2203	520
LPC0032	11/04/2003	20.4052	720
LPC0032	11/18/2003	25.7711	610
LPC0032	12/02/2003	16.0066	2480
LPC0032	12/16/2003	6.0595	5790
LPC0032	01/07/2004	25.4974	180
LPC0032	01/22/2004	45.0265	180
LPC0032	02/05/2004	22.1026	3610
LPC0032	02/19/2004	7.6291	660
LPC0032	03/03/2004	23.2707	220
LPC0032	03/17/2004	21.5733	2140
LPC0032	04/07/2004	21.1535	440
LPC0032	04/21/2004	24.2015	740
LPC0032	05/12/2004	41.4309	2220
LPC0032	05/26/2004	17.5032	130000
LPC0032	06/09/2004	33.5828	2100
LPC0032	06/23/2004	35.5539	2760
LPC0032	07/08/2004	9.8011	24190
LPC0032	07/21/2004	62.9494	1480
LPC0032	08/11/2004	60.0475	930
LPC0032	08/25/2004	65.4316	1230
LPC0032	09/09/2004	65.4316	1470
LPC0032	09/22/2004	67.2203	2910
LPC0091	11/04/2003	20.4052	860
LPC0091	11/18/2003	25.7711	590
LPC0091	12/02/2003	16.0066	420
LPC0091	12/16/2003	6.0595	2610
LPC0091	01/07/2004	25.4974	570
LPC0091	01/22/2004	45.0265	250
LPC0091	02/05/2004	22.1026	3870
LPC0091	02/19/2004	7.6291	5790
LPC0091	03/03/2004	23.2707	210
LPC0091	03/17/2004	21.5733	1020

Sampling Station Identifier	Date	Daily flow frequency	*E. coli* MPN/100ml
LPC0091	04/07/2004	21.1535	1840
LPC0091	04/21/2004	24.2015	820
LPC0091	05/12/2004	41.4309	2480
LPC0091	05/26/2004	17.5032	15530
LPC0091	06/09/2004	33.5828	1730
LPC0091	06/23/2004	35.5539	1440
LPC0091	07/08/2004	9.8011	24190
LPC0091	07/21/2004	62.9494	930
LPC0091	08/11/2004	60.0475	860
LPC0091	08/25/2004	65.4316	910
LPC0091	09/09/2004	65.4316	1330
LPC0091	09/22/2004	67.2203	1180
MEB0000	11/04/2003	20.4052	420
MEB0000	11/18/2003	25.7711	190
MEB0000	12/02/2003	16.0066	390
MEB0000	12/16/2003	6.0595	1540
MEB0000	01/07/2004	25.4974	160
MEB0000	01/22/2004	45.0265	100
MEB0000	02/05/2004	22.1026	1670
MEB0000	02/19/2004	7.6291	70
MEB0000	03/03/2004	23.2707	20
MEB0000	03/17/2004	21.5733	370
MEB0000	04/07/2004	21.1535	160
MEB0000	04/21/2004	24.2015	880
MEB0000	05/12/2004	41.4309	1010
MEB0000	05/26/2004	17.5032	8800
MEB0000	06/09/2004	33.5828	1790
MEB0000	06/23/2004	35.5539	1850
MEB0000	07/08/2004	9.8011	7700
MEB0000	07/21/2004	62.9494	1380
MEB0000	08/11/2004	60.0475	2140
MEB0000	08/25/2004	65.4316	780
MEB0000	09/09/2004	65.4316	17330
MEB0000	09/22/2004	67.2203	730

Sampling Station Identifier	Date	Daily flow frequency	*E. coli* MPN/100ml
SAM0001	11/04/2003	20.4052	600
SAM0001	11/18/2003	25.7711	740
SAM0001	12/02/2003	16.0066	680
SAM0001	12/16/2003	6.0595	730
SAM0001	01/07/2004	25.4974	90
SAM0001	01/22/2004	45.0265	50
SAM0001	02/05/2004	22.1026	2360
SAM0001	02/19/2004	7.6291	110
SAM0001	03/03/2004	23.2707	50
SAM0001	03/17/2004	21.5733	290
SAM0001	04/07/2004	21.1535	500
SAM0001	04/21/2004	24.2015	1300
SAM0001	05/12/2004	41.4309	1870
SAM0001	05/26/2004	17.5032	68700
SAM0001	06/09/2004	33.5828	1380
SAM0001	06/23/2004	35.5539	1580
SAM0001	07/08/2004	9.8011	24190
SAM0001	07/21/2004	62.9494	7700
SAM0001	08/11/2004	60.0475	2360
SAM0001	08/25/2004	65.4316	2480
SAM0001	09/09/2004	65.4316	4110
SAM0001	09/22/2004	67.2203	990

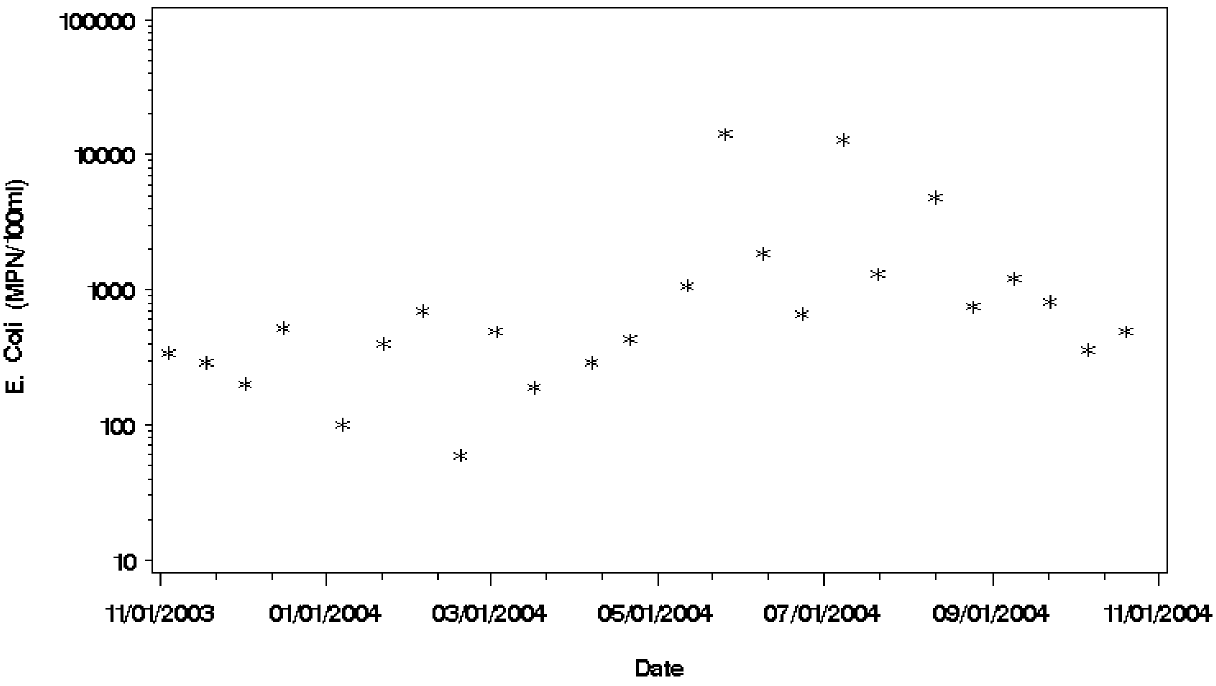

Figure A-1: ***E. coli*** **Concentration vs. Time for Double Pipe Creek Monitoring Station BEB0009**

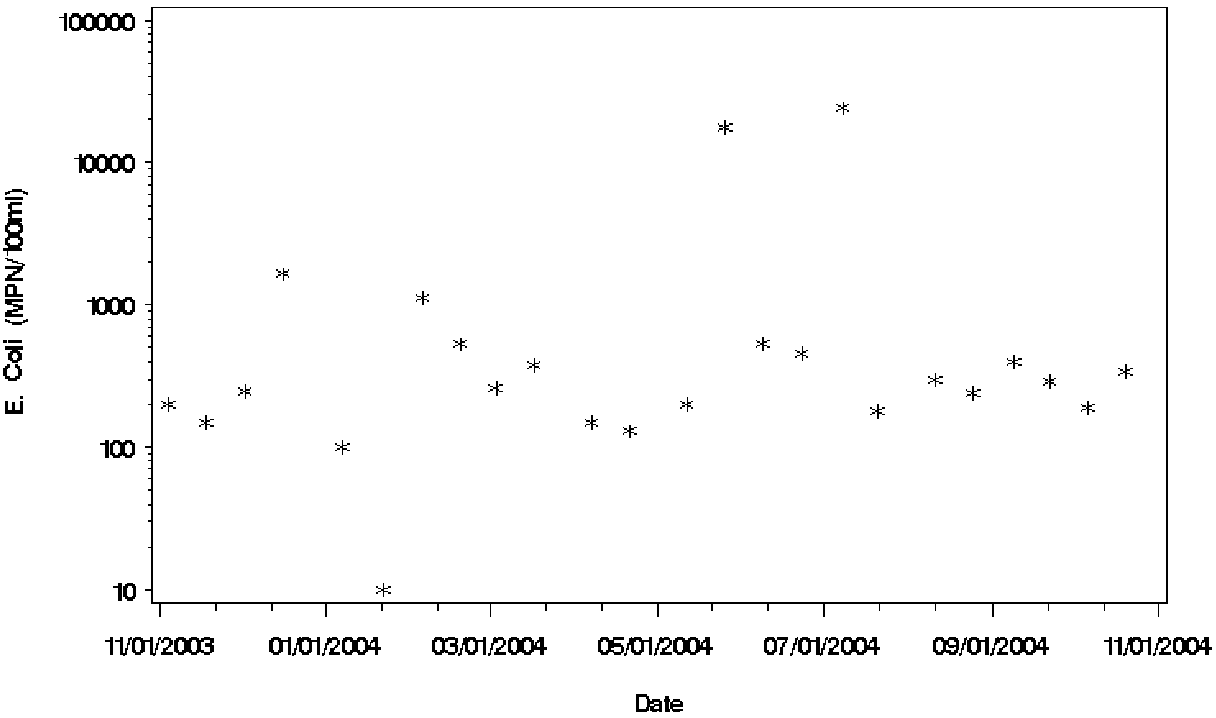

Figure A-2: ***E. coli*** **Concentration vs. Time for Double Pipe Creek Monitoring Station BPC0006**

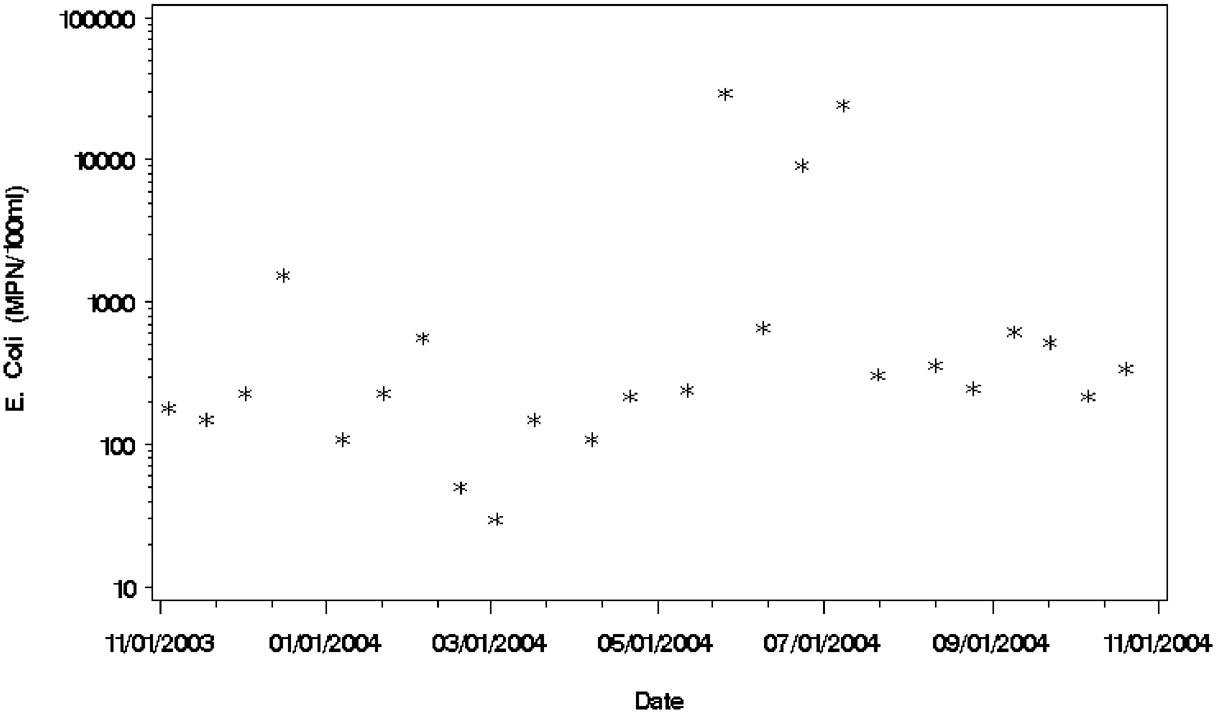

Figure A-3: ***E. coli*** **Concentration vs. Time for Double Pipe Creek Monitoring Station BPC0120**

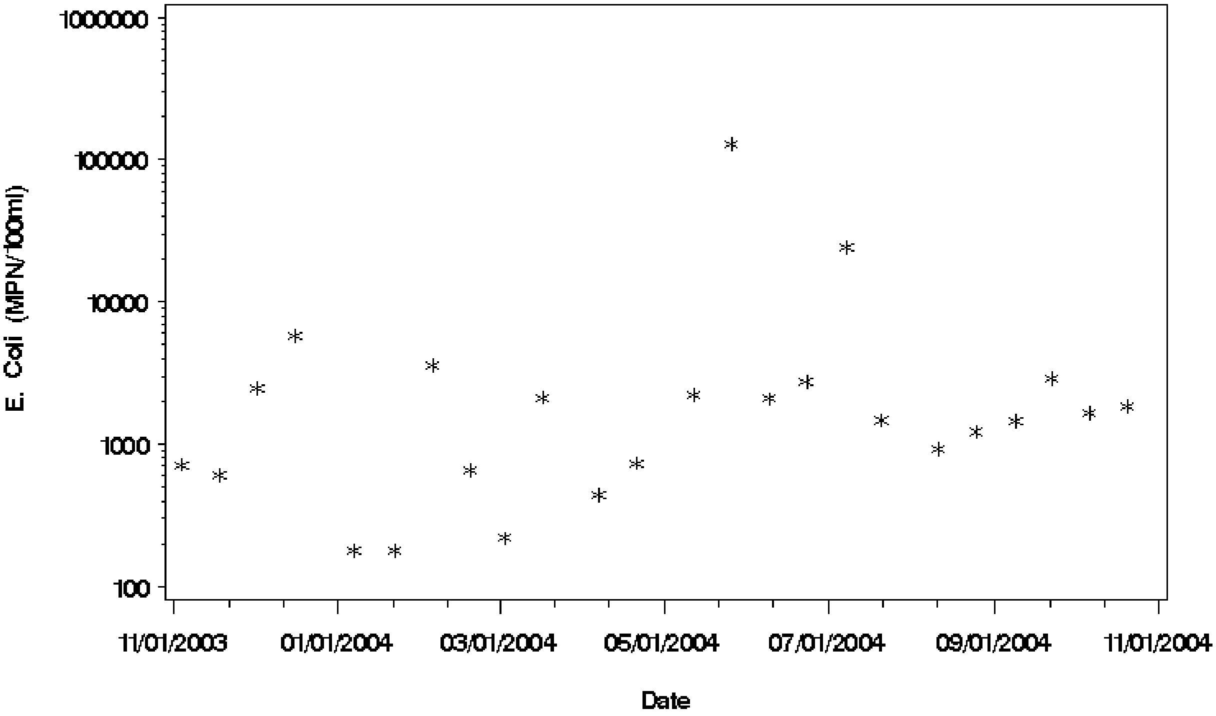

Figure A-4: ***E. coli*** **Concentration vs. Time for Double Pipe Creek Monitoring Station LPC0032**

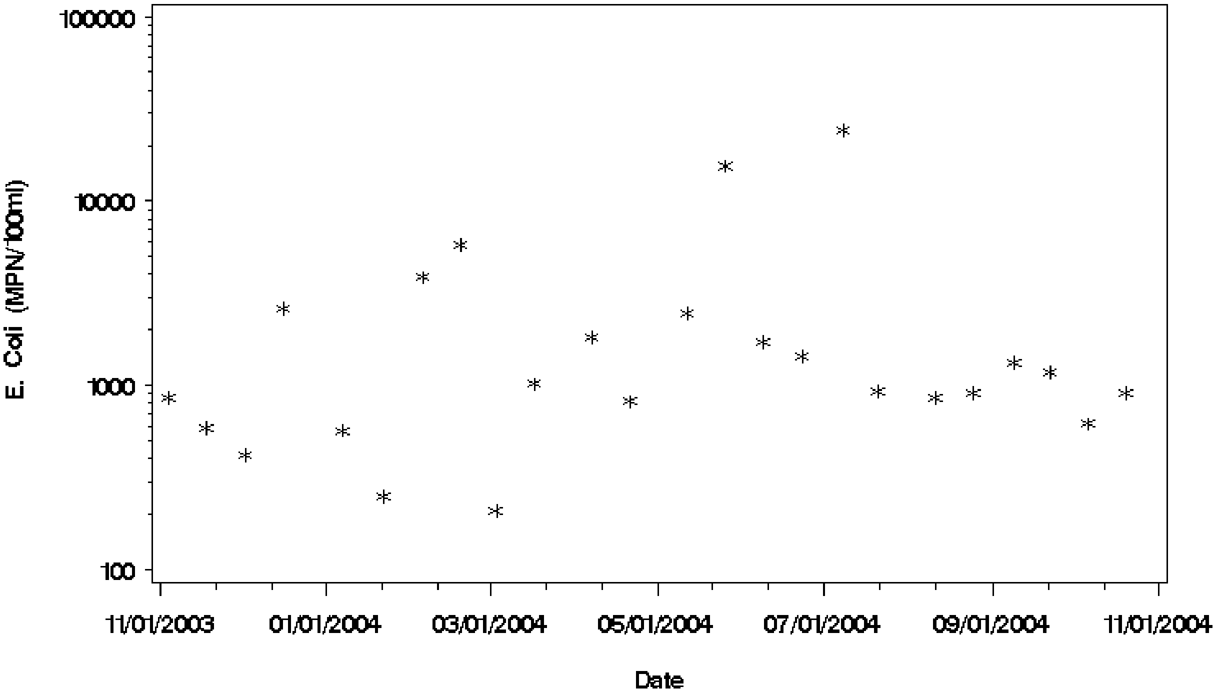

Figure A-5: ***E. coli*** **Concentration vs. Time for Double Pipe Creek Monitoring Station LPC0091**

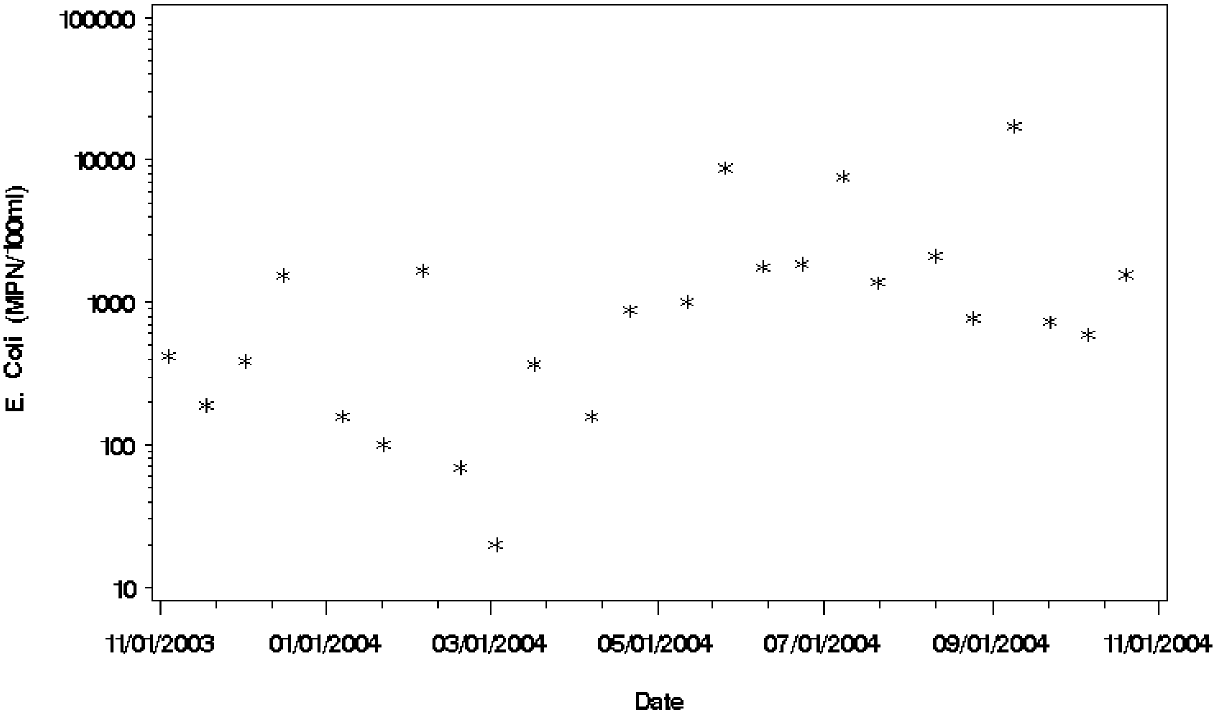

Figure A-6: ***E. coli*** **Concentration vs. Time for Double Pipe Creek Monitoring Station MEB0000**

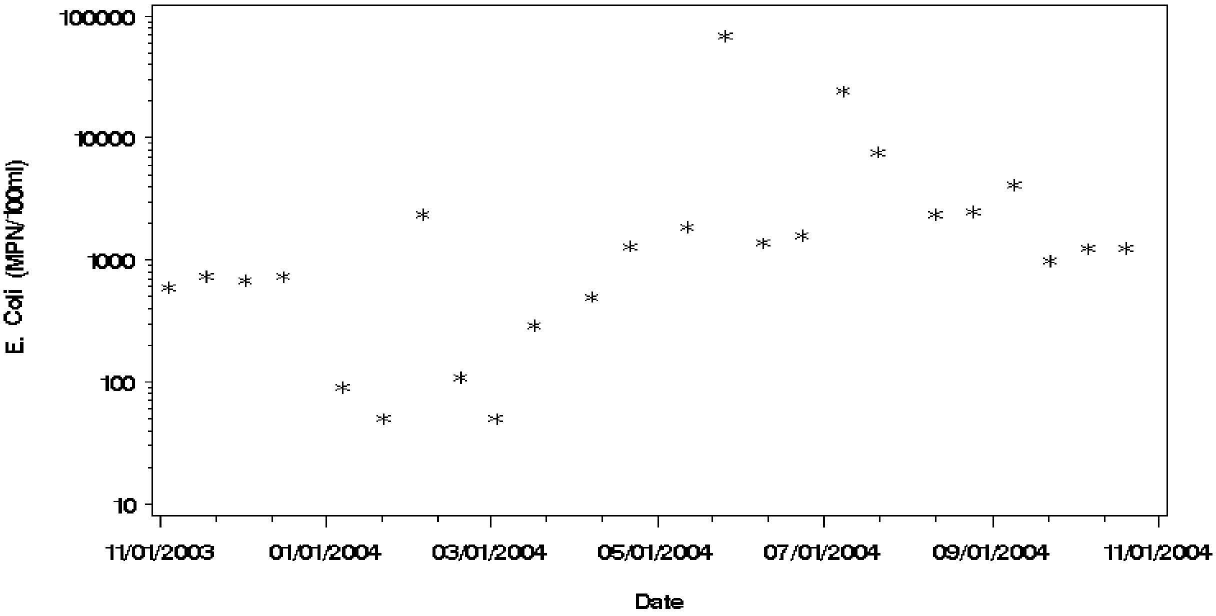

Figure A-7: *E. coli* Concentration vs. Time for Double Pipe Creek Monitoring Station SAM0001

Appendix B – Flow Duration Curve Analysis to Define Strata

The Double Pipe Creek 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 Double Pipe Creek watershed has one active USGS flow gauge (01639500). The gauge and dates of information used are as follows:

Table B-1: USGS Gauges in the Double Pipe Creek Watershed

USGS Gage #	Dates used	Description
01639500	October 1, 1989 to September 30, 2004	Big Pipe Creek near Bruceville, MD

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

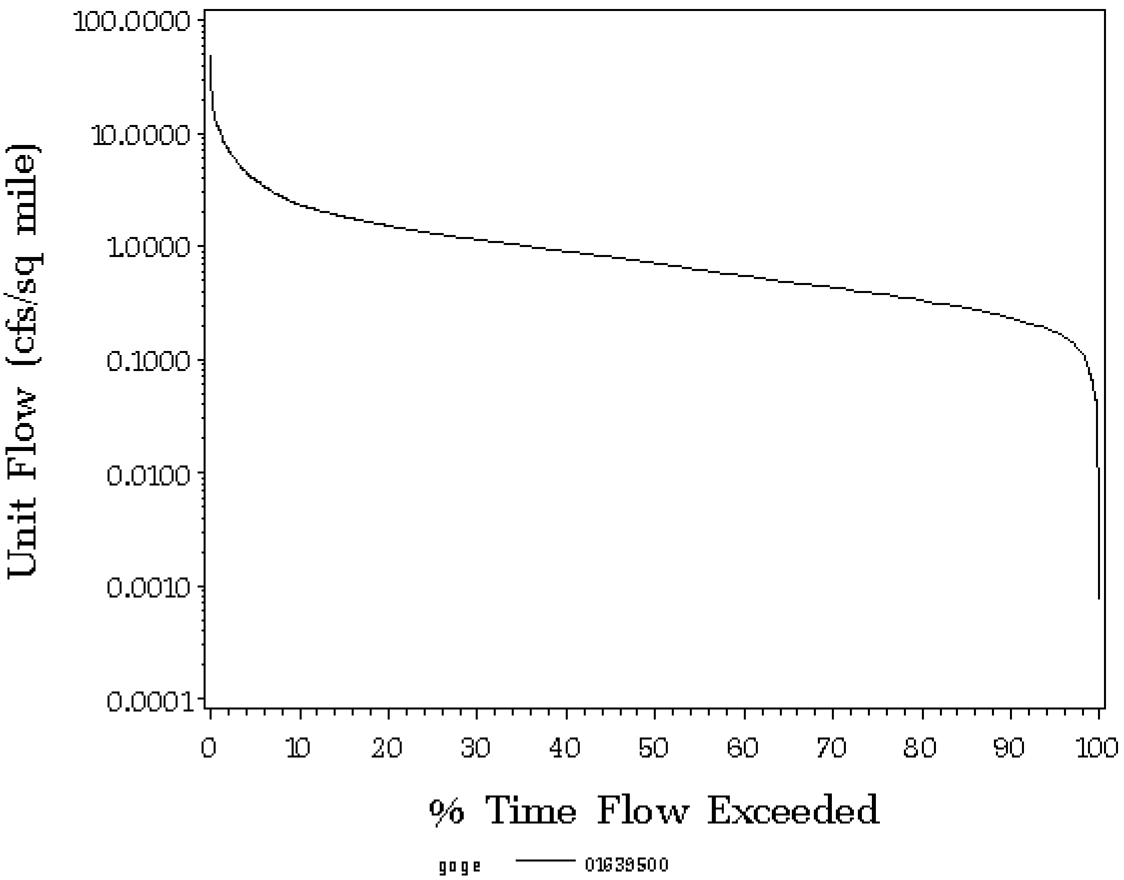

Figure B-1: Double Pipe Creek Flow Duration Curves

Based on the long-term flow data for the Double Pipe Creek watershed and other watersheds in the region (i.e., the Upper Monocacy River 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 21st 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-8 show the Double Pipe Creek *E. coli* monitoring data with corresponding flow frequency for the average annual and the seasonal conditions.

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 Double Pipe Creek, there are sufficient samples in both the high flow strata to estimate the geometric means. For the low flow strata only three samples exist, therefore the mid and low flow strata will be combined to calculate the geometric mean.

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) High Flow Condition
(5) Seasonal (May 1st – September 30th) Low Flow Condition

Weighted geometric means for the average annual and the seasonal conditions are plotted with the monitoring data on Figures B-2 to B-8.

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

Hydrological Condition		Subwatershed	Weighting Factor High Flow	Weighting Factor Low Flow
Annual	Average Condition	All	0.25	0.75
	High	All	0.74	0.26
	Low	All	0.0	1.0
Season	High	All	0.57	0.43
	Low	All	0.0	1.0

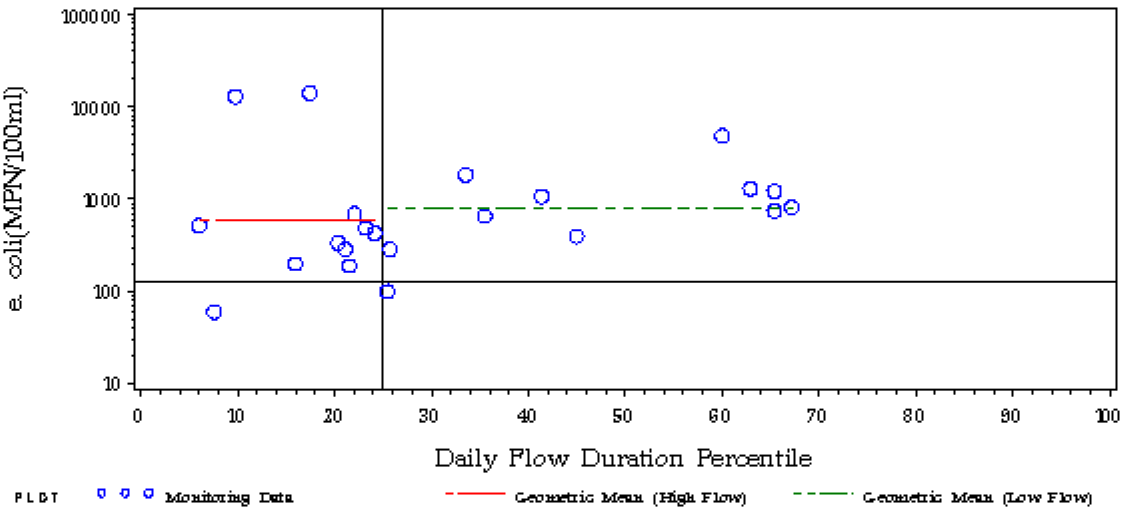

Figure B-2: *E. coli* Concentration vs. Flow Duration for Double Pipe Creek Monitoring Station BEB0009

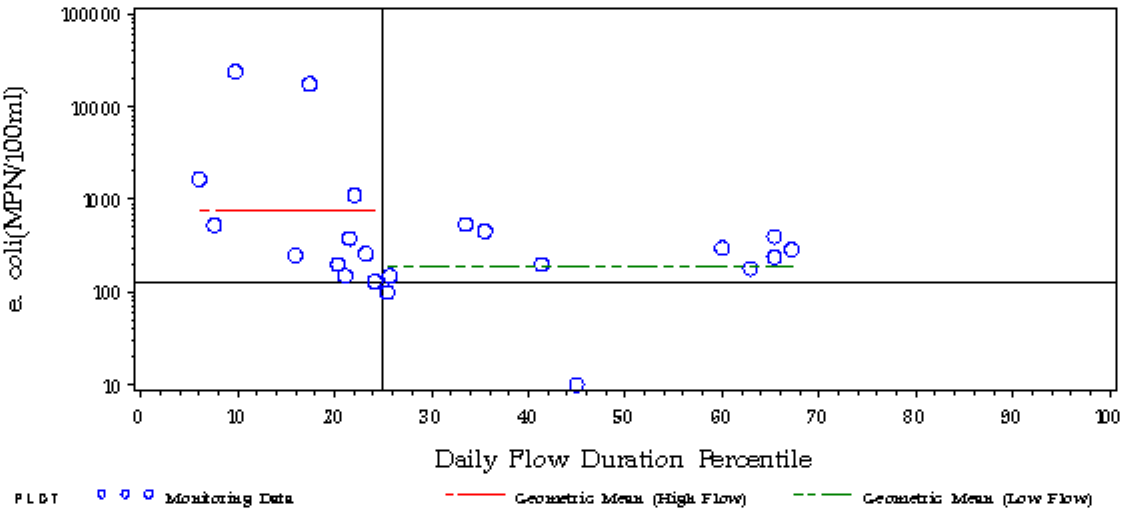

Figure B-3: *E. coli* Concentration vs. Flow Duration for Double Pipe Creek Monitoring Station BPC0006

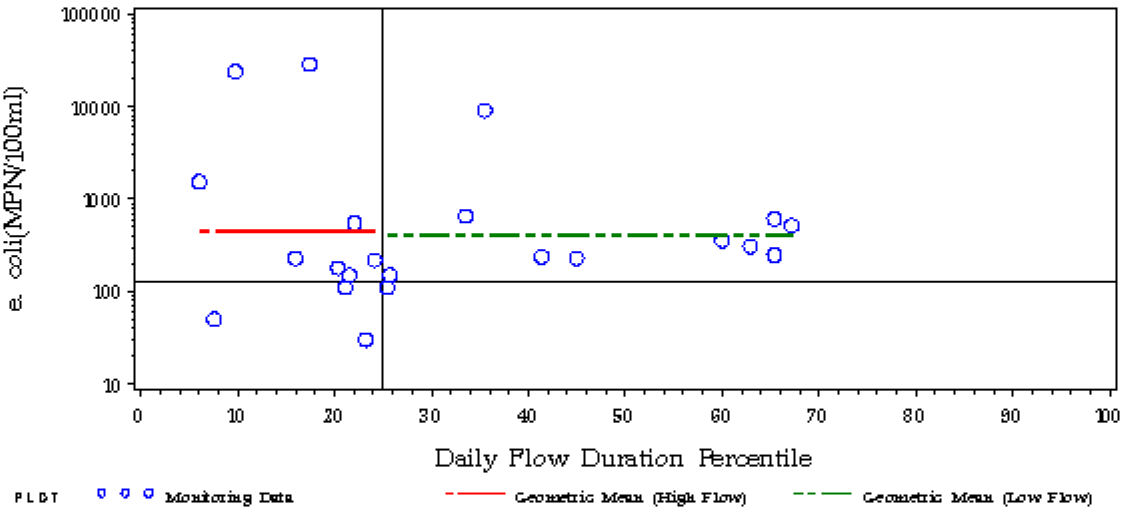

Figure B-4: *E. coli* Concentration vs. Flow Duration for Double Pipe Creek Monitoring Station BPC0120

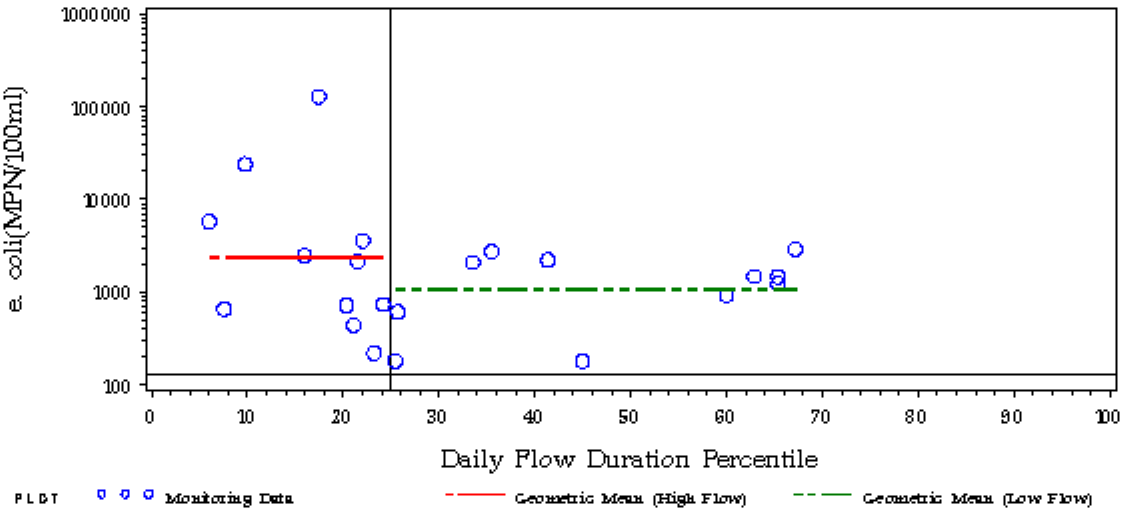

Figure B-5: *E. coli* Concentration vs. Flow Duration for Double Pipe Creek Monitoring Station LPC0032

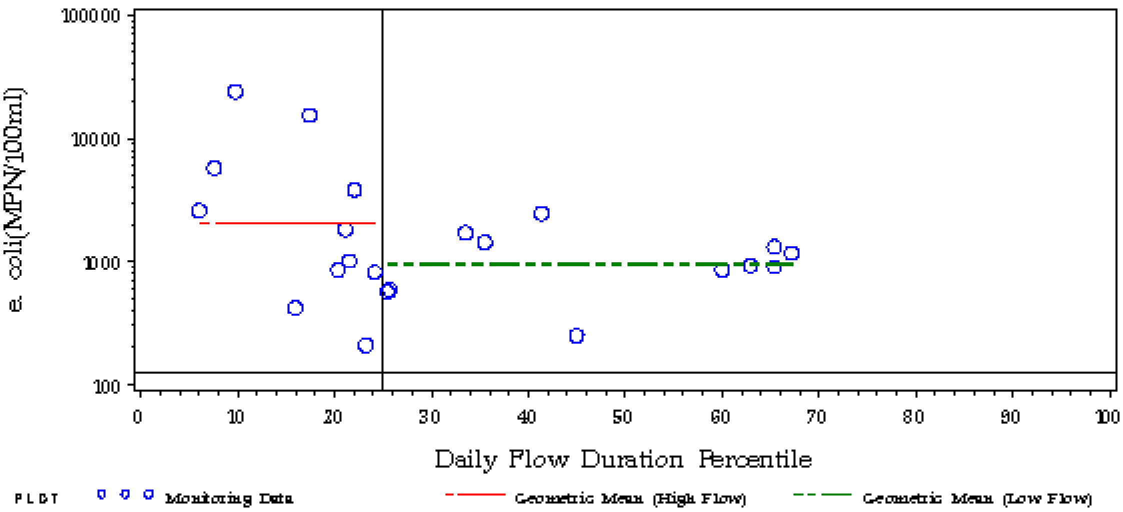

Figure B-6: *E. coli* Concentration vs. Flow Duration for Double Pipe Creek Monitoring Station LPC0091

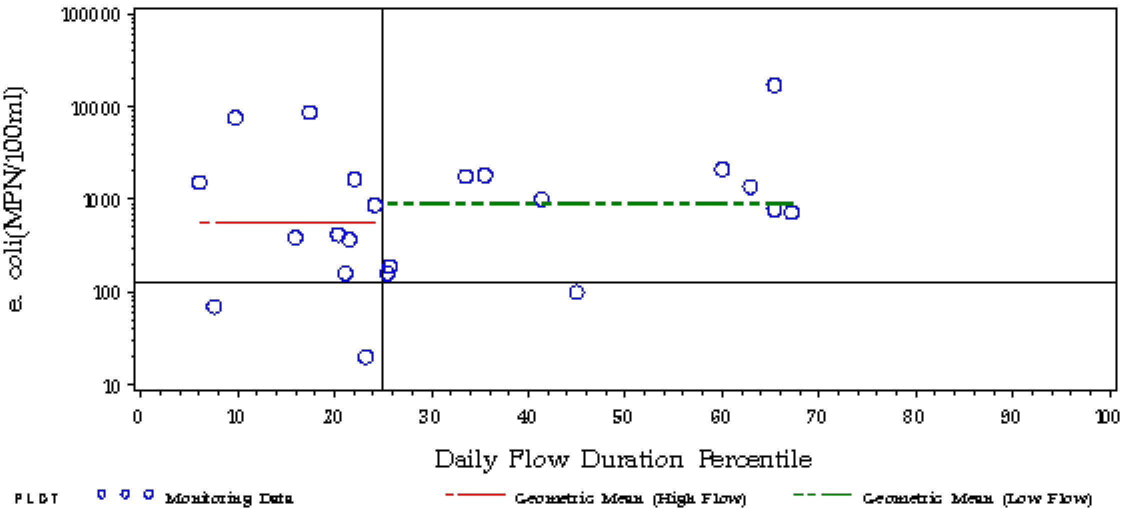

Figure B-7: ***E. coli*** **Concentration vs. Flow Duration for Double Pipe Creek Monitoring Station MEB0000**

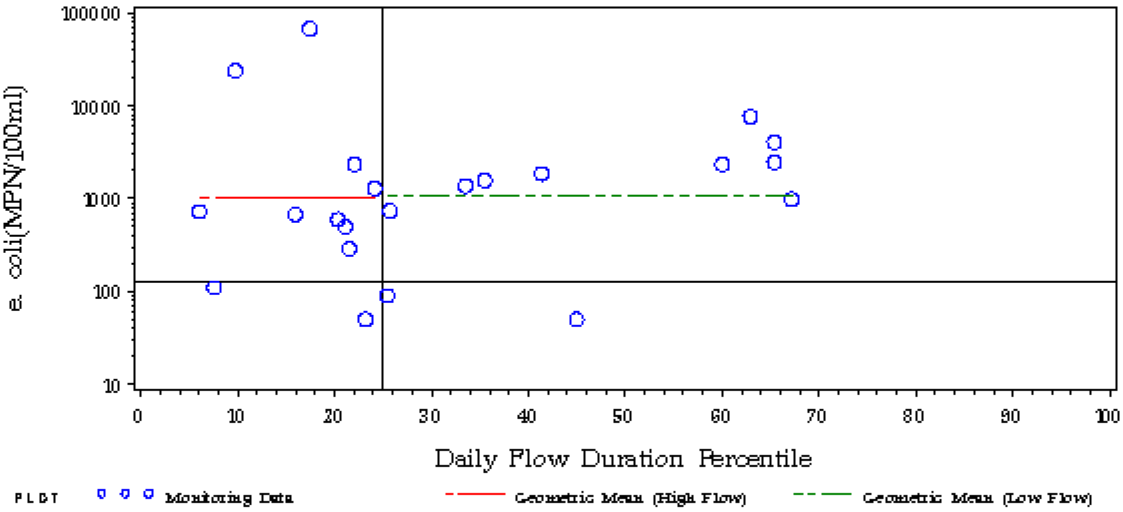

Figure B-8: ***E. coli*** **Concentration vs. Flow Duration for Double Pipe Creek Monitoring Station SAM0001**

Appendix C – BST Report

Identifying Sources of Fecal Pollution in Double Pipe Creek Watershed, Maryland

June 2004 – October 2006

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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.

Double Pipe Creek Watershed ARA Results

Known-Source Library. A 1,684 known-source isolate library was constructed that included 571 isolates from sources in the Double Pipe Creek Watershed (DOP) combined with 559 isolates from the Upper Monocacy River Watershed (UMO), and 554 isolates from the Lower Monocacy River Watershed (LMO). The known sources in the combined DOP-LMO-UMO library were grouped into four categories: humans, livestock (cows and horses), pets (dogs), and wildlife (deer, fox, goose, muskrat, and raccoon) (see Table 2-DOP). 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) were calculated (Table 3-DOP).

Table C-2: Double Pipe Creek. Category, total number, and number of unique patterns in the Double Pipe Creek known-source library and in the combined DOP-LMO-UMO known-source library.

Category	Potential Sources	Total Isolates	Unique Patterns
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
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

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: Double Pipe Creek. Number of isolates not classified, percent unknown, and percent correct for eight (8) threshold probabilities for DOP 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	59.9%	59.9%	61.5%	61.6%	69.4%	89.9%	96.9%	98.1%
% unknown	0.0%	0.0%	4.4%	26.1%	46.8%	70.4%	77.8%	81.8%
# not classified	0	0	25	149	267	402	444	467

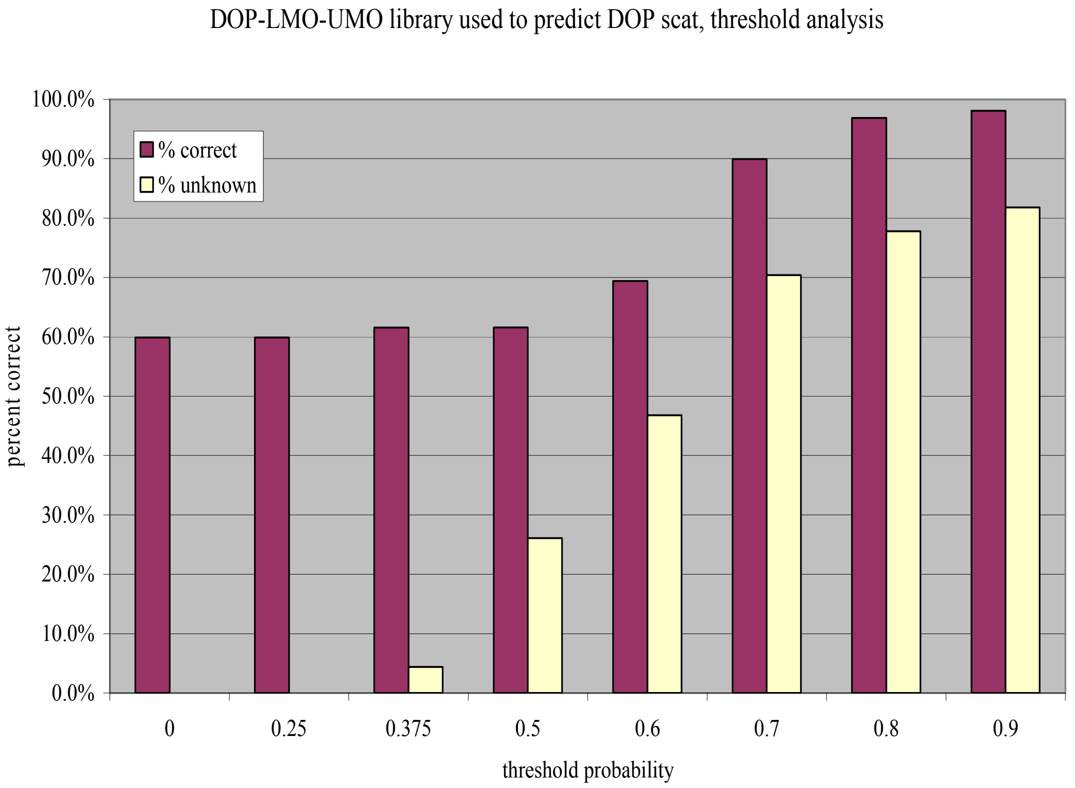
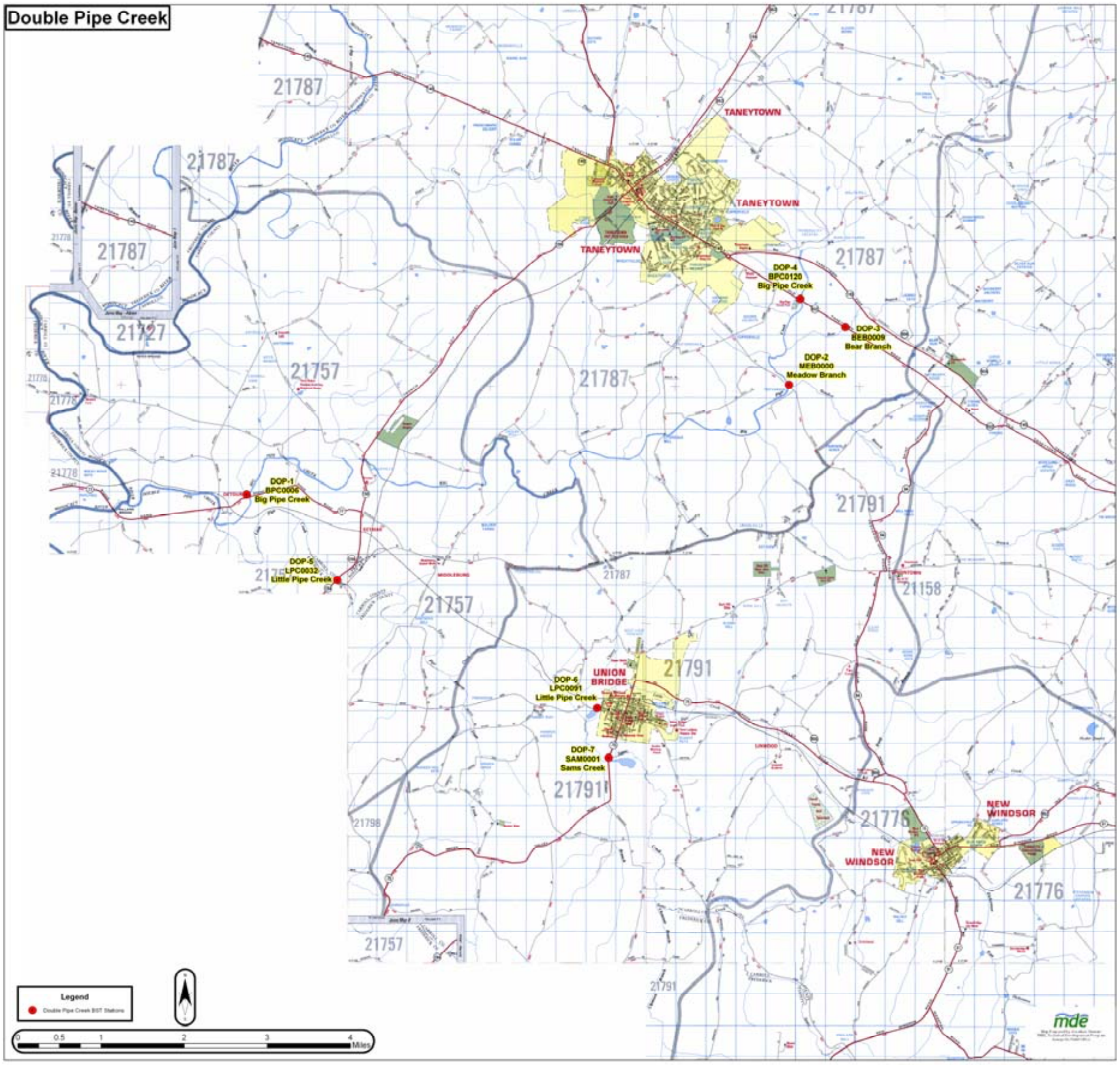


Figure C-1: Double Pipe Creek Classification Model: Percent Correct versus Percent Unknown using a combined DOP-LMO-UMO library.



Note: Red dots indicate water monitoring sites.

Figure C-2: Map of Double Pipe Creek Watershed.

For Double Pipe Creek Watershed, a cutoff probability of 0.50 (50%) was shown to yield an ARCC of 62%. The resulting rates of correct classification for the four categories of sources in the Double Pipe Creek portion of the library, using the cutoff probability of 0.50 (50%), are shown in Table C-4**.**

Table C-4: Double Pipe Creek. 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	61	7	9	2	17	96	77.2%
livestock	6	48	11	56	35	156	39.7%
pet	1	3	60	1	15	80	92.3%
wildlife	5	32	29	91	82	239	58.0%
Total	73	90	109	150	149	571	
*RCC = Actual number of predicted species category / Total number predicted. Example: 163 pet correctly predicted / 175 total number predicted for pet = 163/175 = 93%.							

Double Pipe Creek Water Samples. Monthly monitoring from eight (8) monitoring stations on Double Pipe Creek was the source of water samples. 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 1813 *Enterococcus* isolates were analyzed by statistical analysis. The BST results by species category, shown in Table C-5, indicate that 74% of the water isolates were assigned to a probable host source when using a 0.50 (60%) probability cutoff.

Table C-5: 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**	**% Isolates Classified 50% Prob.**	**% Isolates Classified (excluding unknowns)**
human	269	14.8%	20.1%
livestock	391	21.6%	29.2%
pet	494	27.2%	36.9%
wildlife	184	10.1%	13.8%
unknown	475	26.2%	
Total	1813	100.0%	100.0%
% Classified	**74 %**		

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

Table C-6: Double Pipe Creek. *Enterococcus* isolates obtained from water collected during the spring, summer, fall, and winter seasons, by monitoring station.

Station	**Season**				
	Spring	**Summer**	**Fall**	**Winter**	**Total**
BEB0009	72	72	68	67	279
BPC0006	68	72	65	51	256
BPC0120	72	72	69	61	274
LPC0032	72	72	72	43	259
LPC0091	68	72	62	55	257
MEB0000	65	72	57	40	234
SAM0001	72	72	61	49	254
Total	489	504	454	366	1813

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

Table C-7: Double Pipe Creek. BST Analysis: Number of Isolates per Station per Date.

Predicted Source							
Station	Date	Human	Livestock	Pet	Wildlife	Unknown	Total
BEB0009	11/18/03	3	6	3	3	6	21
BEB0009	12/02/03	3	5	9	4	2	23
BEB0009	01/07/04	4	4	3	3	6	20
BEB0009	02/05/04	4	5	6	5	3	23
BEB0009	03/03/04	4	8	2	1	9	24
BEB0009	04/07/04	2	9	1	2	10	24
BEB0009	05/12/04	4	14	2	1	3	24
BEB0009	06/09/04	3	8	7	0	6	24
BEB0009	07/08/04	6	1	9	0	8	24
BEB0009	08/11/04	1	2	5	4	12	24
BEB0009	09/09/04	0	0	14	1	9	24
BEB0009	10/06/04	1	5	3	4	11	24
BPC0006	11/18/03	2	3	1	6	9	21
BPC0006	12/02/03	6	3	4	5	2	20
BPC0006	01/07/04	1	2	0	1	2	6
BPC0006	02/05/04	6	4	8	4	1	23
BPC0006	03/03/04	6	5	5	3	3	22
BPC0006	04/07/04	3	6	2	3	10	24
BPC0006	05/12/04	2	1	9	0	8	20
BPC0006	06/09/04	3	6	4	5	6	24

BPC0006	07/08/04	5	0	12	1	6	24
BPC0006	08/11/04	1	5	8	1	9	24

Predicted Source							
Station	Date	Human	Livestock	Pet	Wildlife	Unknown	Total
BPC0006	09/09/04	1	2	3	1	17	24
BPC0006	10/06/04	2	9	0	2	11	24
BPC0120	11/18/03	4	1	9	3	4	21
BPC0120	12/02/03	5	7	5	3	4	24
BPC0120	01/07/04	5	3	1	2	2	13
BPC0120	02/05/04	10	5	3	2	4	24
BPC0120	03/03/04	2	4	13	0	5	24
BPC0120	04/07/04	1	4	4	8	7	24
BPC0120	05/12/04	7	4	6	0	7	24
BPC0120	06/09/04	2	3	10	0	9	24
BPC0120	07/08/04	10	1	4	0	9	24
BPC0120	08/11/04	1	1	14	3	5	24
BPC0120	09/09/04	9	6	6	0	3	24
BPC0120	10/06/04	4	2	17	1	0	24
LPC0032	11/18/03	2	13	6	0	3	24
LPC0032	12/02/03	1	7	4	5	7	24
LPC0032	01/07/04	2	6	4	0	3	15
LPC0032	02/05/04	4	3	15	1	0	23
LPC0032	03/03/04	0	1	0	3	1	5
LPC0032	04/07/04	6	2	6	4	6	24
LPC0032	05/12/04	3	11	2	3	5	24
LPC0032	06/09/04	7	6	5	2	4	24
LPC0032	07/08/04	8	1	7	1	7	24
LPC0032	08/11/04	4	4	3	0	13	24
LPC0032	09/09/04	4	9	5	2	4	24
LPC0032	10/06/04	1	5	7	0	11	24
LPC0091	11/18/03	1	2	2	2	7	14
LPC0091	12/02/03	2	10	3	2	7	24
LPC0091	01/07/04	6	4	3	1	10	24
LPC0091	02/05/04	5	4	14	0	0	23
LPC0091	03/03/04	1	3	1	2	1	8
LPC0091	04/07/04	1	9	2	5	3	20
LPC0091	05/12/04	5	2	6	1	10	24
LPC0091	06/09/04	5	8	7	2	2	24
LPC0091	07/08/04	3	3	12	0	6	24
LPC0091	08/11/04	1	6	7	4	6	24
LPC0091	09/09/04	2	8	7	1	6	24
LPC0091	10/06/04	3	10	7	2	2	24
MEB0000	11/18/03	1	5	3	2	6	17

MEB0000	12/02/03	2	3	3	4	6	18
MEB0000	01/07/04	1	2	1	0	2	6
MEB0000	02/05/04	4	5	14	1	0	24
MEB0000	03/03/04	1	1	0	2	6	10
Predicted Source							
Station	Date	Human	Livestock	Pet	Wildlife	Unknown	Total
MEB0000	04/07/04	2	3	0	7	5	17
MEB0000	05/12/04	1	4	8	7	4	24
MEB0000	06/09/04	3	6	9	0	6	24
MEB0000	07/08/04	6	8	2	1	7	24
MEB0000	08/11/04	0	2	9	1	12	24
MEB0000	09/09/04	6	7	4	3	4	24
MEB0000	10/06/04	2	6	6	1	7	22
SAM0001	11/18/03	3	5	2	5	2	17
SAM0001	12/02/03	1	2	5	8	4	20
SAM0001	01/07/04	4	1	5	4	1	15
SAM0001	02/05/04	1	4	13	5	1	24
SAM0001	03/03/04	3	4	2	0	1	10
SAM0001	04/07/04	4	2	15	2	1	24
SAM0001	05/12/04	2	8	8	1	5	24
SAM0001	06/09/04	2	11	4	1	6	24
SAM0001	07/08/04	5	2	15	0	2	24
SAM0001	08/11/04	0	1	2	3	18	24
SAM0001	09/09/04	1	1	9	0	13	24
SAM0001	10/06/04	4	7	8	1	4	24
Total		269	391	494	184	475	1813

Table C-8: Double Pipe Creek. BST Analysis: Percentage of Sources per Station per Date.

		Predicted Source					
Station	Date	Human	Livestock	Pet	Wildlife	Unknown	Total
BEB0009	11/18/03	14%	29%	14%	14%	29%	100%
BEB0009	12/02/03	13%	22%	39%	17%	9%	100%
BEB0009	01/07/04	20%	20%	15%	15%	30%	100%
BEB0009	02/05/04	17%	22%	26%	22%	13%	100%
BEB0009	03/03/04	17%	33%	8%	4%	38%	100%
BEB0009	04/07/04	8%	38%	4%	8%	42%	100%
BEB0009	05/12/04	17%	58%	8%	4%	13%	100%
BEB0009	06/09/04	13%	33%	29%	0%	25%	100%
BEB0009	07/08/04	25%	4%	38%	0%	33%	100%
BEB0009	08/11/04	4%	8%	21%	17%	50%	100%
BEB0009	09/09/04	0%	0%	58%	4%	38%	100%
BEB0009	10/06/04	4%	21%	13%	17%	46%	100%
BPC0006	11/18/03	10%	14%	5%	29%	43%	100%
BPC0006	12/02/03	30%	15%	20%	25%	10%	100%

BPC0006	01/07/04	17%	33%	0%	17%	33%	100%

Predicted Source							
Station	Date	Human	Livestock	Pet	Wildlife	Unknown	Total
BPC0006	02/05/04	26%	17%	35%	17%	4%	100%
BPC0006	03/03/04	27%	23%	23%	14%	14%	100%
BPC0006	04/07/04	13%	25%	8%	13%	42%	100%
BPC0006	05/12/04	10%	5%	45%	0%	40%	100%
BPC0006	06/09/04	13%	25%	17%	21%	25%	100%
BPC0006	07/08/04	21%	0%	50%	4%	25%	100%
BPC0006	08/11/04	4%	21%	33%	4%	38%	100%
BPC0006	09/09/04	4%	8%	13%	4%	71%	100%
BPC0006	10/06/04	8%	38%	0%	8%	46%	100%
BPC0120	11/18/03	19%	5%	43%	14%	19%	100%
BPC0120	12/02/03	21%	29%	21%	13%	17%	100%
BPC0120	01/07/04	38%	23%	8%	15%	15%	100%
BPC0120	02/05/04	42%	21%	13%	8%	17%	100%
BPC0120	03/03/04	8%	17%	54%	0%	21%	100%
BPC0120	04/07/04	4%	17%	17%	33%	29%	100%
BPC0120	05/12/04	29%	17%	25%	0%	29%	100%
BPC0120	06/09/04	8%	13%	42%	0%	38%	100%
BPC0120	07/08/04	42%	4%	17%	0%	38%	100%
BPC0120	08/11/04	4%	4%	58%	13%	21%	100%
BPC0120	09/09/04	38%	25%	25%	0%	13%	100%
BPC0120	10/06/04	17%	8%	71%	4%	0%	100%
LPC0032	11/18/03	8%	54%	25%	0%	13%	100%
LPC0032	12/02/03	4%	29%	17%	21%	29%	100%
LPC0032	01/07/04	13%	40%	27%	0%	20%	100%
LPC0032	02/05/04	17%	13%	65%	4%	0%	100%
LPC0032	03/03/04	0%	20%	0%	60%	20%	100%
LPC0032	04/07/04	25%	8%	25%	17%	25%	100%
LPC0032	05/12/04	13%	46%	8%	13%	21%	100%
LPC0032	06/09/04	29%	25%	21%	8%	17%	100%
LPC0032	07/08/04	33%	4%	29%	4%	29%	100%
LPC0032	08/11/04	17%	17%	13%	0%	54%	100%
LPC0032	09/09/04	17%	38%	21%	8%	17%	100%
LPC0091	10/06/04	13%	42%	29%	8%	8%	100%
LPC0091	11/18/03	7%	14%	14%	14%	50%	100%
LPC0091	12/02/03	8%	42%	13%	8%	29%	100%
LPC0091	01/07/04	25%	17%	13%	4%	42%	100%
LPC0091	02/05/04	22%	17%	61%	0%	0%	100%
LPC0091	03/03/04	13%	38%	13%	25%	13%	100%
LPC0091	04/07/04	5%	45%	10%	25%	15%	100%

LPC0091	05/12/04	21%	8%	25%	4%	42%	100%
LPC0091	06/09/04	21%	33%	29%	8%	8%	100%
LPC0091	07/08/04	13%	13%	50%	0%	25%	100%
LPC0091	08/11/04	4%	25%	29%	17%	25%	100%

Predicted Source

Station	Date	Human	Livestock	Pet	Wildlife	Unknown	Total
LPC0091	09/09/04	8%	33%	29%	4%	25%	100%
LPC0032	10/06/04	4%	21%	29%	0%	46%	100%
MEB0000	11/18/03	6%	29%	18%	12%	35%	100%
MEB0000	12/02/03	11%	17%	17%	22%	33%	100%
MEB0000	01/07/04	17%	33%	17%	0%	33%	100%
MEB0000	02/05/04	17%	21%	58%	4%	0%	100%
MEB0000	03/03/04	10%	10%	0%	20%	60%	100%
MEB0000	04/07/04	12%	18%	0%	41%	29%	100%
MEB0000	05/12/04	4%	17%	33%	29%	17%	100%
MEB0000	06/09/04	13%	25%	38%	0%	25%	100%
MEB0000	07/08/04	25%	33%	8%	4%	29%	100%
MEB0000	08/11/04	0%	8%	38%	4%	50%	100%
MEB0000	09/09/04	25%	29%	17%	13%	17%	100%
MEB0000	10/06/04	9%	27%	27%	5%	32%	100%
SAM0001	11/18/03	18%	29%	12%	29%	12%	100%
SAM0001	12/02/03	5%	10%	25%	40%	20%	100%
SAM0001	01/07/04	27%	7%	33%	27%	7%	100%
SAM0001	02/05/04	4%	17%	54%	21%	4%	100%
SAM0001	03/03/04	30%	40%	20%	0%	10%	100%
SAM0001	04/07/04	17%	8%	63%	8%	4%	100%
SAM0001	05/12/04	8%	33%	33%	4%	21%	100%
SAM0001	06/09/04	8%	46%	17%	4%	25%	100%
SAM0001	07/08/04	21%	8%	63%	0%	8%	100%
SAM0001	08/11/04	0%	4%	8%	13%	75%	100%
SAM0001	09/09/04	4%	4%	38%	0%	54%	100%
SAM0001	10/06/04	17%	29%	33%	4%	17%	100%

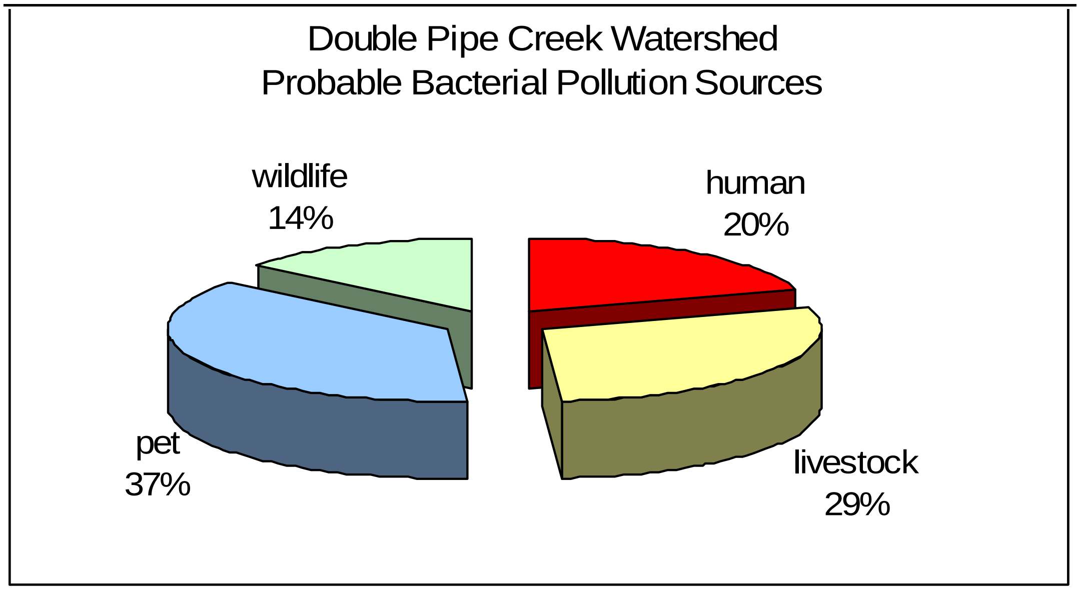


Figure C-3. Double Pipe Creek Watershed relative contributions by probable sources of Enterococcus contamination.

Double Pipe Creek Summary

The use of ARA allowed the identification of probable bacterial sources in the Double Pipe Creek Watershed for source categories in the library. When water isolates were compared to the library and potential sources predicted, 74% of the isolates were classified by statistical analysis. The highest RCC for the library was 92% (for pet), while human and wildlife had RCCs of 77% and 58%, respectively. Again, as was found in the Antietam Creek watershed, the livestock category had a lower RCC of 40%. The largest category of potential sources in the watershed as a whole was pet (37% of classified water isolates), followed by livestock (29%), human (20%), and wildlife (14%) (Figure C-3).

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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 Double Pipe Creek. 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.

Se*__lected Approach for Defining Maximum Daily Loads for Nonpoint Sources and MS4__*

To calculate the Double Pipe Creek 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:

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

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

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 Double Pipe Creek. 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 MEB0000 station. In the case of Double Pipe Creek, a value measured during low-flow conditions at the MEB0000 station resulted in the highest percentile of all three stations and strata. This value translates to the 97.96th 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 are shown in Table D-1.

Table D-1: Percentiles of Maximum Observed Bacteria Concentrations in the Double Pipe Creek Subwatersheds

Station	Strata	Maximum Observed *E. coli* Concentration (MPN/100ml)	Percentile
BEB0009	High Flow	14,200	97.04
	Low Flow	4,880	96.34
BPC0120	High Flow	29,100	97.04
	Low Flow	9,210	96.34
MEB0000	High Flow	8,800	93.03
	Low Flow	17,330	97.96
BPC0006sub	High Flow	24,190	97.18
	Low Flow	540	83.05
LPC0091	High Flow	24,190	95.40
	Low Flow	2,480	93.71
SAM0001	High Flow	68,700	97.62
	Low Flow	7,700	90.06
LPC0032sub	High Flow	130,000	97.36
	Low Flow	2,910	84.70

As seen in Table D-1, the highest percentile value obtained from all three stations and strata is 97.96%, therefore, the upper boundary percentile to be used to estimate MDLs in this analysis will equal 97.96%. This 97.96th percentile value results in a maximum daily load that would not be exceeded 97.96% 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 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* Concentrations (MPN/100ml)
BEB0009	High Flow	20	83
	Low Flow	27	45
BPC0120	High Flow	17	228
	Low Flow	15	31
MEB0000	High Flow	19	104
	Low Flow	30	84
BPC0006sub	High Flow	63	330
	Low Flow	68	124
LPC0091	High Flow	135	395
	Low Flow	63	76
SAM0001	High Flow	11	107
	Low Flow	12	38
LPC0032sub	High Flow	65	382
	Low Flow	30	50

*Only arithmetic parameters are used in the daily loads analysis.

The next step is to calculate the 97.96th 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, Wayne R. 1995).

Therefore, the coefficient of variation estimated using the monitoring data concentrations does not change, and it can be used to estimate the 99.5th percentile of the long-term average TMDL concentrations (LTAC) using equation (D1). These values are shown in Table D-3.

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

Station	Strata	CV	MDL Concentrations (MPN/100ml)
BEB0009	High Flow	4.0	632
	Low Flow	1.3	215
BPC0120	High Flow	13.4	1,798
	Low Flow	1.7	171
MEB0000	High Flow	5.5	831
	Low Flow	2.7	572
BPC0006sub	High Flow	5.1	2,613
	Low Flow	1.5	640
LPC0091	High Flow	2.8	2,712
	Low Flow	0.7	226
SAM0001	High Flow	9.5	868
	Low Flow	3.0	270
LPC0032sub	High Flow	5.8	3,051
	Low Flow	1.3	231

With the 97.96th 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:

$$\text{Daily TMDL (MPN/day)} = Q_H*(97.96^{th}C_{LTA-H})*F_{1H}*W_H + Q_L*(97.96^{th}C_{LTA-L})*F_{1L}*W_L$$

Se***lected Approach for Defining Maximum Daily Loads for Other Point Sources***

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 Double Pipe Creek, to estimate the maximum daily loads for WWTPs, the annual average loads are multiplied by the multiplication factor as follows:

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

The Maximum Daily Loads for the Double Pipe Creek subwatersheds 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)**
BEB0009	High Flow	743	221
	Low Flow	47	
BPC0120	High Flow	8,368	2,202
	Low Flow	147	
MEB0000	High Flow	1,012	350
	Low Flow	129	
BPC0006sub	High Flow	4,699	1,333
	Low Flow	211	
LPC0091	High Flow	9,063	2,370
	Low Flow	139	
SAM0001	High Flow	1,562	458
	Low Flow	90	
LPC0032sub	High Flow	4,412	1,149
	Low Flow	62	

Maximum Daily Loads 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 Double Pipe Creek watershed is presented in Table D-5.

Table D-5: Double Pipe Creek Watershed Maximum Daily Loads

Subwatersheds	**TMDL**	**LA**	**Stormwater WLA**	**WWTP WLA**
	Billions MPN *E. coli*/day			
Bear Branch (BEB0009)	221	163	58	0.6
Big Pipe Creek (BPC0120)	2,201	1,631	570	0
Meadow Branch (MEB0000)	350	252	98	0
Big Pipe Creek (BPC0006sub)	1,333	1,050	283	0.4
Little Pipe Creek (LPC0091)	2,370	1,918	373	79
Sam's Creek (SAM0001)	458	271	187	0
Little Pipe Creek (LPC0032sub)	1,149	864	285	0
TOTAL	8,082	6,148	1,854	80

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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.

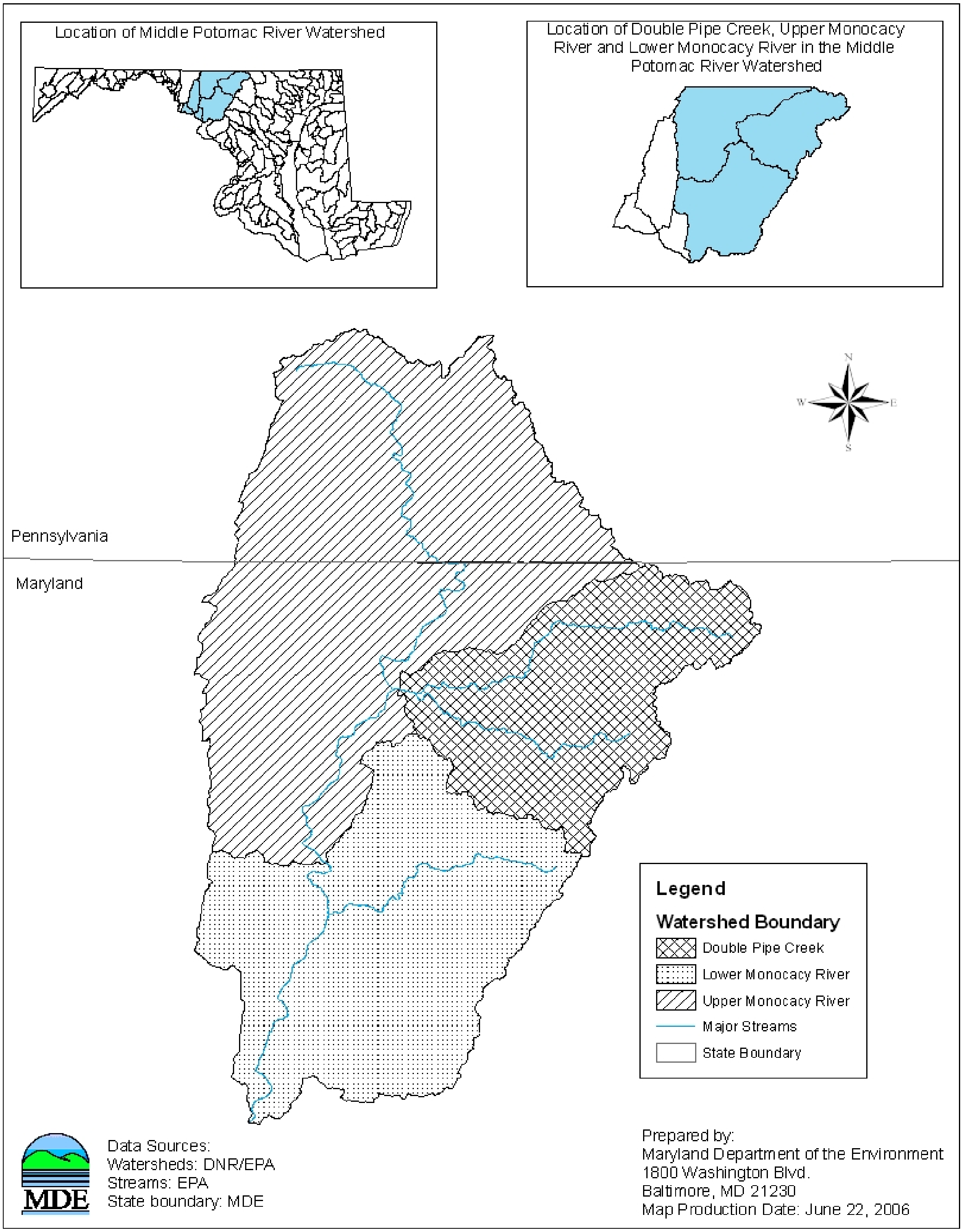

Figure E-1: Location of the Double Pipe Creek, Upper Monocacy River, and Lower Monocacy River Watersheds

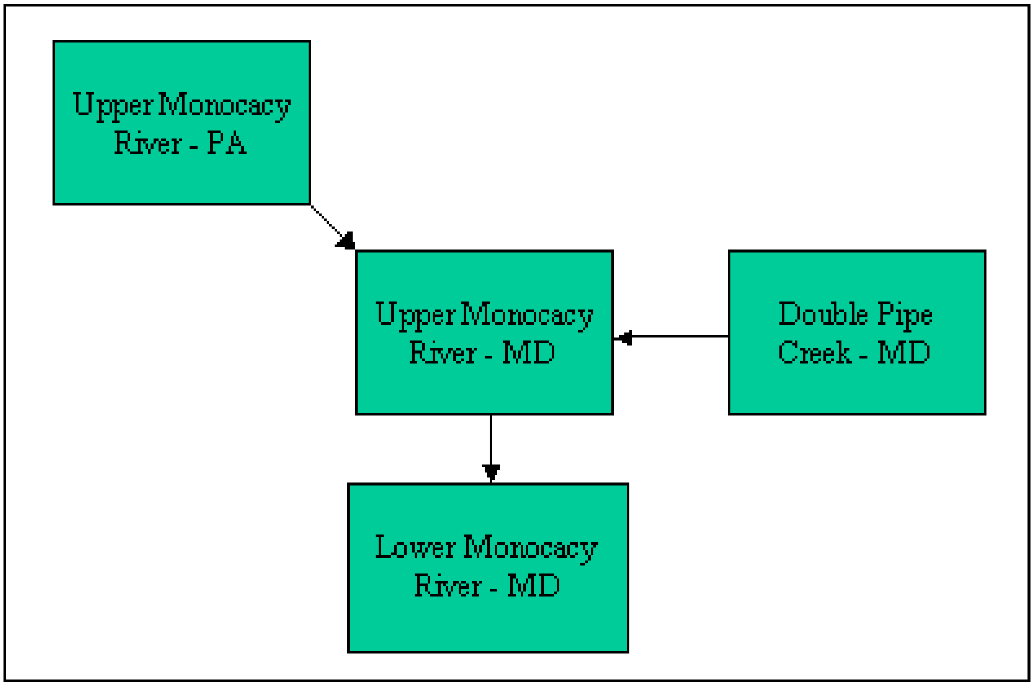

Figure E-2: Flow Schematic of the Double Pipe Creek, Upper Monocacy River, and Lower Monocacy River Watersheds

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	=	483,751	+	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] The upstream load is equivalent to the Upper Monocacy River TMDL.