Total Maximum Daily Loads of Fecal Bacteria for the Conococheague Creek Basin in Washington County, Maryland

REVISED FINAL

DEPARTMENT OF THE ENVIRONMENT
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Submitted to:

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U.S. Environmental Protection Agency, Region III
1650 Arch Street
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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
cfs	Cubic Feet per Second
CFR	Code of Federal Regulations
CFU	Colony Forming Units
COMAR	Code of Maryland Regulations
CSO	Combined Sewer Overflow
CSS	Combined Sewer System
CWA	Clean Water Act
DNR	Department of Natural Resources
EPA	Environmental Protection Agency
GIS	Geographic Information System
LA	Load Allocation
MACS	Maryland Agricultural Cost Share Program
MDE	Maryland Department of the Environment
MDP	Maryland Department of Planning
MGD	Millions of Gallons per Day
ml	Milliliter(s)
MOS	Margin of Safety
MPN	Most Probable Number
MPR	Maximum Practicable Reduction
MS4	Municipal Separate Storm Sewer System
MST	Microbial Source Tracking
NPDES	National Pollutant Discharge Elimination System
NRCS	National Resources Conservation Service
RCC	Rates of Correct Classification
RESAC	Mid-Atlantic Regional Earth Science Applications Center
SSO	Sanitary Sewer Overflows
SW	Stormwater
STATSGO	State Soil Geographic Database
TMDL	Total Maximum Daily Load
USGS	United States Geological Survey
WQIA	Water Quality Improvement Act
WLA	Wasteload Allocation
WQLS	Water Quality Limited Segment
WWTP	Wastewater Treatment Plant

EXECUTIVE SUMMARY

This document, upon approval by the U.S. Environmental Protection Agency (EPA), establishes a Total Maximum Daily Load (TMDL) for fecal bacteria in the Conococheague Creek watershed (MD basin number 02-14-05-04). Section 303(d) of the federal Clean Water Act (CWA) and 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 Conococheague Creek and its tributaries in the State of Maryland's (MD) 303(d) List as impaired by fecal bacteria (listed in 2002), high pH (listed in 2002) and sediments (listed in 1996). Conococheague Creek and the tributaries Meadow Brook, Troupe Run, and Rush Run have also been identified as impaired by impacts to biological communities (listed in 2004). Conococheague Creek and all its tributaries have been designated as Use IV-P (Recreational Trout Waters and Public Water Supply). See Code of Maryland Regulations (COMAR) 26.08.02.08Q. This document proposes to establish a TMDL for fecal bacteria in the Conococheague Creek watershed that will allow for attainment of the beneficial use designation of primary contact recreation. The listings for pH, sediments, and impacts to biological communities will be addressed in separate TMDL documents. MDE monitored the Conococheague Creek watershed from 2003-2004 for fecal bacteria. 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 Conococheague Creek watershed has been divided into nine subwatersheds. For convenience, each subwatershed will be referenced by the downstream bacteria monitoring station's name and location. The nine subwatersheds are CON0217 (Conococheague Creek at the Pennsylvania line), CON0180 (Conococheague Creek near Fairview, MD at USGS gage along Wishard Road), RKD0006 (Rockdale Run at Gossard Mill Road), TMS0006 (Toms Run at Fairview Road), RUS0005 (Rush Run at Rush Run Road), CON0051 (Conococheague Creek upstream of Meadow Brook at Kemps Mill Rd), MEA0009 (Meadow Brook at Pinesburg Road), UWR0000 (Unnamed tributary at Kemps Mill Road northwest of Rock Hill Road) and CON0005 (Conococheague Creek in Williamsport, MD at Route 68). The pollutant loads set forth in this document are for these nine subwatersheds. To establish baseline and allowable pollutant loads for this TMDL, a flow duration curve approach was employed, using bacteria data from MDE and flow strata estimated from United States Geological Survey (USGS) daily flow monitoring. The sources of fecal bacteria are estimated at nine representative stations in the Conococheague 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 baseline load is estimated from current monitoring data using a long-term geometric mean and weighting factors from the flow duration curve. The TMDL for fecal bacteria entering the Conococheague Creek watershed is established after considering four different hydrological conditions: high flow and low flow annual conditions, and high flow and low flow seasonal conditions (the period between May 1st and September 30th when water contact recreation is more prevalent). The allowable load quantified by the TMDL 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 nine subwatersheds, it was estimated that water quality standards could not be attained with MPRs; thus, higher maximum reductions were applied.

The MD 8-digit Conococheague Creek Total Baseline Load is 4,812,341 billion MPN *E. coli*/year. This baseline load consists of upstream loads generated outside the assessment unit (i.e., the MD 8-digit watershed): a Pennsylvania Upstream Baseline (BL_{PA}) of 3,966,535 billion MPN *E. coli*/year, plus loads generated within the assessment unit: a MD 8-digit Conococheague Creek Baseline Load Contribution of 845,806 billion MPN *E. coli*/year. The baseline loads are summarized in the following table:

MD 8-Digit Conococheague Creek Fecal Bacteria Baseline Loads (Billion MPN *E. coli*/year)

Total Baseline Load	=	**Upstream Baseline Load**[1] **(BL_{PA})**	+	**MD 8-digit Conococheague Creek Baseline Load Contribution**
4,812,341	=	3,966,535	+	845,806

[1] Although the upstream baseline load is reported here as a single value, it could include point and nonpoint sources.

The MD 8-digit Conococheague Creek TMDL of fecal bacteria consists of an annual average allocation attributed to loads generated outside the assessment unit: a Pennsylvania Upstream Load Allocation (LA_{PA}), plus allocations attributed to loads generated within the assessment unit: a MD 8-digit Conococheague Creek TMDL Contribution.

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

The MD 8-digit Conococheague Creek TMDL of fecal bacteria is presented in the following table:

MD 8-Digit Conococheague Creek Fecal Bacteria TMDL (Billion MPN *E. coli*/year)

TMDL	=	**LA**			+	**WLA**			+	**MOS**
		LA$_{PA}$[1]	+	**LA$_{CON}$**		**SW WLA$_{CON}$**	+	**WWTP WLA$_{CON}$**		
1,013,386	=	907,512	+	81,626	+	17,088	+	7,160	+	Incorporated

Upstream Load Allocation

MD 8-digit Conococheague Creek TMDL Contribution (105,874)

[1] Although the upstream load is reported here as a single value, it could include point and nonpoint sources.

The LA$_{PA}$, accounting for portions of subwatersheds located in Pennsylvania, is determined to be necessary in order to meet MD water quality standards in the MD portion of the Conococheague Creek watershed. The LA$_{PA}$ represents a reduction of approximately 77% from the PA baseline load of 3,966,535 billion MPN *E. coli*/year. The MD 8-digit TMDL Contribution (105,874 billion MPN *E. coli*/year) represents a reduction of approximately 87% from the MD 8-digit Baseline Load Contribution of 845,806 billion MPN *E. coli*/year.

Pursuant to recent EPA guidance (US EPA 2006), maximum daily load (MDL) expressions of the long-term annual average TMDLs are also provided, as shown in the following table:

MD 8-Digit Conococheague Creek Fecal Bacteria MDL Summary (Billion MPN *E. coli*/day)

MDL	=	**LA**			+	**WLA**			+	**MOS**
		LA$_{PA}$[1]	+	**LA$_{CON}$**		**SW WLA$_{CON}$**	+	**WWTP WLA$_{CON}$**		
29,699	=	26,266	+	2,722	+	650	+	61	+	Incorporated

Upstream MDL

MD 8-digit Conococheague Creek MDL Contribution (3,433)

Once EPA has approved a TMDL, MDE intends for the required reductions to be implemented in an iterative process that first addresses those sources most severely impacting water quality and posing 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 nine subwatersheds using the MPR scenario. MPRs may not be sufficient in subwatersheds where wildlife is a significant component or where very high reductions of fecal bacteria loads are required to meet water quality standards. In these cases, it is expected that the MPR scenario will be the first stage of TMDL implementation. Progress will be made through the iterative implementation process described above, and the situation will be reevaluated in the future.

1.0 INTRODUCTION

This document, upon approval by the U.S. Environmental Protection Agency (EPA), establishes a Total Maximum Daily Load (TMDL) for fecal bacteria in the Conococheague Creek watershed (basin number 02-14-05-04). 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.

Conococheague Creek and its tributaries have been identified in the State of Maryland's (MD) 303(d) List as impaired by fecal bacteria (listed in 2002), high pH (listed in 2002) and sediments (listed in 1996). Conococheague Creek and the tributaries Meadow Brook, Troupe Run, and Rush Run have also been identified as impaired by impacts to biological communities (listed in 2004). Conococheague Creek and all its tributaries have been designated as Use IV-P (Recreational Trout Waters and Public Water Supply). See Code of Maryland Regulations (COMAR) 26.08.02.08Q. This document proposes to establish a TMDL for fecal bacteria in the Conococheague Creek watershed that will allow for attainment of the beneficial use designation of primary contact recreation. The listings for pH, sediments and impacts to biological communities will be addressed in separate TMDL documents. MDE monitored the Conococheague Creek watershed from 2003-2004 for fecal bacteria. 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 MD's current bacteria water quality criteria, either *E. coli* or enterococci. The indicator organism used in the Conococheague Creek TMDL analysis was *E. coli*.

2.0 SETTING AND WATER QUALITY DESCRIPTION

2.1 General Setting

Location

The Conococheague Creek watershed is located in both Maryland (MD) and Pennsylvania (PA) with a drainage area of 568 square miles (363,567 acres). The majority (88.4%) of the watershed is in PA (in Franklin, Adams, Cumberland and Perry Counties) with a portion in Washington County, MD (see Figure 2.1.1).

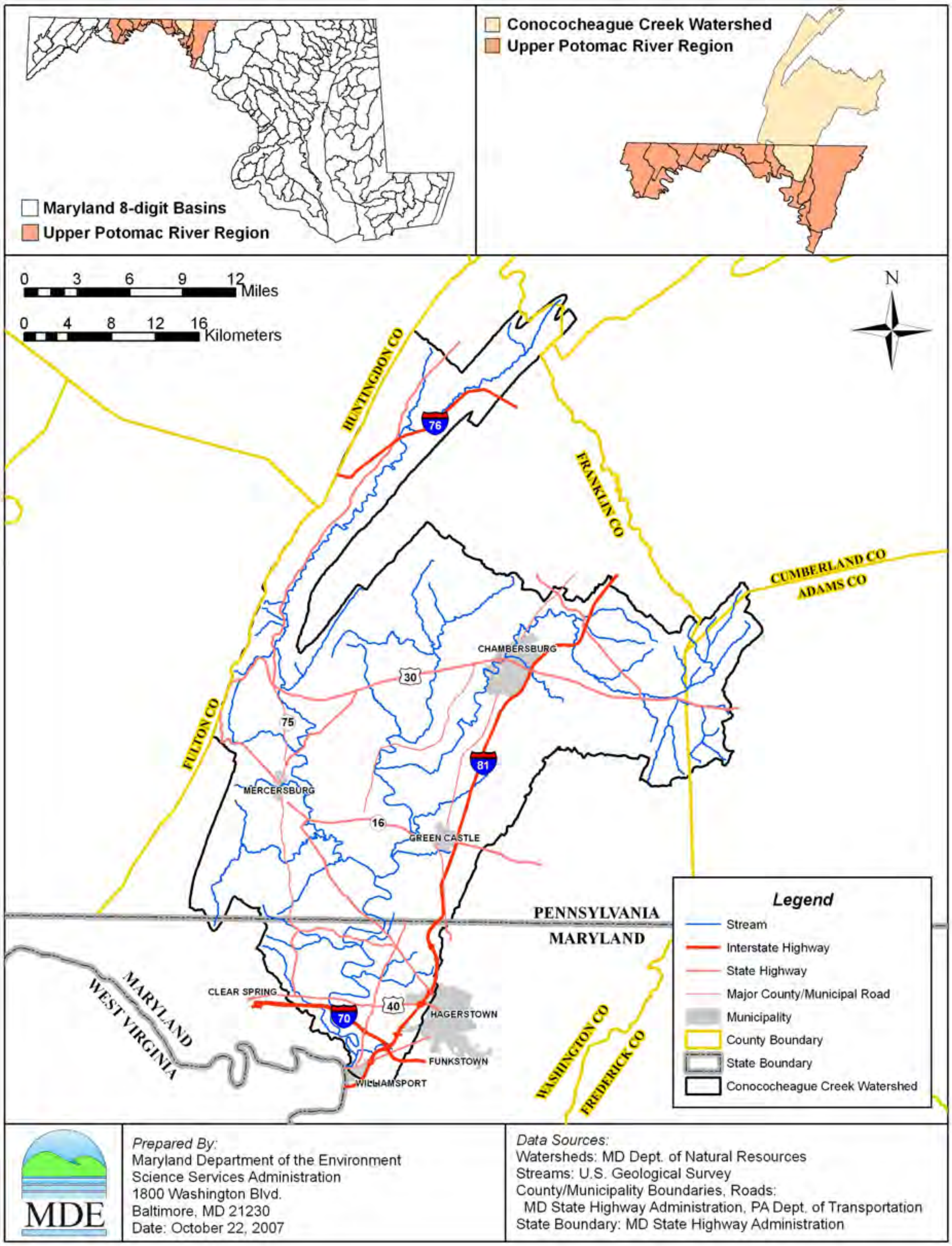
Conococheague Creek and its tributaries flow through several towns including Chambersburg, Greencastle and Mercersburg in PA and Williamsport in MD. The headwaters of Conococheague Creek originate approximately 13 miles east of Chambersburg, PA. Passing through Chambersburg it continues flowing southwest through PA and into MD and finally empties into the Potomac River near the town of Williamsport.

The tributaries of Conococheague Creek in MD include Semple Run, Meadow Brook, Rush Run, Toms Run, and Rockdale Run (see Figure 2.1.2).

Geology/Soils

Conococheague Creek is located in the Valley and Ridge physiographic region. The watershed lies in an area known as the Great Valley, also called the Hagerstown Valley. The geology of this valley is comprised of Cambrian and Ordovician limestone and dolomite (Edwards 1981). This carbonate bedrock is the reason for the valley’s karst landscape. A characteristic of karst terrains is the loss of surface water to the subsurface (Reger 2007).

The overlying soils are composed predominantly of the Weikert-Berks soil association around the mainstem of Conococheague Creek and the Hagerstown-Duffield-Clarksburg soil association on either side. Spatial distributions for each soil series are shown in Figure 2.1.3. The Weikert-Berks association is comprised of shallow to moderately deep, well drained soils formed in shale, siltstone and fine-grained sandstone. The Hagerstown-Duffield-Clarksburg association consists of deep and very deep, well drained soils formed from limestone bedrock.



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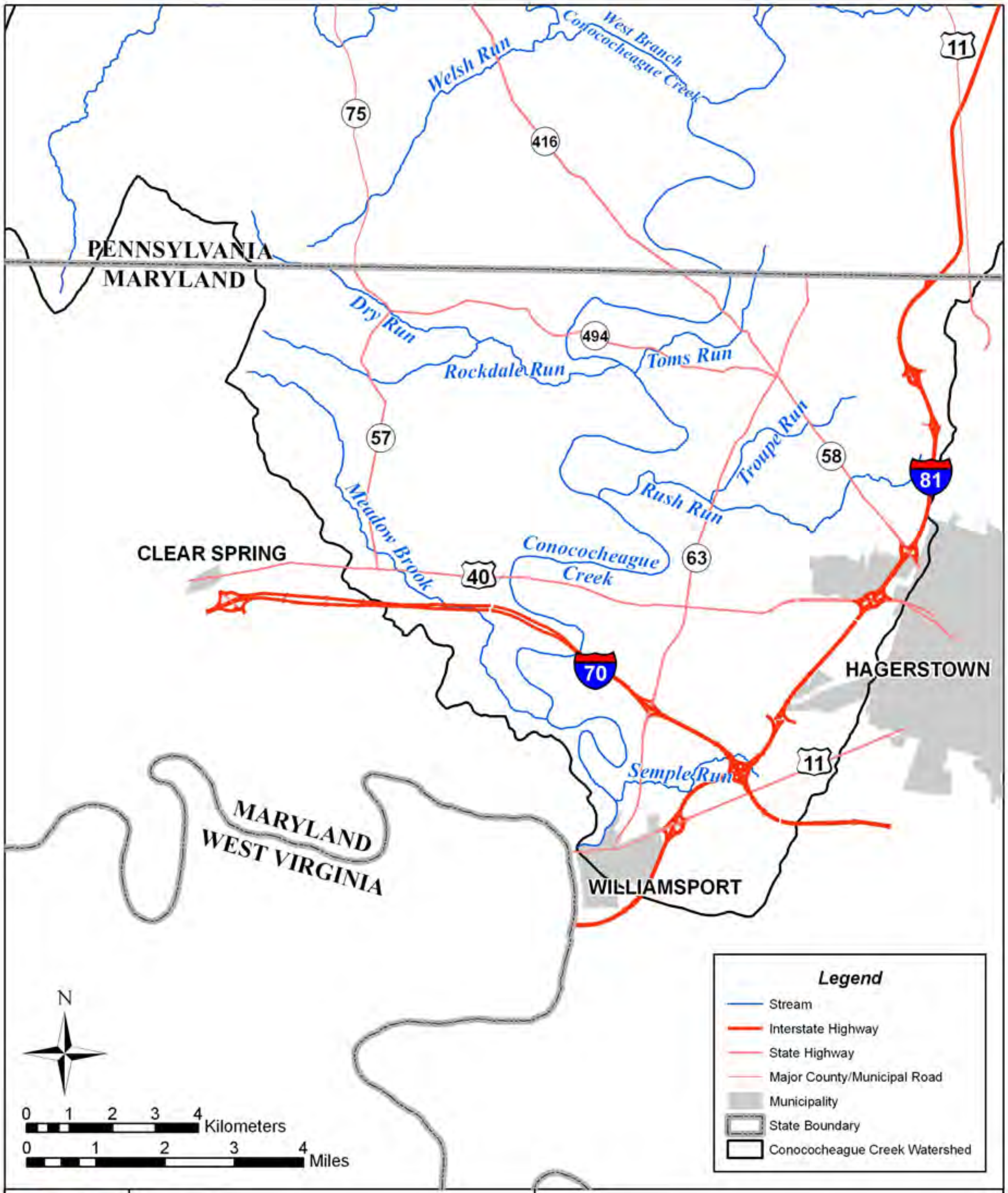
Date: October 22, 2007

Data Sources:
Watersheds: MD Dept. of Natural Resources
Streams: U.S. Geological Survey
County/Municipality Boundaries, Roads:
MD State Highway Administration, PA Dept. of Transportation
State Boundary: MD State Highway Administration

Figure 2.1.1: Location Map of the Conococheague Creek Watershed



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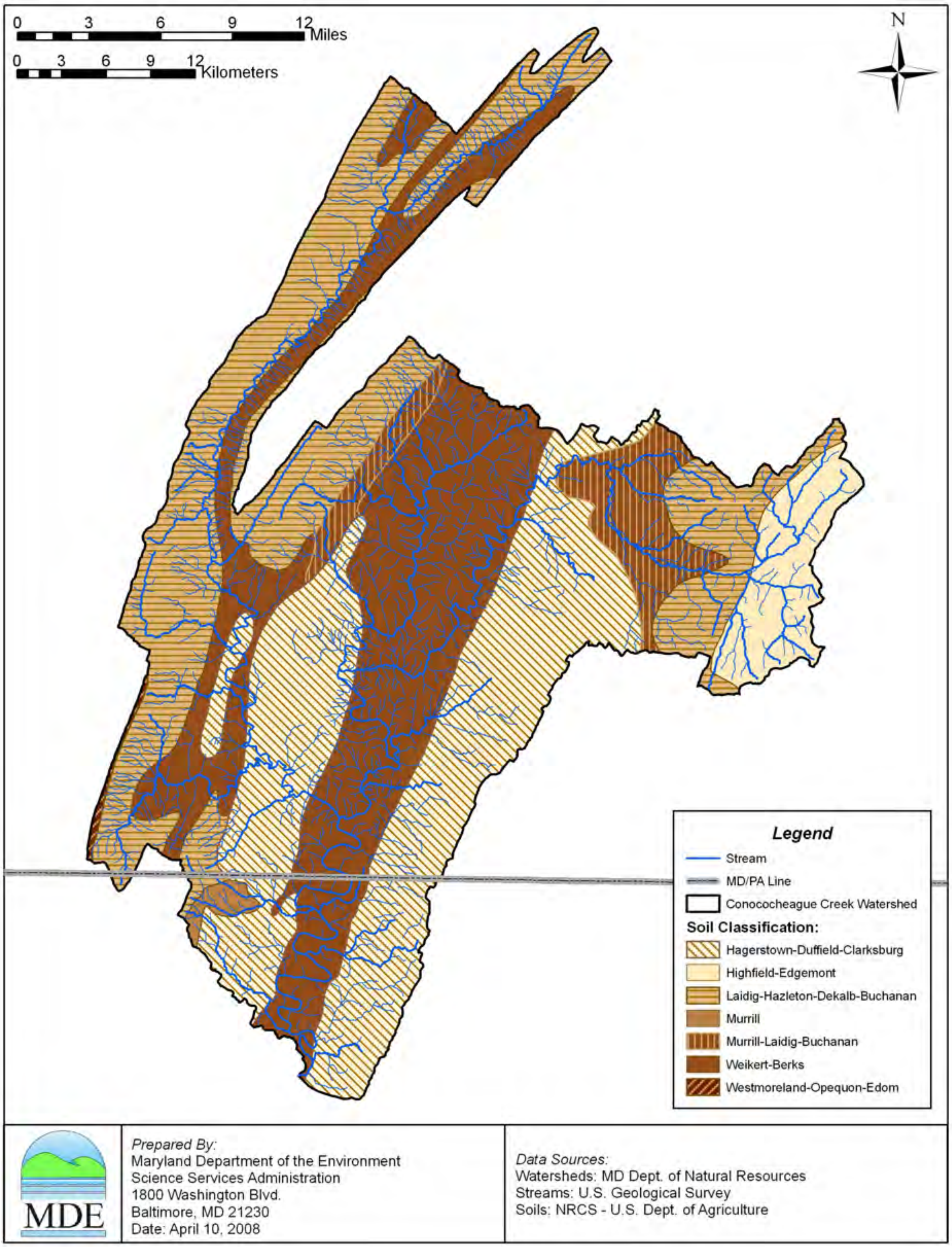
Data Sources:
Watersheds: MD Dept. of Natural Resources
Streams: U.S. Geological Survey
State/Municipality Boundaries, Roads:
MD State Highway Administration

Figure 2.1.2: Location Map of the MD 8-digit Conococheague Creek Watershed


0 3 6 9 12 Miles
0 3 6 9 12 Kilometers
N
Legend
Stream
MD/PA Line
Conococheague Creek Watershed
Soil Classification:
Hagerstown-Duffield-Clarksburg
Highfield-Edgemont
Laidig-Hazleton-Dekalb-Buchanan
Murrill
Murrill-Laidig-Buchanan
Weikert-Berks
Westmoreland-Opequon-Edom
MDE
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Data Sources:
Watersheds: MD Dept. of Natural Resources
Streams: U.S. Geological Survey
Soils: NRCS - U.S. Dept. of Agriculture

Figure 2.1.3: General Soil Associations in the Conococheague Creek Watershed

Land Use

The Conococheague Creek Watershed covers an area of 363,567 acres in MD and PA. Based on the 2002 Maryland Department of Planning (MDP) land use/land cover data, MD's portion of the watershed is primarily cropland with significant urban and forest land as well. Regional Earth Science Application Center (RESAC) land use/land cover was used to estimate the land use for the PA portion of the watershed. RESAC shows that the PA portion is largely forest and cropland.

The forested areas are mainly in the western and eastern portions of the watershed. The major urban areas of the watershed are Halfway and Williamsport in MD and Chambersburg in PA.

The land use acreage and percentage distribution is shown in Table 2.1.1, and spatial distributions for each land use are shown in Figure 2.1.4. Table 2.1.2 shows the land use percentage distribution for each of the nine subwatersheds considered in the analysis. Note that the subwatersheds are identified by the MDE monitoring stations located in the mainstem of the river and its main tributaries, and are listed by flow from upstream to downstream.

Table 2.1.1: Land Use Percentage Distribution for the Conococheague Creek Watershed

Land Type	**Maryland Area**		**Pennsylvania Area**		***Total***	
	Acres	**%**	**Acres**	**%**	**Acres**	**%**
Agricultural	20,150	47.7	112,663	35.1	132,814	36.5
Forest	8,444	20.0	158,128	49.2	166,572	45.8
Pasture	2,799	6.6	27,260	8.5	30,059	8.3
Urban	10,372	24.6	22,754	7.1	33,126	9.1
Water	434	1.0	561	0.2	995	0.3
Total	**42,200**	**100**	**321,367**	**100**	**363,567**	**100**

Table 2.1.2: Land Use Percentage Distribution for the Conococheague Creek Subwatersheds

Station / Subwatershed	Land Use Area (%)				
	Agricultural	Forest	Pasture	Urban	Water
CON0217 / Conococheague Creek (CC) at PA line	34.7	49.4	8.5	7.2	0.2
CON0180 / CC near Fairview	54.9	31.0	6.7	5.5	1.9
RKD0006 / Rockdale Run	64.2	20.4	4.5	10.8	0.1
TMS0006 / Toms Run	60.5	13.8	4.1	21.6	0.05
RUS0005 / Rush Run	60.3	8.5	5.7	25.5	0.01
CON0051 / CC upstream of Meadow Brook	47.5	28.9	5.5	15.5	2.7
MEA0009 / Meadow Brook	65.1	18.3	7.8	8.8	0.0
UWR0000 / Unnamed tributary near Kemps	31.2	17.3	16.7	34.5	0.3
CON0005 / CC in Williamsport	20.3	22.9	5.6	49.8	1.4

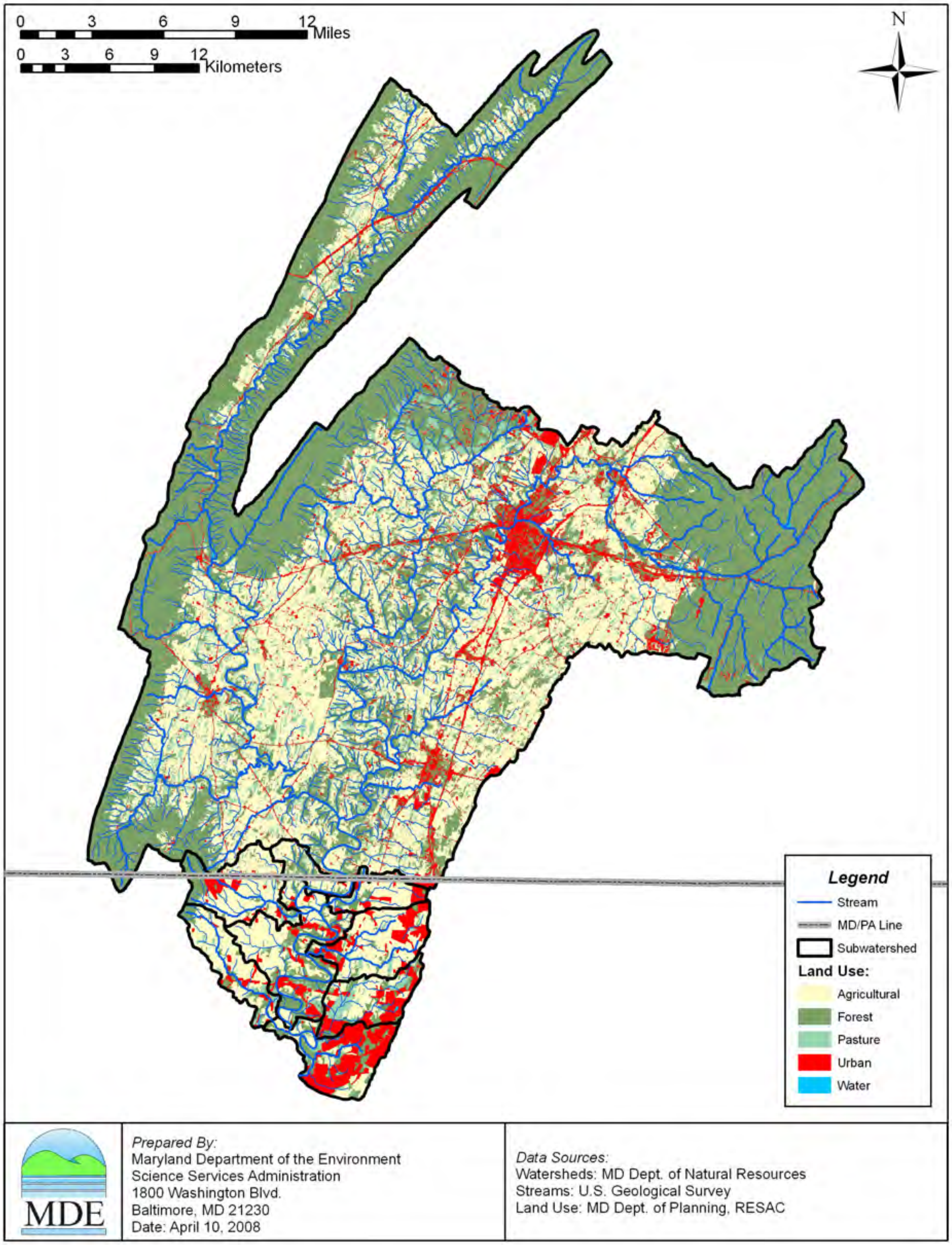


Figure 2.1.4: Land Use of the Conococheague Creek Watershed

Population

The total population in the Conococheague Creek watershed is estimated to be 108,702 people. Figure 2.1.5 illustrates the population density in the watershed. The human population and the number of households were estimated based on a weighted average from the 2000 Census GIS Block Groups and the 2002 MDP Land Use Land Cover and the RESAC for PA. Since the boundaries of the watershed differ from the boundaries of the block groups, residential land use data were used to extract the necessary areas of the Census block groups. The residential density designations used for this estimation are shown in Table 2.1.3 and were based on MDP and RESAC information.

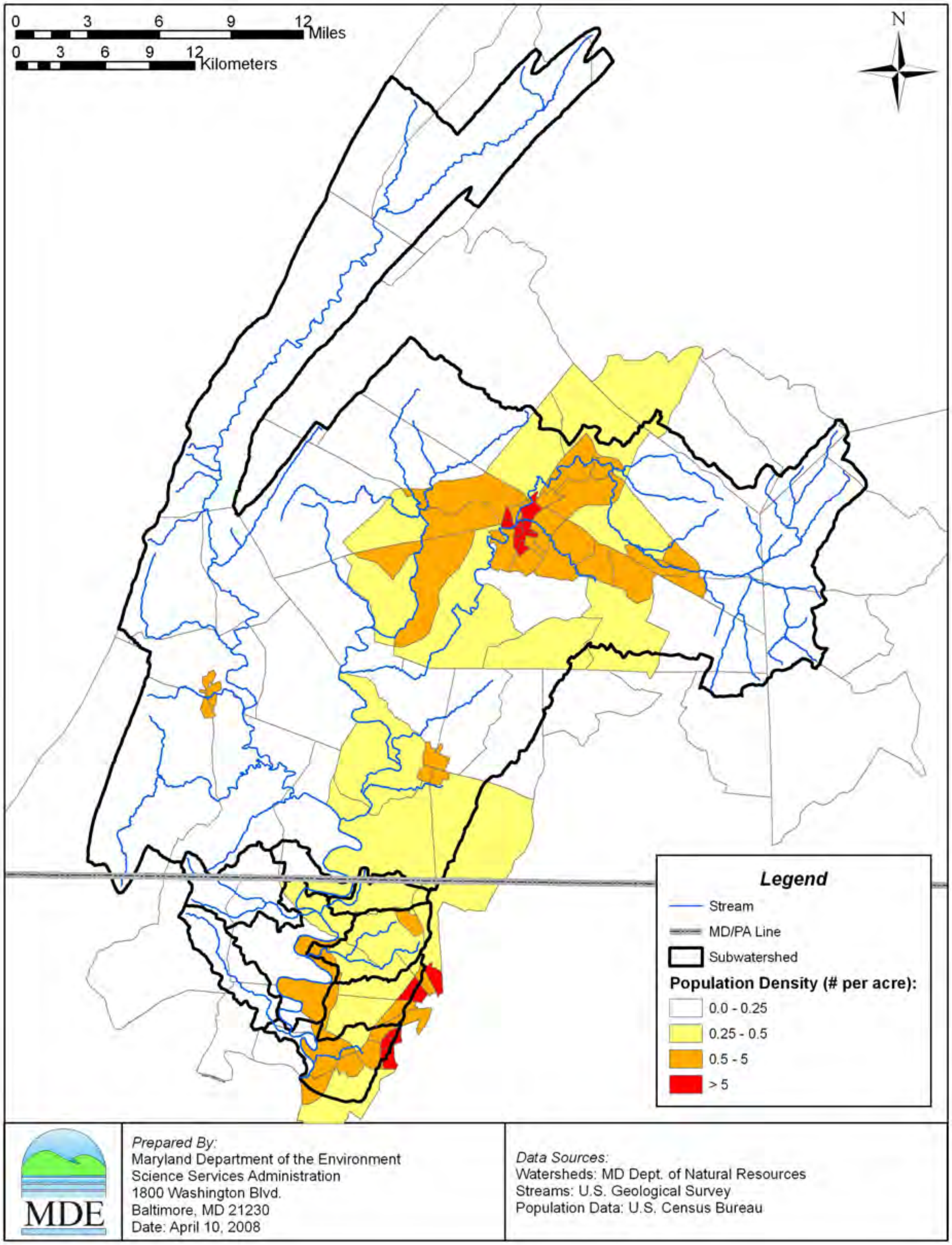
Table 2.1.3: Number of Dwellings Per Acre

Land Use Code	Dwellings Per Acre
Low Density Residential	1
Medium Density Residential	5
High Density Residential	8

Based on these densities and the population data from the census block groups the population for each subwatershed was estimated and is presented in Table 2.1.4.

Table 2.1.4: Total Population per Subwatershed in the Conococheague Creek Watershed

Station / Subwatershed	Population
CON0217 / Conococheague Creek (CC) at PA line	87,066
CON0180 / CC near Fairview	430
RKD0006 / Rockdale Run	1,233
TMS0006 / Toms Run	659
RUS0005 / Rush Run	3,718
CON0051 / CC upstream of Meadow Brook	2,963
MEA0009 / Meadow Brook	790
UWR0000 / Unnamed tributary near Kemps	2,562
CON0005 / CC in Williamsport	9,282
Total	**108,702**



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Data Sources:
Watersheds: MD Dept. of Natural Resources
Streams: U.S. Geological Survey
Population Data: U.S. Census Bureau

Figure 2.1.5: Population Density in the Conococheague Creek Watershed

2.2 Water Quality Characterization

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

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

Bacteria Monitoring

Table 2.2.1 lists the historical monitoring data for the Conococheague Creek watershed. MDE conducted monitoring sampling at nine stations in the Conococheague Creek watershed from November 2003 through October 2004. The United States Geological Survey (USGS) gage station 01614500, located at Fairview, MD, was used in deriving the surface water flow. The locations of these stations are shown in Tables 2.2.2 to 2.2.4 and in Figure 2.2.1. Observations recorded from the nine MDE monitoring stations are provided in Appendix A.

Bacteria counts are highly variable which is typical due to the nature of bacteria and their relationship to flow. The *E. coli* counts for the nine stations ranged between 10 and 24,192 MPN/100 ml.

Table 2.2.1: Historical Monitoring Data in the Conococheague Creek Watershed

Organization	Date	Design	Summary
DNR	01/1986 through 11/2003	Fecal Coliform*	2 stations 1 sample per month
MDE	10/2002 through 10/2003	*E. coli*	9 stations 2 samples per month
MDE	10/2002 through 10/2003	BST (*Enterococcus)*	9 stations 1 sample per month

*Only *E. coli* was used for this analysis.

Table 2.2.2: Location of DNR Core & Trend Stations in the Conococheague Creek Watershed

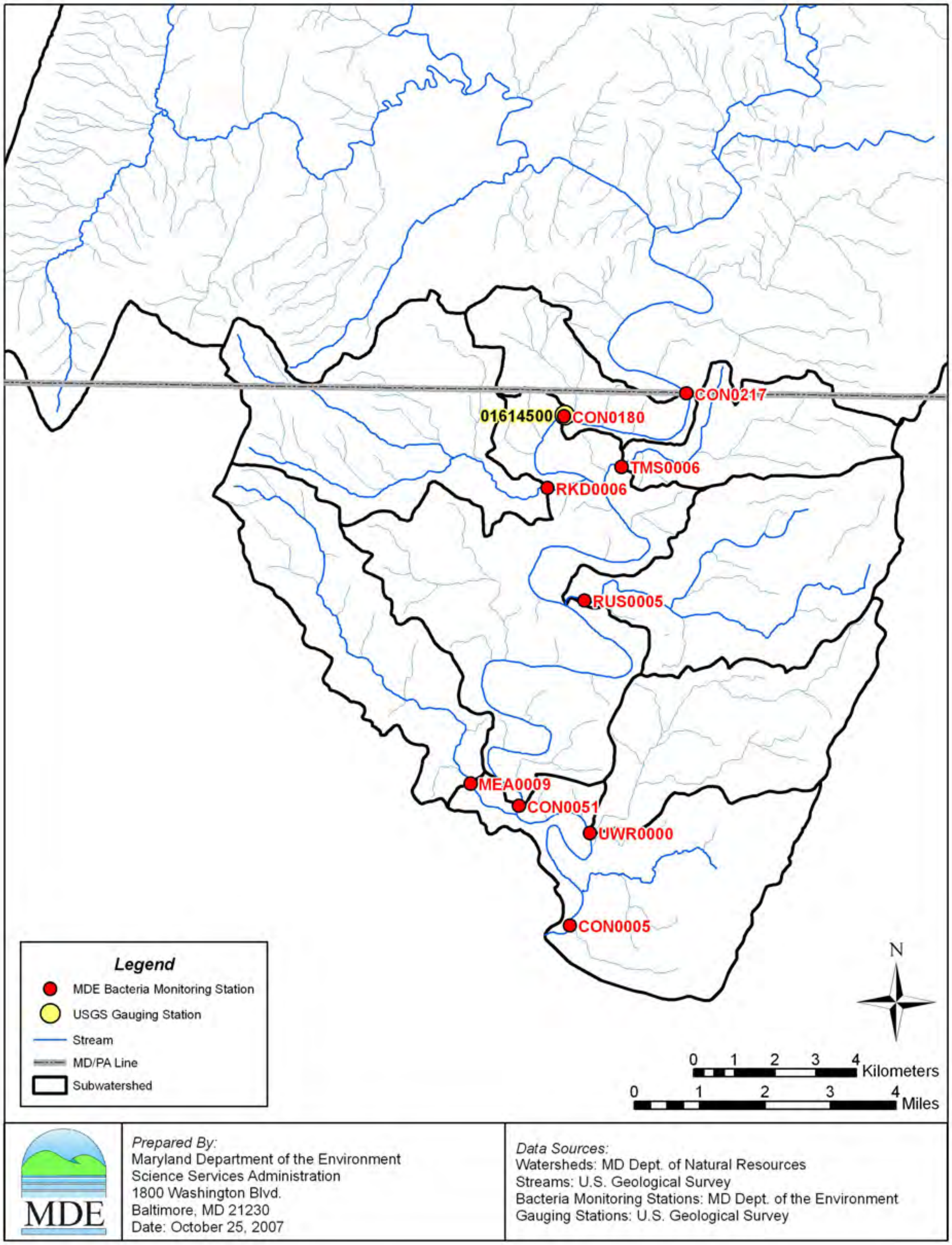
Station	Tributary	Latitude (Decimal Degrees)	Longitude (Decimal Degrees)
CON0005	Conococheague Creek	39.603	-77.822
CON0180	Conococheague Creek	39.716	-77.825

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

Tributary	Station	Observation Period	Total Observations	Latitude (Decimal Degrees)	Longitude (Decimal Degrees)
Conococheague Creek (at PA line)	CON0217	2003 - 2004	22	39.723	-77.793
Conococheague Creek (near Fairview along Wishard Road)	CON0180	2003 - 2004	24	39.716	-77.824
Rockdale Run (at Gossard Mill Road)	RKD0006	2003 - 2004	23	39.700	-77.830
Toms Run (at Fairview Road)	TMS0006	2003 - 2004	24	39.705	-77.808
Rush Run (at Rush Run Road)	RUS0005	2003 - 2004	24	39.675	-77.819
Conococheague Creek (at Kemps Mill Road near Snug Harbor Lane)	CON0051	2003 - 2004	23	39.630	-77.837
Meadow Brook (at Pinesburg Road)	MEA0009	2003 - 2004	24	39.635	-77.851
Unnamed stream (at Kemps Mill Road NW of Rock Hill Road)	UWR0000	2003 - 2004	24	39.624	-77.817
Conococheague Creek (at Route 68)	CON0005	2003 - 2004	24	39.603	-77.822

Table 2.2.4: Location of USGS Gauging Station in Conococheague Creek Watershed

Site Number	Observation Period Used	Total Observations	Latitude	Longitude
01614500	1982-2007	9131	39.716	-77.825


CON0217
01614500
CON0180
TMS0006
RKD0006
RUS0005
MEA0009
CON0051
UWR0000
CON0005
Legend
MDE Bacteria Monitoring Station
USGS Gauging Station
Stream
MD/PA Line
Subwatershed
N
0 1 2 3 4 Kilometers
0 1 2 3 4 Miles
MDE
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Date: October 25, 2007
Data Sources:
Watersheds: MD Dept. of Natural Resources
Streams: U.S. Geological Survey
Bacteria Monitoring Stations: MD Dept. of the Environment
Gauging Stations: U.S. Geological Survey

Figure 2.2.1: Monitoring Stations and Subwatersheds in the MD 8-digit Conococheague Creek Watershed

2.3 Water Quality Impairment

Designated Uses and Water Quality Standard

The Maryland water quality standards Surface Water Use Designation for Conococheague Creek and its tributaries is Use IV-P (Recreational Trout Waters and Public Water Supply). (COMAR 26.08.02.08Q) The Conococheague Creek watershed was listed on Maryland's 303(d) List as impaired by fecal bacteria in 2002, due to elevated fecal coliform concentrations detected at the DNR Core monitoring station CON0005, which showed a geometric mean of 216 MPN/100ml.

Water Quality Criteria

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

Table 2.3.1: Bacteria Criteria Values
(Source: 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/100ml

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 Conococheague 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 Conococheague 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.

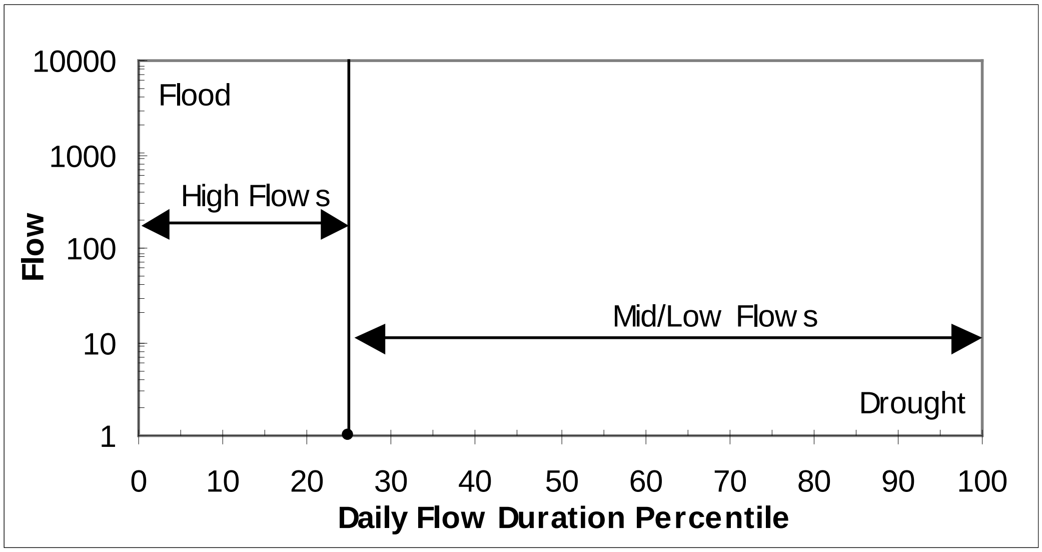

Figure 2.3.1: Conceptual Diagram of Flow Duration Zones

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 flow data of USGS gage 01614500 it was determined that the long-term average daily flow corresponds to a daily flow duration of 29.7%. Hence for this analysis it is defined that flows greater than the 29.7 percentile flow represent low/mid flows, and flows lesser than the 29.7 percentile flow represent high 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 Conococheague 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 Conococheague Creek Watershed

Flow Duration Zone	Duration Interval	Weighting Factor
High Flows	0 – 29.7%	0.297
Mid/Low Flows	29.7 – 100%	0.703

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:

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

where,

C_{gm} = Steady-state geometric mean concentration

Tables 2.3.3 and 2.3.4 present the maximum and minimum concentrations and the geometric means by stratum, and the overall steady-state geometric mean for the Conococheague Creek subwatersheds for the annual and seasonal (May 1st –September 30th) periods.

Table 2.3.3: Conococheague Creek Watershed Annual Steady-State Geometric Means by Flow Stratum per Subwatershed

Station / Tributary	Flow Stratum	Number 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)
CON0217 Conococheague Creek (CC) at PA line	**High**	12	31	3,448	460	215
	Low	10	63	479	156	
CON0180 CC near Fairview	**High**	14	63	4,884	471	223
	Low	10	41	460	162	
RKD0006 Rockdale Run	**High**	14	52	6,867	876	900
	Low	9	52	4,352	910	
TMS0006 Toms Run	**High**	14	10	24,192	233	131
	Low	10	10	813	103	
RUS0005 Rush Run	**High**	14	199	7,701	1,089	895
	Low	10	173	3,255	824	
CON0051 CC upstream of Meadow Brook	**High**	13	10	4,106	318	137
	Low	10	10	223	96	
MEA0009 Meadow Brook	**High**	14	187	4,884	761	623
	Low	10	41	5,475	572	
UWR0000 Unnamed tributary near Kemps	**High**	14	132	1,989	682	597
	Low	10	110	1,789	565	
CON0005 CC in Williamsport	**High**	14	41	6,867	379	177
	Low	10	31	269	129	

Table 2.3.4: Conococheague Creek Watershed Seasonal Period (May 1 - September 30) Steady-State Geometric Means by Flow Stratum per Subwatershed

Station / Tributary	Flow Stratum	Number 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)
CON0217 Conococheague Creek (CC) at PA line	**High**	5	364	3,448	1,132	342
	Low	5	132	309	206	
CON0180 CC near Fairview	**High**	5	292	4,884	1,407	360
	Low	5	121	460	202	
RKD0006 Rockdale Run	**High**	5	1,669	6,867	2,999	2,022
	Low	4	1,130	2,489	1,712	
TMS0006 Toms Run	**High**	5	185	24,192	1,356	404
	Low	5	86	813	242	
RUS0005 Rush Run	**High**	5	1,137	7,701	2,574	2,119
	Low	5	1,112	3,255	1,952	
CON0051 CC upstream of Meadow Brook	**High**	5	108	4,106	934	274
	Low	5	132	223	164	
MEA0009 Meadow Brook	**High**	5	1,076	3,255	1,773	2,349
	Low	5	1,145	5,475	2,645	
UWR0000 Unnamed tributary near Kemps	**High**	5	495	1,989	1,030	1,087
	Low	5	754	1,789	1,111	
CON0005 CC in Williamsport	**High**	5	199	6,867	1,349	345
	Low	5	97	269	194	

2.4 Source Assessment

Nonpoint Source Assessment

Nonpoint sources of fecal bacteria do not have one discharge point but occur over the entire length of a stream or waterbody. During rain events, surface runoff transports water and fecal bacteria over the land surface and discharges to the stream system. This transport is dictated by rainfall, soil type, land use, and topography of the watershed. Many types of nonpoint sources introduce fecal bacteria to the land surface, including the manure spreading process, direct deposition from livestock during the grazing season, and excretions from pets and wildlife. The deposition of non-human fecal bacteria directly to the stream occurs when livestock or wildlife have direct access to the waterbody. Nonpoint source contributions from human sources generally arise from failing septic systems and their associated drain fields or leaking infrastructure (i.e., sewer systems). The entire Conococheague Creek watershed in MD is covered by the general Phase II NPDES Municipal Separate Storm Sewer System (MS4) permit for Washington County and Hagerstown. Therefore, contributions from domestic animal and human sources will be categorized under point sources as part of a Stormwater (SW) Waste Load Allocation (WLA_{CON}). 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_{CON}) in this analysis. Wildlife contributions will be distributed between WLAs and LAs due to the presence of wildlife in both developed and undeveloped areas of the watershed.

Sewer Systems

The MD Conococheague Creek watershed is serviced by both sewer systems and septic systems. Sewer systems are present in the towns of Maugansville, Hagerstown, Halfway and Williamsport.

Septic Systems

On-site disposal (septic) systems are located throughout the Conococheague Creek watershed. Table 2.4.1 presents the number of septic systems per subwatershed. Figure 2.4.1 displays the areas that are serviced by sewers and the locations of the septic systems in MD.

Table 2.4.1: Septic Systems and Households per Subwatershed in the MD 8-digit Conococheague Creek Watershed

Station / Subwatershed	Septic Systems	Households
CON0217 / Conococheague Creek (CC) at PA line	33	95
CON0180 / CC near Fairview	64	40
RKD0006 / Rockdale Run	288	346
TMS0006 / Toms Run	202	211
RUS0005 / Rush Run	493	1,415
CON0051 / CC upstream of Meadow Brook	831	1,061
MEA0009 / Meadow Brook	305	286
UWR0000 / Unnamed tributary near Kemps	367	980
CON0005 / CC in Williamsport	243	3,791
Total	**2,826**	**8,225**

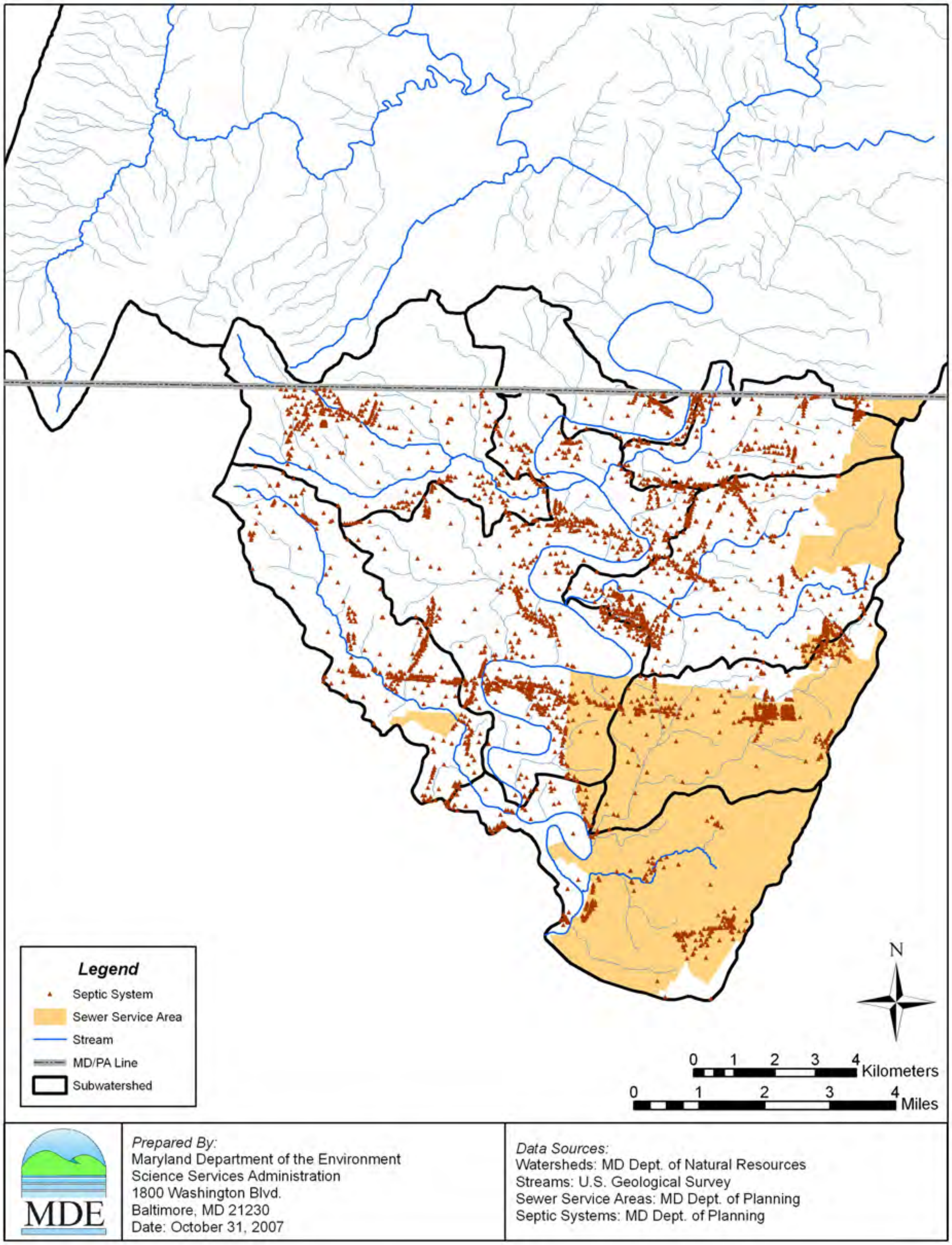

Figure 2.4.1: Sanitary Sewer Service Areas and Septic Locations in the MD 8-digit Conococheague Creek Watershed

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 are issued for industrial and municipal WWTPs and Phase I municipal separate storm sewer systems (MS4s). MDE general permits have been established for surface water discharges from: Phase II and other MS4 entities, surface coal mines, mineral mines, quarries, borrow pits, ready-mix concrete, asphalt plants, seafood processors, hydrostatic testing of tanks and pipelines, marinas, concentrated animal feeding operations, and stormwater associated with industrial activities.

NPDES Regulated Stormwater

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

Maryland’s portion of the Conococheague Creek watershed is located entirely in Washington County. Washington County, along with Hagerstown, is covered by a general Phase II NPDES MS4 permit. Bacteria loads associated with these MS4s are therefore included in the Stormwater (SW) WLA_{CON} of this TMDL, which also encompasses any other NPDES regulated Phase I and Phase II stormwater discharges in the watershed, including state and federal entities.

Sanitary Sewer Overflows

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

There were a total of 5 SSOs events reported to MDE between November 2003 and October 2004 in the Conococheague Creek watershed. Approximately 13,070 gallons of untreated or partially treated wastewater from SSOs were discharged through various waterways (surface water, groundwater, sanitary sewers, etc.). Figure 2.4.2 shows the locations where SSOs occurred in the MD portion of the watershed between November 2003 and October 2004.

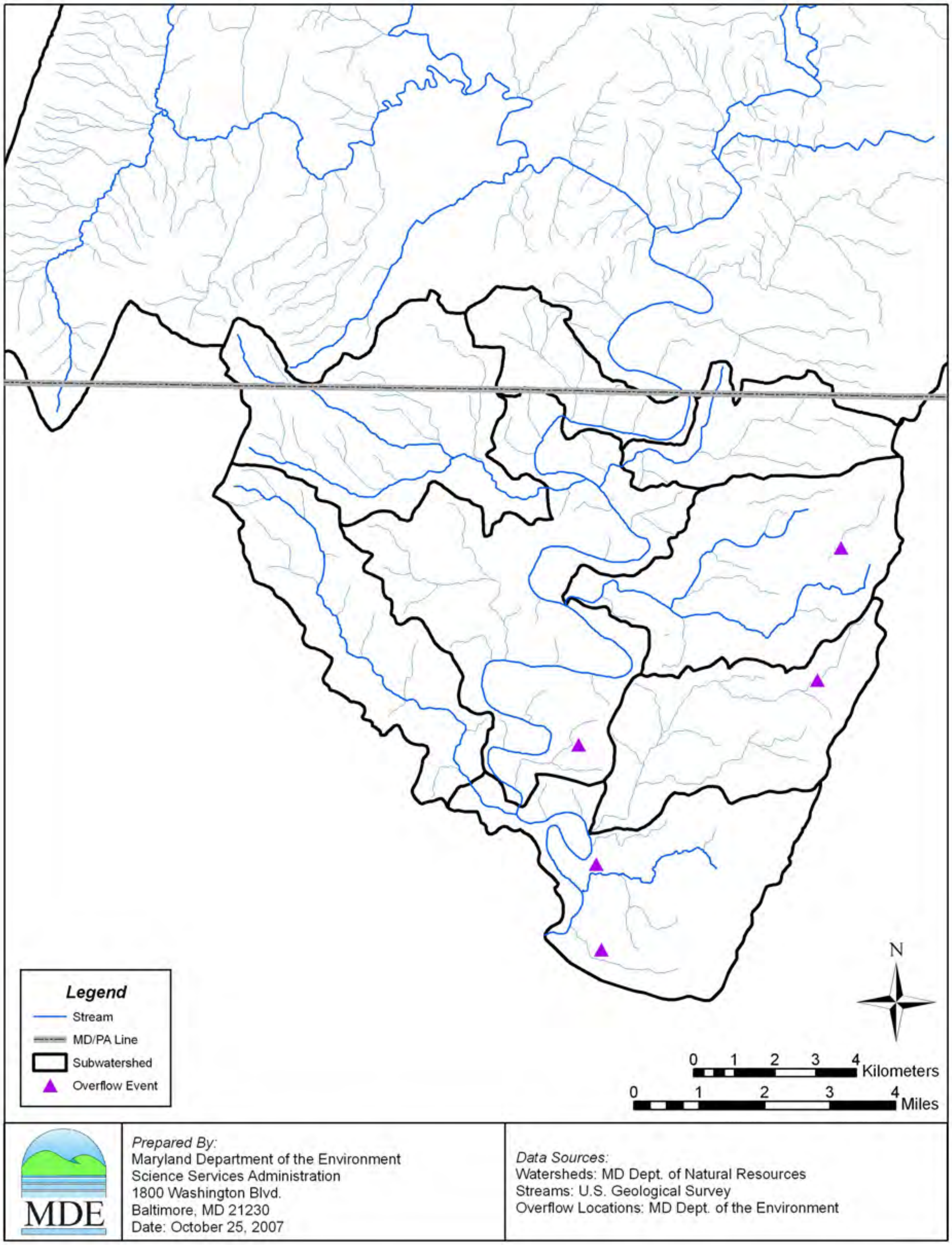
Legend
Stream
MD/PA Line
Subwatershed
Overflow Event
N
0 1 2 3 4 Kilometers
0 1 2 3 4 Miles
MDE
Prepared By:
Maryland Department of the Environment
Science Services Administration
1800 Washington Blvd.
Baltimore, MD 21230
Date: October 25, 2007
Data Sources:
Watersheds: MD Dept. of Natural Resources
Streams: U.S. Geological Survey
Overflow Locations: MD Dept. of the Environment

Figure 2.4.2: Sanitary Sewer Overflow Areas in the MD 8-digit Conococheague Creek Watershed

Municipal and Industrial Wastewater Treatment Plants (WWTPs)

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

Based on MDE's point source permitting information, there are three active municipal NPDES permitted point source facilities with permits regulating the discharge of fecal bacteria in the Conococheague Creek watershed. These three facilities combined treat approximately 2.9 MGD (million gallons per day). There are no industrial facilities in the Conococheague Creek watershed with NPDES permits regulating the discharge of fecal bacteria. Table 2.4.2 lists these facilities and Figure 2.4.3 shows their location in the watershed.

Table 2.4.2: NPDES Permit Holders Regulated for Fecal Bacteria Discharge in the MD 8-digit Conococheague Creek Watershed

Facility	NPDES Permit No.	County	Average Flow (MGD)	Fecal Coliform Concentration Annual AVG (MPN/100ml)	Fecal Coliform Load (Billion MPN/day)
Broadfording Bible Brethren Church WWTP	MD0051373	Washington	0.001	16.64*	0.001*
Cedar Ridge Children's Home and School WWTP	MD0067881	Washington	0.015	4.80	0.003
Conococheague WWTP	MD0063509	Washington	2.874	0.56	0.061

*Average daily maximum.

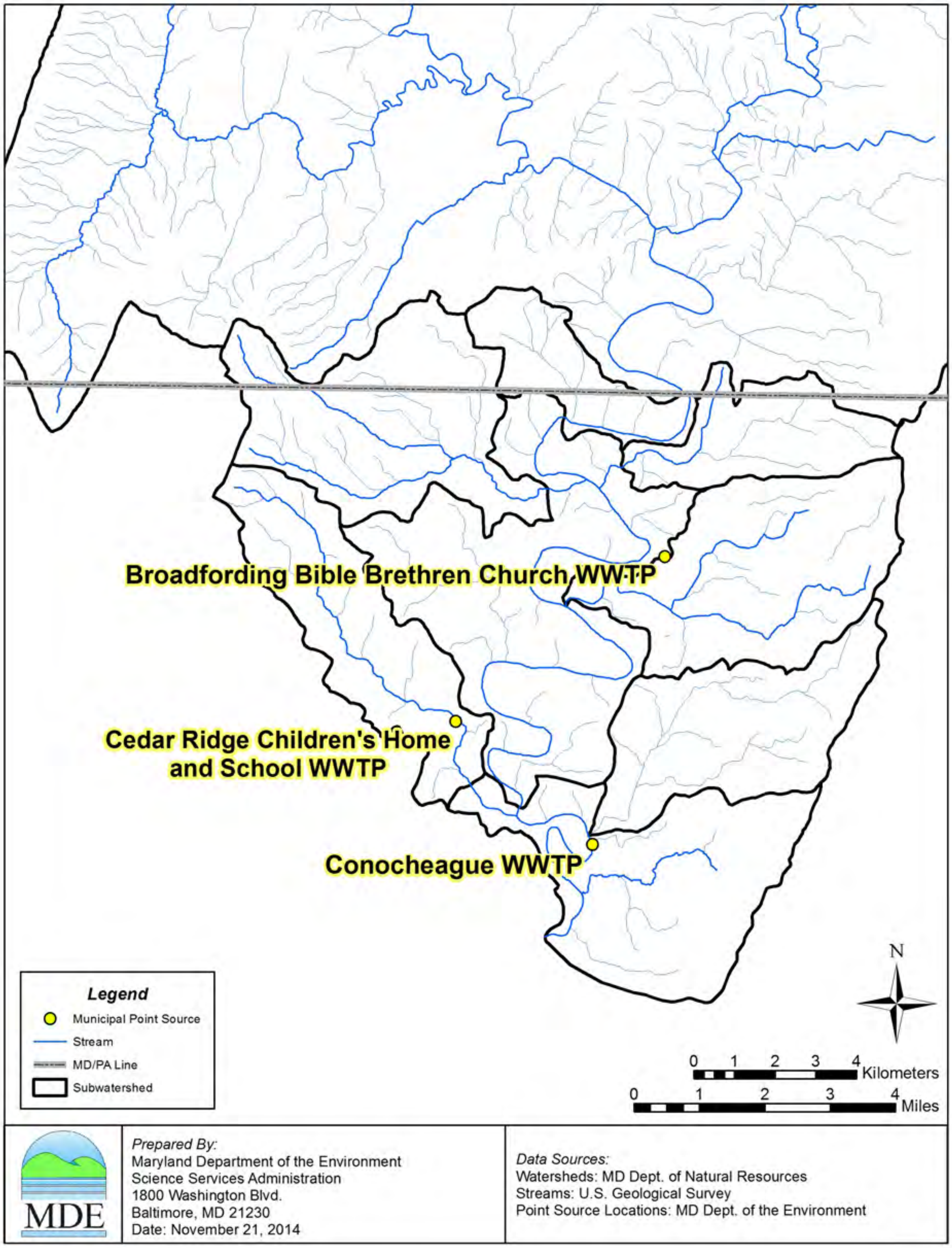
Broadfording Bible Brethren Church WWTP
Cedar Ridge Children's Home and School WWTP
Conocheague WWTP
Legend
Municipal Point Source
Stream
MD/PA Line
Subwatershed
N
0 1 2 3 4 Kilometers
0 1 2 3 4 Miles
MDE
Prepared By:
Maryland Department of the Environment
Science Services Administration
1800 Washington Blvd.
Baltimore, MD 21230
Date: November 21, 2014
Data Sources:
Watersheds: MD Dept. of Natural Resources
Streams: U.S. Geological Survey
Point Source Locations: MD Dept. of the Environment

Figure 2.4.3: Permitted Point Sources Discharging Fecal Bacteria in the MD 8-digit Conococheague Creek Watershed

Bacteria Source Tracking

Bacteria source tracking (BST) was used to identify the relative contributions of different sources of bacteria to in-stream water samples. BST monitoring was conducted at nine stations in the Conococheague Creek watershed, where samples were collected once per month 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 contribution of each 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 an initial 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. Adjust the weighted percentage based on the classification of known sources.
4. The final weighted mean source percentage, for each source category, is based on the proportion of time in each flow duration zone.

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

$$MS_l = \sum_{i=1}^{2} MS_{i,l} * W_i \tag{4}$$

where,

$$MS_{i,l} = \sum_{k=1}^{5} \frac{A_{l,k} * IMS_{i,k}}{P_k} \tag{5}$$

where,

$$IMS_{i,k} = \frac{\sum_{j=1}^{n_i} \log_{10}(C_{i,j}) * S_{i,j,k}}{\sum_{j=1}^{n_i} \log_{10}(C_{i,j})} \tag{6}$$

and where,

MS_l = weighted mean proportion of isolates of source *l*
$MS_{i,l}$ = adjusted weighted mean proportion of isolates for source *l* in stratum *i*
$IMS_{i,k}$ = initial weighted mean proportion of isolates for source *k* in stratum *i*
W_i = proportion covered by stratum *i*
$A_{l,k}$ = number of known source *l* isolates initially predicted as source *k*
P_k = number of total known isolates initially predicted as source *k*
i = stratum
j = sample
k = source category (1=human, 2=domestic, 3=livestock, 4=wildlife, 5=unknown)
l = final source category (1=human, 2=domestic, 3=livestock, 4=wildlife)
$C_{i,j}$ = 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 Conococheague Creek Watershed for the Average Annual Period

Station	Flow Stratum	% Domestic Animals	% Human	% Livestock	% Wildlife
CON0217	**High**	17.2	15.7	33.5	33.7
	Low	15.6	15.3	28.8	40.2
	Weighted	16.1	15.4	30.2	38.3
CON0180	**High**	22.0	17.1	31.4	29.5
	Low	16.7	22.5	29.4	31.3
	Weighted	18.3	20.9	30.0	30.8
RKD0006	**High**	20.6	20.4	31.2	27.8
	Low	16.8	20.3	29.8	33.1
	Weighted	17.9	20.3	30.2	31.6
TMS0006	**High**	22.0	14.2	30.4	33.4
	Low	28.9	13.4	26.9	30.8
	Weighted	26.9	13.6	27.9	31.5
RUS0005	**High**	18.9	14.4	36.0	30.7
	Low	20.4	13.0	33.2	33.4
	Weighted	20.0	13.4	34.0	32.6
CON0051	**High**	21.7	19.5	32.7	26.1
	Low	20.6	9.3	28.2	41.9
	Weighted	20.9	12.4	29.5	37.2
MEA0009	**High**	22.3	23.5	28.4	25.8
	Low	22.9	13.8	29.2	34.1
	Weighted	22.7	16.7	29.0	31.6
UWR0000	**High**	23.0	16.0	28.8	32.1
	Low	23.9	18.0	32.2	25.8
	Weighted	23.7	17.4	31.2	27.7
CON0005	**High**	15.6	16.9	34.7	32.9
	Low	14.1	16.0	27.0	42.9
	Weighted	14.5	16.2	29.3	39.9

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

Station	Flow Stratum	% Domestic Animals	% Human	% Livestock	% Wildlife
CON0217	**High**	29.0	17.5	27.9	25.6
	Low	18.7	8.0	27.7	45.6
	Weighted	21.7	10.8	27.7	39.7
CON0180	**High**	35.7	10.3	28.2	25.8
	Low	21.7	11.3	30.2	36.7
	Weighted	25.9	11.0	29.6	33.5
RKD0006	**High**	26.1	14.5	30.6	28.8
	Low	14.5	14.1	30.9	40.5
	Weighted	17.9	14.2	30.8	37.0
TMS0006	**High**	30.9	16.2	29.4	23.6
	Low	35.1	12.9	23.8	28.2
	Weighted	33.8	13.8	25.5	26.9
RUS0005	**High**	25.4	13.1	33.2	28.3
	Low	21.5	13.0	33.1	32.3
	Weighted	22.7	13.1	33.1	31.1
CON0051	**High**	26.5	17.7	31.7	24.0
	Low	19.8	7.3	26.5	46.4
	Weighted	21.8	10.4	28.1	39.7
MEA0009	**High**	25.3	28.4	24.9	21.4
	Low	23.5	14.2	29.4	32.9
	Weighted	24.0	18.4	28.1	29.5
UWR0000	**High**	31.3	17.8	27.3	23.6
	Low	32.9	12.8	28.1	26.2
	Weighted	32.4	14.3	27.9	25.4
CON0005	**High**	18.9	16.4	35.7	29.1
	Low	13.4	8.4	28.7	49.5
	Weighted	15.0	10.8	30.8	43.4

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 Maryland 8-digit Conococheague Creek watershed. These standards are described fully in Section 2.3, "Water Quality Impairment."

4.0 TOTAL MAXIMUM DAILY LOADS AND SOURCE ALLOCATION

4.1 Overview

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

To be most effective, the TMDL provides a basis for allocating loads among the known pollutant sources in the watershed so that appropriate control measures can be implemented and water quality standards achieved. By definition, the TMDL is the sum of the individual waste load allocations (WLAs) for point sources and load allocations (LAs) for nonpoint sources 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, as well as the limits in scientific and technical understanding of water quality in natural systems. Although this formulation suggests that the TMDL be expressed as a load, the Code of Federal Regulations (40 CFR 130.2(i)) states that the TMDL can be expressed in terms of “mass per time, toxicity or other appropriate measure.”

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

Bacteria concentrations, determined through laboratory analysis of in-stream water samples for bacteria indicators (e.g., enterococci), are expressed in either colony forming units (CFU) or most probable number (MPN) of colonies. The first method (US EPA 1985) is a direct estimate of the bacteria colonies (Method 1600). The second method 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 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 Analytical Framework

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

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

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

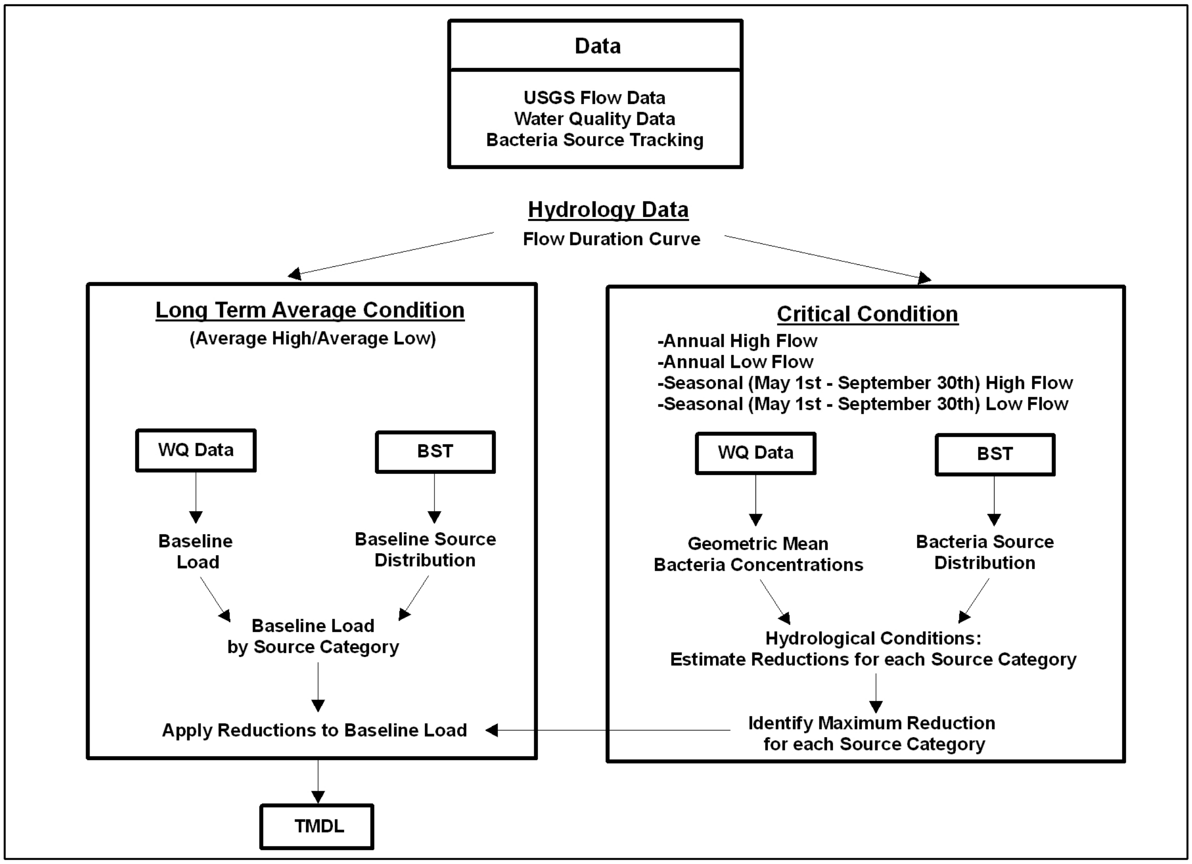

Figure 4.2.1: Diagram of the Non-tidal Bacteria TMDL Analysis Framework

4.3 Estimating Baseline Loads

Baseline loads are estimated for all subwatersheds of Conococheague Creek, including, for computational purposes, those partially located in PA. Baseline loads estimated in this TMDL analysis are reported as long-term average annual loads. These loads are estimated using geometric mean concentrations and bias correction factors (calculated from bacteria monitoring data) and daily average flows (estimated from 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.

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

$$F_{1i} = A_i/C_i \qquad (7)$$

where,

F_{1i} = bias correction factor for stratum i
A_i = long term annual arithmetic mean for stratum i
C_i = long term annual geometric mean for stratum i

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

The loads for each stratum are estimated as follows:

$$L_i = Q_i * C_i * F_{1i} * F_2 \qquad (8)$$

where,

L_i = daily average load (Billion MPN/day) at monitoring station for stratum i
Q_i = daily average flow (cfs) for stratum i
C_i = geometric mean for stratum i
F_{1i} = bias correction factor for stratum i
F_2 = unit conversion factor (0.0245)

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

$$L = \sum_{i=1}^{2} L_i * W_i \qquad (9)$$

where,

L = daily average load at station (MPN/day)
W_i = proportion of stratum i

In the Conococheague Creek watershed, weighting factors of 0.297 for high flow and 0.703 for low/mid flows were used to estimate the annual baseline load expressed as Billion MPN *E. coli*/year.

Estimating Subwatershed Loads

Subwatersheds with more than one monitoring station were subdivided into unique watershed segments, thus allowing individual load and reduction targets to be determined for each. In the Conococheague Creek watershed three stations have upstream monitoring stations, as listed in Table 4.3.1. In these three cases, the subwatershed is differentiated by adding the extension "sub" to the name of the downstream monitoring station. For example, "CON0180sub" signifies only the area and load between stations CON0180 and CON0217, while "CON0180" refers to the cumulative area draining to that station. There are a total of nine subwatersheds considered in this analysis, corresponding to the nine monitoring stations.

Table 4.3.1: Subdivided Watersheds in the Conococheague Creek Watershed

Station / Tributary	Upstream Station(s)
CON0180sub / Conococheague Creek (CC) near Fairview	CON0217
CON0051sub / CC upstream of Meadow Brook	CON0180, RKD0006, TMS0006 and RUS0005
CON0005sub / CC in Williamsport	CON0051, MEA0009 and UWR0000

Bacteria loads from these subwatersheds are joined by loads from their upstream subwatersheds to result in the concentration measured at the downstream monitoring station. However, for the purposes of this TMDL, the bacteria concentration measured at each monitoring station is assumed to be representative of that corresponding subwatershed and independent of flow from upstream subwatersheds. For example, the load transported from upstream station CON0217 is not considered in the estimation of the load from the subwatershed CON0180sub. Instead the bacteria concentration measured at station CON0180 is assigned to that subwatershed.

This assumption is necessary due to a particular phenomenon, an example of which is observed in the subwatershed of CON0051sub. The bacteria loadings in the subwatersheds upstream of CON0051sub are significantly greater than the load measured at that downstream station. This occurrence indicates that bacteria loads are significantly diminished as they are transported downstream. Bacteria are either dying off quickly, possibly due to environmental conditions such as extreme pH levels, elevated temperature, etc., or are being diverted due to the Karst geology present in the area. Given this phenomenon, the measured concentration at each station is attributed solely to its immediate subwatershed. This will result in a slightly conservative estimate of bacteria loads, but will also allow a more consistent methodology throughout the watershed than applying unpredictable upstream loads.

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 the subwatersheds defined in Table 4.3.1 were assigned from the analysis of their downstream stations.

Results of the baseline load calculations, including subwatersheds partially located in PA, are presented in Table 4.3.2.

Table 4.3.2: Baseline Loads Calculations

Subwatershed	**Area** (mi^2)	**High Flow** (Unit Flow = 3.01 cfs/mi^2)		**Low Flow** (Unit Flow = 0.55 cfs/mi^2)		**Baseline *E. coli* Load (Billion MPN/year)**
		Average Flow (cfs)	***E. coli* Concentration. (MPN/100ml)**	**Average Flow (cfs)**	***E. coli* Concentration (MPN/100ml)**	
CON0217[1]	497.0	1495.0	460	272.7	156	3,882,857
CON0180sub[1]	3.7	11.1	471	2.0	162	34,061
RKD0006[1]	10.3	31.0	876	5.7	910	193,370
TMS0006[1]	4.7	14.1	233	2.6	103	85,102
RUS0005	10.3	31.0	1089	5.7	824	194,990
CON0051sub[1]	15.8	47.6	318	8.7	96	120,621
MEA0009	7.9	23.8	761	4.3	572	128,775
UWR0000	7.8	23.6	682	4.3	565	74,881
CON0005sub	10.5	31.5	379	5.7	129	97,684

[1] Subwatersheds partially located in Pennsylvania

Baseline loads for subwatersheds located in both MD and PA were estimated using the ratios of the areas of the MD and PA portions to the total area of the subwatershed. The total baseline load for all subwatersheds or portions thereof located in MD is estimated as 845,806 billion MPN *E.coli*/year. The total baseline load for the portions of subwatersheds located in PA is 3,966,535 billion MPN E. coli/year.

4.4 Critical Condition and Seasonality

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

For this TMDL the critical condition is determined by assessing annual and seasonal hydrological conditions for high flow and low flow periods. Seasonality is assessed as the time period when water contact recreation is expected, specifically May 1st through September 30th. For this TMDL analysis, the average hydrological condition over a 25-year period has been estimated as 29.7% high flow and 70.3% 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 29.7% and a low flow condition as occurring when the daily flow duration interval is greater than 29.7%, critical hydrological condition can be estimated by the percent of high or low flows during a specific period.

Using long term flow data from USGS station 01614500, critical condition and seasonality has been determined by assessing various hydrological conditions to account for seasonal and annual averaging periods. The five conditions listed in Table 4.4.1 were used to account for the critical condition.

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

Hydrological Condition		Averaging Period	Water Quality Data Used	Fraction High Flow	Fraction Low Flow	Condition Period
Annual	Average	365 days	All	0.297	0.703	Long-Term Average
	Wet (High Flow)	365 days	All	0.739	0.261	Jan. 1996 – Jan. 1997
	Dry (Low Flow)	365 days	All	0.038	0.962	June 2001 – June 2002
Seasonal	Wet (High Flow)	May 1st – Sept. 30th	May 1st – Sept. 30th	0.612	0.388	May – Sept. 1996
	Dry (Low Flow)	May 1st – Sept. 30th	May 1st – Sept. 30th	0	1.000	May – Sept. 2007

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

The bacteria monitoring data for all stations located in the Conococheague Creek watershed cover a sufficient temporal span (at least one year) to estimate annual conditions. Sufficient data were also available to establish geometric means for the seasonal period.

The reductions of fecal bacteria required to meet water quality standards in each subwatershed of the Conococheague Creek watershed are shown in Table 4.4.2. For computational purposes, the calculations include those subwatersheds partially located in PA.

Table 4.4.2: Required Fecal Bacteria Reductions (by Hydrological Condition per Subwatershed) to Meet Water Quality Standards

Station / Tributary	Hydrological Condition		Domestic Animals %	Human %	Livestock %	Wildlife %
CON0217[1] Conococheague Creek (CC) at PA line	Annual	Average	69.1	89.4	64.0	0.0
		Wet	98.0	98.0	98.0	6.1
		Dry	49.0	98.0	11.8	0.0
	Seasonal	Wet	98.0	98.0	98.0	42.7
		Dry	74.4	98.0	73.0	0.0
	Maximum Source Reduction		**98.0**	**98.0**	**98.0**	**42.7**
CON0180sub[1] CC near Fairview	Annual	Average	64.2	82.7	57.3	0.0
		Wet	98.0	98.0	90.8	0.0
		Dry	43.0	98.0	0.0	0.0
	Seasonal	Wet	98.0	98.0	98.0	44.6
		Dry	62.3	98.0	53.8	0.0
	Maximum Source Reduction		**98.0**	**98.0**	**98.0**	**44.6**
RKD0006[1] Rockdale Run	Annual	Average	98.0	98.0	98.0	62.2
		Wet	98.0	98.0	98.0	58.5
		Dry	98.0	98.0	98.0	64.1
	Seasonal	Wet	98.0	98.0	98.0	89.1
		Dry	98.0	98.0	98.0	85.7
	Maximum Source Reduction		**98.0**	**98.0**	**98.0**	**89.1**
TMS0006[1] Toms Run	Annual	Average	2.6	58.3	0.0	0.0
		Wet	50.4	80.5	44.5	0.0
		Dry	0.0	0.0	0.0	0.0
	Seasonal	Wet	98.0	98.0	98.0	38.1
		Dry	64.7	91.2	68.0	0.0

	Maximum Source Reduction		**98.0**	**98.0**	**98.0**	**38.1**
Station / Tributary	**Hydrological Condition**		**Domestic Animals %**	**Human %**	**Livestock %**	**Wildlife %**
RUS0005 Rush Run	Annual	Average	98.0	98.0	98.0	63.1
		Wet	98.0	98.0	98.0	66.7
		Dry	98.0	98.0	98.0	60.8
	Seasonal	Wet	98.0	98.0	98.0	87.4
		Dry	98.0	98.0	98.0	85.2
	Maximum Source Reduction		**98.0**	**98.0**	**98.0**	**87.4**
CON0051sub[1] CC upstream of Meadow Brook	Annual	Average	22.0	63.7	0.2	0.0
		Wet	66.2	89.7	61.1	0.0
		Dry	0.0	0.0	0.0	0.0
	Seasonal	Wet	98.0	98.0	98.0	27.0
		Dry	50.1	81.3	41.5	0.0
	Maximum Source Reduction		**98.0**	**98.0**	**98.0**	**27.0**
MEA0009 Meadow Brook	Annual	Average	98.0	98.0	98.0	43.5
		Wet	98.0	98.0	98.0	44.6
		Dry	98.0	98.0	98.0	42.6
	Seasonal	Wet	98.0	98.0	98.0	83.4
		Dry	98.0	98.0	98.0	90.3
	Maximum Source Reduction		**98.0**	**98.0**	**98.0**	**90.3**
UWR0000 Unnamed tributary near Kemps	Annual	Average	98.0	98.0	98.0	32.8
		Wet	98.0	98.0	98.0	44.0
		Dry	98.0	98.0	98.0	24.9
	Seasonal	Wet	98.0	98.0	98.0	60.3
		Dry	98.0	98.0	98.0	64.5
	Maximum Source Reduction		**98.0**	**98.0**	**98.0**	**64.5**
CON0005sub CC in Williamsport	Annual	Average	62.4	55.0	49.6	0.0
		Wet	98.0	55.0	98.0	5.9
		Dry	2.9	55.0	5.6	0.0
	Seasonal	Wet	98.0	55.0	98.0	67.9
		Dry	77.7	55.0	80.6	0.0

	Maximum Source Reduction	**98.0**	**55.0**	**98.0**	**67.9**

[1] Subwatersheds partially located in Pennsylvania

4.5 Margin of Safety

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

Based on EPA guidance, the MOS can be achieved through two approaches (EPA 1991). One approach is to reserve a portion of the loading capacity as a separate term in the TMDL (i.e., TMDL = LA + WLA + MOS). The second approach is to incorporate the MOS as conservative assumptions used in the TMDL analysis. The second approach was used for this TMDL 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. 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 CON0180sub, CON0051sub, and CON0005sub were based on the sources identified at stations CON0180, CON0051, and CON0005 respectively.

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

Subwatershed	Domestic		Human		Livestock		Wildlife		Total Load (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)	
CON0217[1]	16.1	623,501	15.4	599,633	30.2	1,172,927	38.3	1,486,801	3,882,857
CON0180sub[1]	18.3	6,238	20.9	7,119	30.0	10,221	30.8	10,484	34,061
RKD0006[1]	17.9	34,612	20.3	39,260	30.2	58,490	31.6	61,009	193,370
TMS0006[1]	26.9	22,885	13.6	11,612	27.9	23,769	31.5	26,836	85,102
RUS0005	20.0	38,996	13.4	26,106	34.0	66,353	32.6	63,534	194,990
CON0051sub[1]	20.9	25,203	12.4	14,915	29.5	35,598	37.2	44,905	120,621
MEA0009	22.7	29,222	16.7	21,538	29.0	37,292	31.6	40,722	128,775
UWR0000	23.7	17,725	17.4	13,047	31.2	23,391	27.7	20,718	74,881
CON0005sub	14.5	14,200	16.2	15,872	29.3	28,604	39.9	39,009	97,684

[1] Subwatersheds partially located in Pennsylvania

First Scenario: Fecal Bacteria Practicable Reduction Targets

The maximum practicable reduction (MPR) for each of the four source categories is listed in Table 4.6.2. These values are based on review of the available literature and best professional judgment. It is assumed that human sources would potentially have the highest risk of causing gastrointestinal illness and therefore should have the highest reduction. If a domestic WWTP is located in the upstream watershed, this is considered in the MPR so as to not violate the permitted loads. For this reason, in the subwatershed of CON0005 the human source reduction had to be limited in order to maintain the permitted loads of the WWTP. 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 (BMPs). 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:

$$\text{Risk Score} = \text{Min} \sum_{i=1}^{4} P_j * W_j \qquad (10)$$

where,

$$P_j = \frac{(1 - R_i) * Pb_j}{1 - TR} \qquad (11)$$

and,

$$TR = \frac{C - C_{cr}}{C} \qquad (12)$$

Therefore the risk score can be represented as:

$$Risk\ Score = Min \sum_{i=1}^{4} \left[\frac{(1 - R_j) * Pb_j}{(1 - \frac{C - Ccr}{C})} * W_j \right] \qquad (13)$$

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	= weight 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:

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

The human source reduction for the subwatershed CON0005sub was further constrained to no greater than 55.0% in order to maintain the permitted load of the WWTP.

In all nine 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: Maximum Practicable Reduction Scenario Results

Subwatershed	Applied Reductions				Total Reduction %	Target Reduction %
	Domestic %	Human %	Livestock %	Wildlife %		
CON0217[1]	75.0	95.0	75.0	0.0	49.4	76.8
CON0180sub[1]	75.0	95.0	75.0	0.0	56.1	81.6
RKD0006[1]	75.0	95.0	75.0	0.0	55.4	95.2
TMS0006[1]	75.0	95.0	75.0	0.0	54.1	79.1
RUS0005	75.0	95.0	75.0	0.0	53.2	94.5
CON0051sub[1]	75.0	95.0	75.0	0.0	49.6	71.6
MEA0009	75.0	95.0	75.0	0.0	54.6	95.6
UWR0000	75.0	95.0	75.0	0.0	57.7	88.7
CON0005sub	75.0	55.0	75.0	0.0	41.8	79.0

[1] Subwatersheds partially located in Pennsylvania

Second Scenario: Fecal Bacteria Reductions Higher than MPRs

The TMDL must specify load allocations that will meet the water quality standards. In the practicable reduction targets scenario, none of the subwatersheds 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 these subwatersheds, the maximum allowable reduction was increased to 98% for all sources, including wildlife. A similar optimization procedure as before 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 considered in the practicable reduction scenario but subject to the following constraints:

$C = C_{cr}$
$0 \le R_{human} \le 98\%$
$0 \le R_{pets} \le 98\%$
$0 \le R_{livestock} \le 98\%$
$0 \le R_{wildlife} \le 98\%$
$P_j \ge 1\%$

A summary of the results of this second scenario analysis is presented in Table 4.6.4.

Table 4.6.4: Reduction Results Based on Optimization Model Allowing Up to 98% Reduction

Subwatershed	Applied Reductions				Total Reduction %	Target Reduction %
	Domestic %	Human %	Livestock %	Wildlife %		
CON0217[1]	98.0	98.0	98.0	42.7	76.8	76.8
CON0180sub[1]	98.0	98.0	98.0	44.6	81.6	81.6
RKD0006[1]	98.0	98.0	98.0	89.1	95.2	95.2
TMS0006[1]	98.0	98.0	98.0	38.1	79.1	79.1
RUS0005	98.0	98.0	98.0	87.4	94.5	94.5
CON0051sub[1]	98.0	98.0	98.0	27.0	71.6	71.6
MEA0009	98.0	98.0	98.0	90.3	95.6	95.6
UWR0000	98.0	98.0	98.0	64.5	88.7	88.7
CON0005sub	98.0	55.0	98.0	67.9	79.0	79.0

[1] Subwatersheds partially located in Pennsylvania

4.7 TMDL Loading Caps

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

The TMDL loading caps are provided in billion MPN *E. coli*/year. These loading caps are for the nine subwatersheds located upstream of their respective monitoring stations: CON0217, CON0180sub, RKD0006, TMS0006, RUS0005, CON0051sub, MEA0009, UWR0000 and CON0005sub. Loading caps for subwatersheds of Conococheague Creek partially located in PA were included in the TMDL scenario. A TMDL summary for the entire Conococheague Creek watershed will include an upstream load allocation for the portion of the watershed located in PA to indicate estimated loads necessary to meet MD water quality standards in the MD 8-digit assessment unit for the Conococheague Creek watershed.

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 the long-term annual average daily flow for each flow stratum. The loads from these two strata are then weighted to represent average conditions (see Table 4.3.1), based on the proportion of each stratum, to estimate the total long-term loading rate.

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

$$\text{TMDL Loading Cap} = L_b * (1 - R) \qquad (14)$$

where,

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

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

Table 4.7.1: Annual Average TMDL Loading Caps

Subwatershed	*E. coli* Baseline Load (Billion MPN/year)	Long-Term Average *E. coli* TMDL Load (Billion MPN/year)	% Target Reduction
CON0217[1]	3,882,857	900,433	76.8
CON0180sub[1]	34,061	6,283	81.6
RKD0006[1]	193,370	9,289	95.2
TMS0006[1]	85,102	17,780	79.1
RUS0005	194,990	10,656	94.5
CON0051sub[1]	120,621	34,280	71.6
MEA0009	128,775	5,705	95.6
UWR0000	74,881	8,438	88.7
CON0005sub	97,684	20,521	79.0
Total	**4,812,341**	**1,013,385**	**78.9**

[1] Subwatersheds partially located in Pennsylvania

Table 4.7.2: Annual Average TMDL Loading Caps by Source Category

Subwatershed	Domestic		Human		Livestock		Wildlife		Total Load (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)	
CON0217[1]	1.4	12,470	1.3	11,993	2.6	23,459	94.7	852,515	900,433
CON0180sub[1]	2.0	125	2.3	142	3.3	204	92.5	5,812	6,283
RKD0006[1]	7.5	692	8.5	785	12.6	1,170	71.5	6,641	9,289
TMS0006[1]	2.6	458	1.3	232	2.7	475	93.4	16,615	17,780
RUS0005	7.3	780	4.9	522	12.5	1,327	75.3	8,027	10,656
CON0051sub[1]	1.5	504	0.9	298	2.1	712	95.6	32,766	34,280
MEA0009	10.2	584	7.6	431	13.1	746	69.1	3,944	5,705
UWR0000	4.2	354	3.1	261	5.5	468	87.2	7,355	8,438
CON0005sub	1.4	284	34.8	7,138	2.8	572	61.0	12,527	20,521

[1] Subwatersheds partially located in Pennsylvania

Maximum Daily Loads

Recent EPA guidance (US EPA 2006a) recommends that maximum daily load (MDL) expressions of long-term annual average TMDLs should also be provided as part of the TMDL analysis and report. Selection of an appropriate method for translating a TMDL based on a longer time period into one using a daily time period requires decisions regarding 1) the level of resolution, and 2) the level of protection. The level of resolution pertains to the amount of detail used in specifying the maximum daily load. The level of protection represents how often the maximum daily load (MDL) is expected to be exceeded. Draft EPA/TetraTech guidance on daily loads (Limno-Tech 2007) provides three categories of options for both level of resolution and level of protection, and discusses these categories in detail.

For the Conococheague Creek MDLs, a “representative daily load” option was selected as the level of resolution, and a value “that will be exceeded with a pre-defined probability” was selected as the level of protection. In these options, the MDLs are two single daily loads that correspond to the two flow strata, with an upper bound percentile that accounts for the variability of daily loads. The upper bound percentile and the MDLs were estimated following EPA’s

"*Technical Support Document for Water Quality-Based Toxics Control*" (1991 TSD) (EPA 1991); and "*Approaches For Developing a Daily Load Expression for TMDLs Computed for Longer Term Averages*" (EPA 2006b).

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

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

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

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

Table 4.7.3: Conococheague Creek Watershed Maximum Daily Loads Summary

Subwatershed	Flow Stratum	Maximum Daily Load (Billion *E. coli* MPN/day)	
		by Stratum	Weighted by Stratum
CON0217[1]	High Low	84,987 1,162	26,058
CON0180sub[1]	High Low	478 8	147
RKD0006[1]	High Low	806 129	330
TMS0006[1]	High Low	1,746 56	558
RUS0005	High Low	558 68	214
CON0051sub[1]	High Low	5,061 49	1,537
MEA0009	High Low	251 182	202
UWR0000	High Low	273 53	118
CON0005sub	High	1,743	535

	Low	24	

[1] Subwatersheds partially located in Pennsylvania

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

4.8 TMDL Allocations

The MD 8-digit Conococheague Creek fecal bacteria TMDL is composed of the following components:

$$TMDL = LA_{PA} + LA_{CON} + WLA_{CON} + MOS \qquad (15)$$

where,

LA_{PA} = Pennsylvania Upstream Load Allocation
LA_{CON} = MD Conococheague Creek Load Allocation
WLA_{CON} = MD Conococheauge Creek Waste Load Allocation
MOS = Margin of Safety

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

In addition to these allocation categories for the MD 8-digit watershed, the MD Conococheague Creek TMDL includes an upstream load allocation for the portion of the watershed located in PA (LA_{PA}). The LA_{PA} was calculated using the ratios of the areas of the watershed in MD and in PA to the total area of the watershed, and is presented as a "lump-sum" upstream load comprising all bacteria source categories. The LA_{PA}, determined to be necessary in order to meet MD water quality standards in the MD 8-digit Conococheague Creek basin, will not be distributed between nonpoint sources (LA) and point sources (WLA).

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

Bacteria Source Categories and Allocation Distributions

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

Table 4.8.1: Potential Source Contributions for TMDL Allocation Categories in the MD 8-digit Conococheague Creek Watershed

Source Category	**TMDL Allocation Categories**		
	LA	**WLA**	
		WWTP	**Stormwater**
Human		X	X
Domestic			X
Livestock	X		
Wildlife	X		X

* These allocations apply only to the portion of the watershed in MD. The upstream load allocation attributed to PA includes all four bacteria source categories in one single load.

LA_{CON}

All four bacteria source categories could potentially contribute to nonpoint source loads. For human sources, if the watershed has no MS4s or other NPDES-regulated Phase I or Phase II stormwater discharges, the nonpoint source contribution is estimated by subtracting any WWTP and/or CSO loads from the TMDL human load, and is then assigned to the LA_{CON}. However, in watersheds covered by NPDES-regulated stormwater permits, any such nonpoint sources of human bacteria (i.e., beyond the reach of the sanitary sewer systems) are assigned to the SW-WLA_{CON} (see below). There are three municipal and no industrial wastewater treatment facilities with NPDES permits regulating the discharge of fecal bacteria in the Conococheague Creek watershed. There are no subwatersheds with assigned NPDES CSO WLA.

Livestock loads are all assigned to the LA_{CON}. Domestic animals (pets) loads are assigned to the LA in watersheds with no MS4s or other NPDES-regulated stormwater systems. Since the entire Conococheague Creek watershed is covered by an NPDES MS4 permit, bacteria loads from domestic animal sources are assigned to the SW-WLA_{CON} in all nine subwatersheds of

Conococheague Creek. However, wildlife sources will be distributed between the LA_{CON} and the SW- WLA_{CON} based on a ratio of the amount of pervious area in non-urban land to pervious area in urban land.

$\mathbf{WLA_{CON}}$

NPDES Regulated Stormwater

EPA's guidance document, "Establishing Total Maximum Daily Load (TMDL) Wasteload Allocations (WLAs) for Storm Water Sources and NPDES Permit Requirements Based on Those WLAs" (November 2002), advises that all individual and general NPDES Phase I and Phase II stormwater permits are point sources subject to WLA assignment in the TMDL. The document acknowledges that quantification of rainfall-driven nonpoint source loads is uncertain, stating that available data and information usually are not detailed enough to determine WLAs for NPDES-regulated stormwater discharges on an outfall-specific basis; therefore, the EPA guidance allows the stormwater WLA to be expressed as an aggregate allotment. Thus, in watersheds with existing NPDES-regulated stormwater permits, domestic animal bacteria loads are grouped together into a single SW-WLA along with other potential nonpoint source loads such as human and wildlife loads. This allowable human load in the SW-WLA is estimated by subtracting any WWTP and CSO loads (if present) from the total allowable (TMDL) human load. (There are three municipal and no industrial wastewater treatment facilities with NPDES permits regulating the discharge of fecal bacteria in the Conococheague Creek watershed. There are no NPDES CSO permits in the watershed.) The SW-WLA_{CON} wildlife load is estimated as explained above. In watersheds with no existing NPDES-regulated stormwater permits, these loads will be included in the LA.

Within the MD portion of the Conococheague Creek watershed, the jurisdiction of Washington County is covered by the general Phase II MS4 program regulations. Based on EPA's guidance, the SW-WLA is presented as one combined load for the entire land area of each county in each subwatershed. The SW-WLA_{CON} category encompasses any other Phase I and Phase II NPDES-regulated stormwater discharges in the watershed, including State and federal entities. The SW-WLA_{CON} includes loads from sources such as leaks from broken sanitary infrastructure and failing septic systems, which may be transported through the storm drain system. These loads may be more effectively controlled through other management programs, but at this time such components cannot be determined separately. As stormwater assessment and/or other program monitoring efforts result in a more refined source assessment, MDE reserves the right to revise the current SW-WLA_{CON}, provided the revisions are consistent with achieving water quality standards. Upon approval of the TMDL, "NPDES-regulated municipal stormwater and small construction storm water discharges effluent limits should be expressed as BMPs or other similar requirements, rather than as numeric effluent limits" (US EPA 2002a). The SW-WLA_{CON} distribution in Washington County is presented in Table 4.8.2.

Table 4.8.2: Annual Average Stormwater Allocations in MD

Subwatershed	Washington County SW-WLA (Billion MPN *E. coli*/year)
CON0217[1]	92
CON0180sub[1]	177
RKD0006[1]	1,370
TMS0006[1]	2,244
RUS0005	2,511
CON0051sub[1]	4,216
MEA0009	1,258
UWR0000	1,804
CON0005sub	3,422
Total	**17,088**

[1] MD portion of the subwatershed only.

Municipal and Industrial WWTPs

As explained in the source assessment section above, there are three NPDES permitted point source facilities with permits regulating the discharge of fecal bacteria in the MD 8-digit Conococheague Creek watershed. These three facilities discharge into three subwatersheds: Conococheague Creek upstream of Meadow Brook (CON0051), Meadow Brook (MEA0009), and Conococheague Creek in Williamsport (CON0005).

The WLA for each WWTP is estimated using the design flow of the plant stated in the facility's NPDES permit and the *E. coli* criterion of 126 MPN/100ml. Bacteria loads assigned to the WWTPs are allocated as the WWTP-WLA_{CON}.

4.9 Summary

The long-term annual average TMDL and TMDL allocations are presented in Table 4.9.1. Table 4.9.2 presents the maximum daily loads for the subwatersheds or portions thereof within the Conococheague Creek MD 8-digit basin. Both tables include the upstream load allocation to Pennsylvania determined to be necessary in order to meet MD water quality standards in the MD portion of the watershed.

Table 4.9.1: MD 8-Digit Conococheague Creek Annual Average TMDL

Subwatershed	**Total Allocation**	**LA**	**SW-WLA**	**WWTP-WLA**
	(Billion MPN *E. coli* /year)			
CON0217[1]	1,615	1,523	92	0
CON0180sub[1]	2,427	2,250	177	0
RKD0006[1]	6,382	5,012	1,370	0
TMS0006[1]	15,862	13,618	2,244	0
RUS0005	10,656	8,146	2,511	0
CON0051sub[1]	34,268	30,047	4,216	4
MEA0009	5,705	4,435	1,253	17
UWR0000	8,438	6,634	1,804	0
CON0005sub	20,521	9,962	3,422	7,138
MD Total	105,874	81,626	17,088	7,160
PA Upstream Load	907,512			
TMDL[2]	**1,013,386**			

[1] MD portion of the subwatershed only.
[2] The MOS is incorporated.

Table 4.9.2: MD 8-Digit Conococheague Creek Maximum Daily Loads

Subwatershed	Total Allocation	LA	SW-WLA	WWTP-WLA
	(Billion MPN *E. coli* /day)			
CON0217[1]	47	44	3	0
CON0180sub[1]	57	53	4	0
RKD0006[1]	227	178	49	0
TMS0006[1]	498	427	70	0
RUS0005	214	163	50	0
CON0051sub[1]	1,537	1,347	189	0.04
MEA0009	202	157	45	0.15
UWR0000	118	93	25	0
CON0005sub	535	260	214	61
MD Total	3,433	2,722	650	61
PA Upstream Load	26,266			
TOTAL	**29,699**			

[1] MD portion of the subwatershed only.

The long-term annual average fecal bacteria TMDL summary for the MD 8-digit Conococheague Creek watershed is presented in Table 4.9.3. Note that the upstream PA load allocation (LA_{PA}) is determined to be necessary in order to meet MD water quality standards in the MD portion of the Conococheague Creek watershed. Although reported here as a single value, it may include both point and nonpoint sources.

Table 4.9.3: MD 8-Digit Conococheague Creek Watershed Annual Average TMDL Summary

(Billion MPN *E. coli*/year)										
TMDL	=	**LA**			+	**WLA**			+	**MOS**
		LA_{PA}	+	**LA_{CON}**		**SW WLA_{CON}**	+	**WWTP WLA_{CON}**		
1,013,386	=	907,512	+	81,626	+	17,088	+	7,160	+	Incorporated

Upstream Load Allocation

MD 8-digit Conococheague Creek TMDL Contribution (105,874)

The maximum daily loads of fecal bacteria for the MD 8-digit Conococheague Creek watershed, including the PA upstream load, are summarized in Table 4.9.4.

Table 4.9.4: MD 8-Digit Conococheague Creek Watershed MDL Summary

(Billion MPN *E. coli*/day)										
MDL	=	**LA**			+	**WLA**			+	**MOS**
		LA_{PA}	+	**LA_{CON}**		**SW WLA_{CON}**	+	**WWTP WLA_{CON}**		
29,699	=	26,266	+	2,722	+	650	+	61	+	Incorporated

Upstream MDL

MD 8-digit Conococheague Creek MDL Contribution (3,433)

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 subwatersheds of Conococheague Creek, 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 Conococheague Creek watershed, the TMDL analysis indicates that, for all nine subwatersheds, the reductions of fecal bacteria loads 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. Conococheague Creek and its tributaries may not be able to attain water quality standards. The fecal bacteria load reductions required to meet water quality criteria in the nine subwatersheds of Conococheague 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.

While a portion of the bacteria loads that contribute to the MD 8-digit Conococheague Creek impairment originate in the Pennsylvania portion of the watershed, implementation actions in this area of the watershed are beyond the jurisdictional and regulatory authority of the Maryland Department of the Environment. MDE looks forward to working with the Commonwealth of Pennsylvania and the EPA to ensure that the Upstream Load Allocations presented in this document are achieved to meet Maryland’s downstream water quality standards.

In summary, through the use of the aforementioned funding mechanisms and best management practices and assuming the cooperation of upstream jurisdictions, there is reasonable assurance that this TMDL can be implemented.

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. However, while neither Maryland nor EPA is proposing the elimination of wildlife to allow for the attainment of water quality standards, 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 non-point sources may also reduce some wildlife inputs to the waters.

6.0 PUBLIC PARTICIPATION

Stakeholders were informed by a July 11, 2007 MDE mailing of a notice of intent to develop a fecal bacteria TMDL for the non-tidal Conococheague Creek basin. The notice letters provided MDE contact information and offered upon request an informational briefing on the proposed TMDL. In response to a request by Washington County officials, a briefing and presentation on the TMDL was provided by MDE on March 20, 2008, at the Washington County Departments of Planning and Engineering.

A public notice of intent to establish the Conococheague Creek fecal bacteria TMDL, announcing the opening and closing dates of the formal 30-day Public Comment Period, was published in the Washington County Herald-Mail. The notice was also sent to MDE's stakeholder distribution list for the Conococheague Creek watershed and all other interested parties. All were invited to send written comments on the draft TMDL to MDE. The public notice announced the availability of the draft TMDL document, copies of which were placed in the Williamsport Branch of the Washington County Free Library. The public notice also provided information on how to access the draft TMDL documents on MDE's website.

All written comments received by the close of the comment period are recorded and formally responded to in a Comment Response Document (CRD), to be included in the draft final TMDL documentation package submitted to EPA for the Agency's approval. Receipt of each set of comments is acknowledged by MDE, either by letter or email to comment authors. Following EPA approval of the TMDL, the responses are made available when the CRD is posted on MDE's website, together with the final approved TMDL documentation. The CRD is also mailed to stakeholders, including all those who sent comments to MDE, along with an approval notification letter.

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Appendix A – Bacteria Data

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

Station	Date	Daily flow frequency	*E. coli* Concentration (MPN/100ml)
CON0005	11/03/2003	23.3027	98
	11/17/2003	30.2124	158
	12/01/2003	16.6557	313
	12/15/2003	4.8073	364
	01/05/2004	9.2203	369
	01/20/2004	38.2173	160
	02/02/2004	51.4017	31
	02/17/2004	33.5414	31
	03/01/2004	10.3154	41
	03/15/2004	21.4520	63
	04/05/2004	9.3298	278
	04/19/2004	12.6040	199
	05/10/2004	24.9562	199
	05/24/2004	25.5366	472
	06/07/2004	16.2834	6867
	06/21/2004	40.5169	240
	07/06/2004	62.8887	97
	07/19/2004	56.9207	269
	08/09/2004	51.6316	201
	08/23/2004	26.7630	1785
	09/07/2004	70.4117	216
	09/20/2004	3.3728	3873
	10/04/2004	15.0350	488
	10/18/2004	39.4547	189

Station	Date	Daily flow frequency	*E. coli* Concentration (MPN/100ml)
CON0051	11/03/2003	23.3027	216
	11/17/2003	30.2124	98
	12/01/2003	16.6557	439
	01/05/2004	9.2203	495
	01/20/2004	38.2173	63
	02/02/2004	51.4017	10
	02/17/2004	33.5414	52
	03/01/2004	10.3154	10
	03/15/2004	21.4520	31
	04/05/2004	9.3298	364
	04/19/2004	12.6040	265
	05/10/2004	24.9562	318
	05/24/2004	25.5366	108
	06/07/2004	16.2834	4106
	06/21/2004	40.5169	187
	07/06/2004	62.8887	132
	07/19/2004	56.9207	223
	08/09/2004	51.6316	146
	08/23/2004	26.7630	1376
	09/07/2004	70.4117	146
	09/20/2004	3.3728	3654
	10/04/2004	15.0350	345
	10/18/2004	39.4547	173

Station	**Date**	**Daily flow frequency**	***E. coli*** **Concentration (MPN/100ml)**
CON0180	11/03/2003	23.3027	233
	11/17/2003	30.2124	110
	12/01/2003	16.6557	262
	12/15/2003	4.8073	309
	01/05/2004	9.2203	1722
	01/20/2004	38.2173	120
	02/02/2004	51.4017	161
	02/17/2004	33.5414	41
	03/01/2004	10.3154	121
	03/15/2004	21.4520	63
	04/05/2004	9.3298	275
	04/19/2004	12.6040	171
	05/10/2004	24.9562	292
	05/24/2004	25.5366	504
	06/07/2004	16.2834	3448
	06/21/2004	40.5169	285
	07/06/2004	62.8887	121
	07/19/2004	56.9207	460
	08/09/2004	51.6316	148
	08/23/2004	26.7630	2224
	09/07/2004	70.4117	145
	09/20/2004	3.3728	4884
	10/04/2004	15.0350	408
	10/18/2004	39.4547	426

Station	**Date**	**Daily flow frequency**	***E. coli* Concentration (MPN/100ml)**
CON0217	11/17/2003	30.2124	98
	12/01/2003	16.6557	299
	01/05/2004	9.2203	1430
	01/20/2004	38.2173	63
	02/02/2004	51.4017	119
	02/17/2004	33.5414	63
	03/01/2004	10.3154	109
	03/15/2004	21.4520	31
	04/05/2004	9.3298	350
	04/19/2004	12.6040	173
	05/10/2004	24.9562	364
	05/24/2004	25.5366	496
	06/07/2004	16.2834	2035
	06/21/2004	40.5169	309
	07/06/2004	62.8887	160
	07/19/2004	56.9207	309
	08/09/2004	51.6316	185
	08/23/2004	26.7630	1467
	09/07/2004	70.4117	132
	09/20/2004	3.3728	3448
	10/04/2004	15.0350	556
	10/18/2004	39.4547	479

Station	Date	Daily flow frequency	*E. coli* Concentration (MPN/100ml)
MEA0009	11/03/2003	23.3027	309
	11/17/2003	30.2124	160
	12/01/2003	16.6557	292
	12/15/2003	4.8073	314
	01/05/2004	9.2203	4884
	01/20/2004	38.2173	41
	02/02/2004	51.4017	146
	02/17/2004	33.5414	51
	03/01/2004	10.3154	323
	03/15/2004	21.4520	282
	04/05/2004	9.3298	298
	04/19/2004	12.6040	187
	05/10/2004	24.9562	1076
	05/24/2004	25.5366	1112
	06/07/2004	16.2834	3255
	06/21/2004	40.5169	1483
	07/06/2004	62.8887	5475
	07/19/2004	56.9207	2851
	08/09/2004	51.6316	1145
	08/23/2004	26.7630	2613
	09/07/2004	70.4117	4884
	09/20/2004	3.3728	1723
	10/04/2004	15.0350	1779
	10/18/2004	39.4547	591

Station	Date	Daily flow frequency	*E. coli* Concentration (MPN/100ml)
RKD0006	11/03/2003	23.3027	697
	11/17/2003	30.2124	933
	12/01/2003	16.6557	571
	12/15/2003	4.8073	933
	01/05/2004	9.2203	906
	01/20/2004	38.2173	275
	02/02/2004	51.4017	857
	02/17/2004	33.5414	52
	03/01/2004	10.3154	74
	03/15/2004	21.4520	52
	04/05/2004	9.3298	331
	04/19/2004	12.6040	583
	05/10/2004	24.9562	3282
	05/24/2004	25.5366	2098
	06/07/2004	16.2834	3076
	06/21/2004	40.5169	1565
	07/19/2004	56.9207	1130
	08/09/2004	51.6316	2489
	08/23/2004	26.7630	1669
	09/07/2004	70.4117	1951
	09/20/2004	3.3728	6867
	10/04/2004	15.0350	2602
	10/18/2004	39.4547	4352

Station	**Date**	**Daily flow frequency**	***E. coli* Concentration (MPN/100ml)**
RUS0005	11/03/2003	23.3027	556
	11/17/2003	30.2124	450
	12/01/2003	16.6557	487
	12/15/2003	4.8073	504
	01/05/2004	9.2203	2098
	01/20/2004	38.2173	216
	02/02/2004	51.4017	341
	02/17/2004	33.5414	173
	03/01/2004	10.3154	199
	03/15/2004	21.4520	218
	04/05/2004	9.3298	594
	04/19/2004	12.6040	1017
	05/10/2004	24.9562	1935
	05/24/2004	25.5366	1935
	06/07/2004	16.2834	3448
	06/21/2004	40.5169	2035
	07/06/2004	62.8887	1989
	07/19/2004	56.9207	1935
	08/09/2004	51.6316	3255
	08/23/2004	26.7630	1137
	09/07/2004	70.4117	1112
	09/20/2004	3.3728	7701
	10/04/2004	15.0350	3873
	10/18/2004	39.4547	884

Station	Date	Daily flow frequency	*E. coli* Concentration (MPN/100ml)
TMS0006	11/03/2003	23.3027	41
	11/17/2003	30.2124	148
	12/01/2003	16.6557	262
	12/15/2003	4.8073	240
	01/05/2004	9.2203	74
	01/20/2004	38.2173	10
	02/02/2004	51.4017	20
	02/17/2004	33.5414	10
	03/01/2004	10.3154	10
	03/15/2004	21.4520	31
	04/05/2004	9.3298	110
	04/19/2004	12.6040	63
	05/10/2004	24.9562	1017
	05/24/2004	25.5366	185
	06/07/2004	16.2834	3076
	06/21/2004	40.5169	332
	07/06/2004	62.8887	331
	07/19/2004	56.9207	109
	08/09/2004	51.6316	86
	08/23/2004	26.7630	327
	09/07/2004	70.4117	813
	09/20/2004	3.3728	24192
	10/04/2004	15.0350	744
	10/18/2004	39.4547	529

Station	**Date**	**Daily flow frequency**	***E. coli* Concentration (MPN/100ml)**
UWR0000	11/03/2003	23.3027	1309
	11/17/2003	30.2124	794
	12/01/2003	16.6557	620
	12/15/2003	4.8073	459
	01/05/2004	9.2203	906
	01/20/2004	38.2173	301
	02/02/2004	51.4017	203
	02/17/2004	33.5414	110
	03/01/2004	10.3154	132
	03/15/2004	21.4520	624
	04/05/2004	9.3298	591
	04/19/2004	12.6040	189
	05/10/2004	24.9562	530
	05/24/2004	25.5366	1291
	06/07/2004	16.2834	1989
	06/21/2004	40.5169	839
	07/06/2004	62.8887	1198
	07/19/2004	56.9207	1250
	08/09/2004	51.6316	1789
	08/23/2004	26.7630	495
	09/07/2004	70.4117	754
	09/20/2004	3.3728	1722
	10/04/2004	15.0350	1317
	10/18/2004	39.4547	364

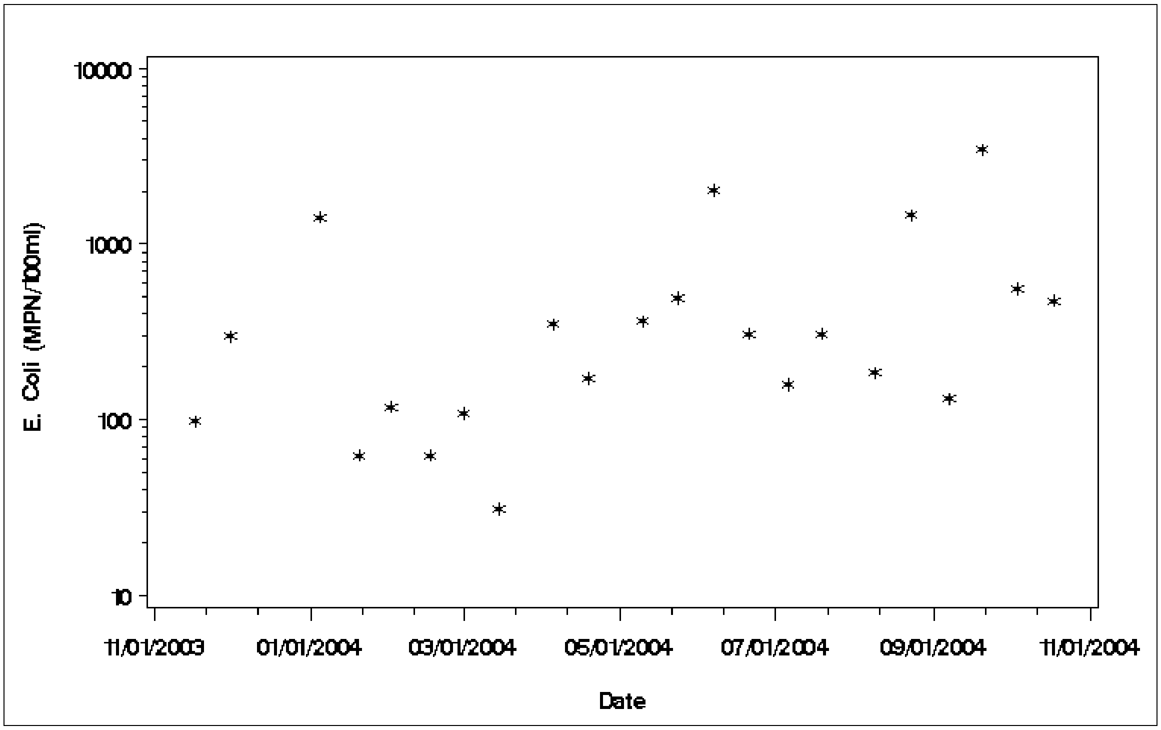

Figure A-1: *E. coli* Concentration vs. Time for MDE Monitoring Station CON0217

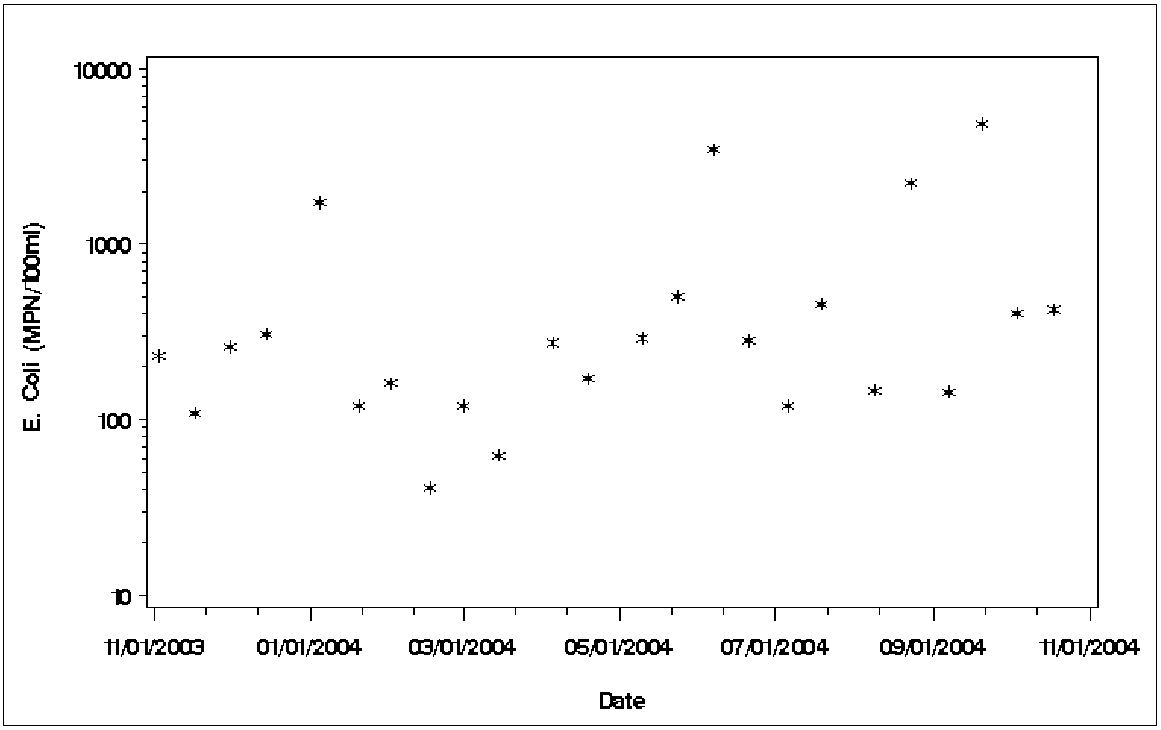

Figure A-2: *E. coli* Concentration vs. Time for MDE Monitoring Station CON0180

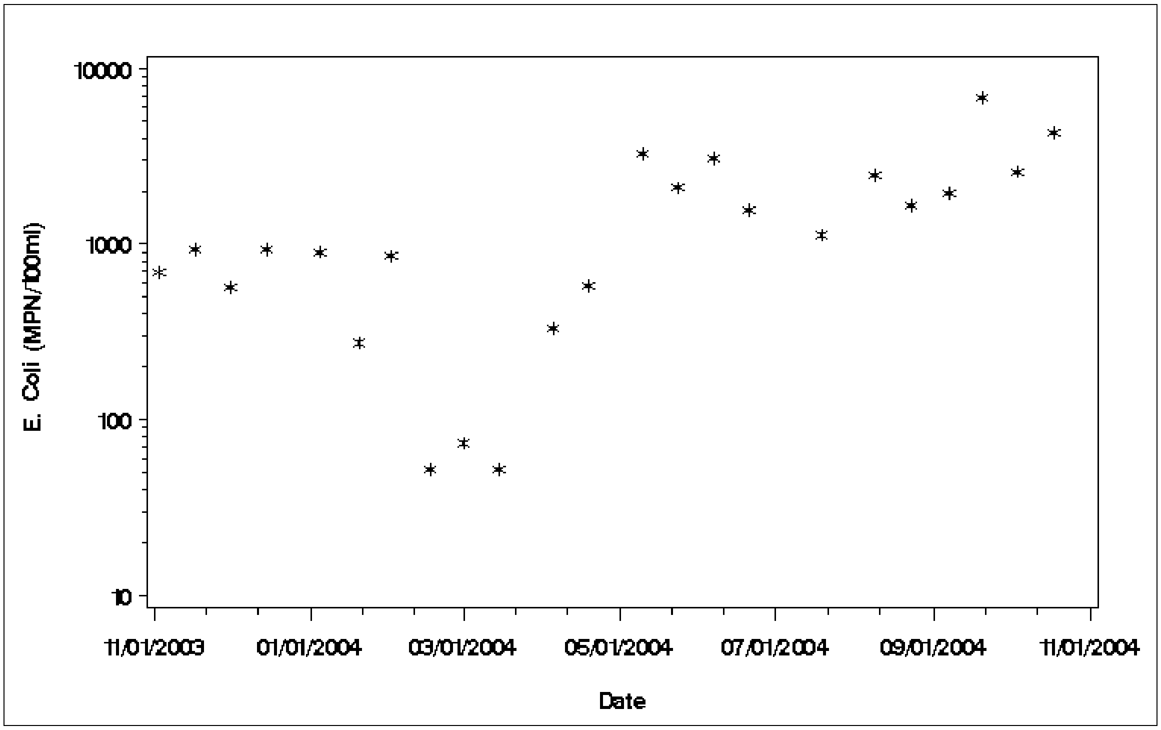

Figure A-3: *E. coli* Concentration vs. Time for MDE Monitoring Station RKD0006

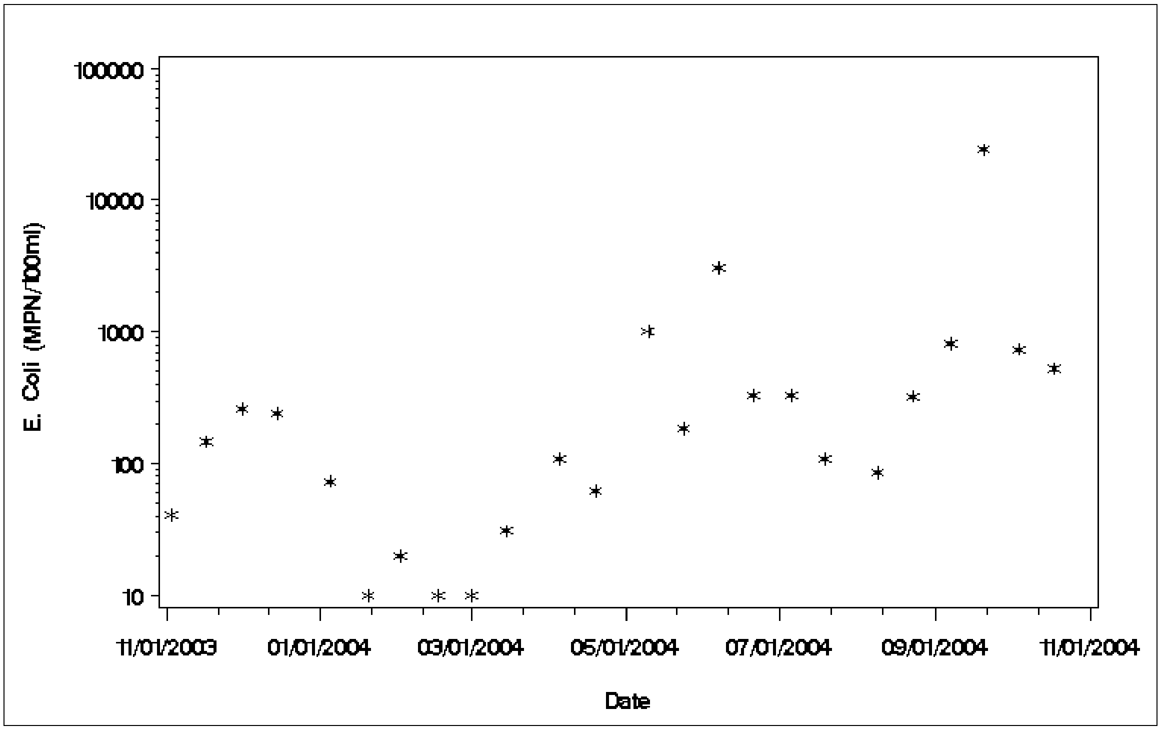

Figure A-4: *E. coli* Concentration vs. Time for MDE Monitoring Station TMS0006

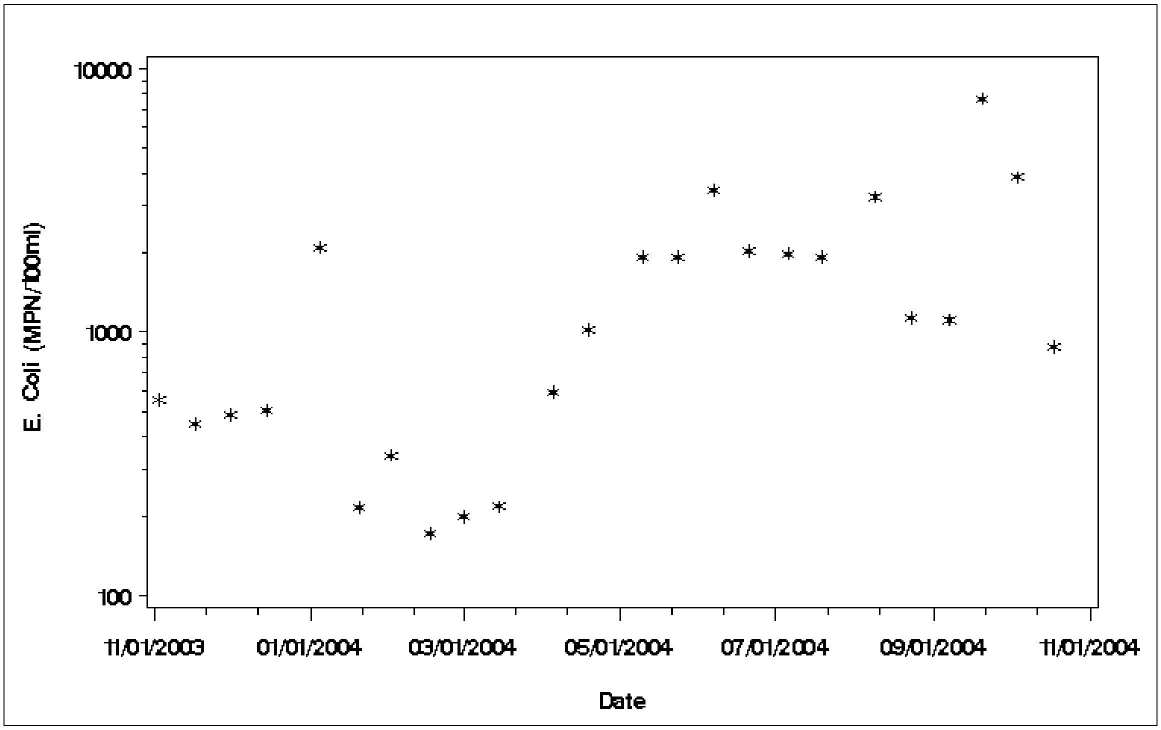

Figure A-5: ***E. coli*** **Concentration vs. Time for MDE Monitoring Station RUS0005**

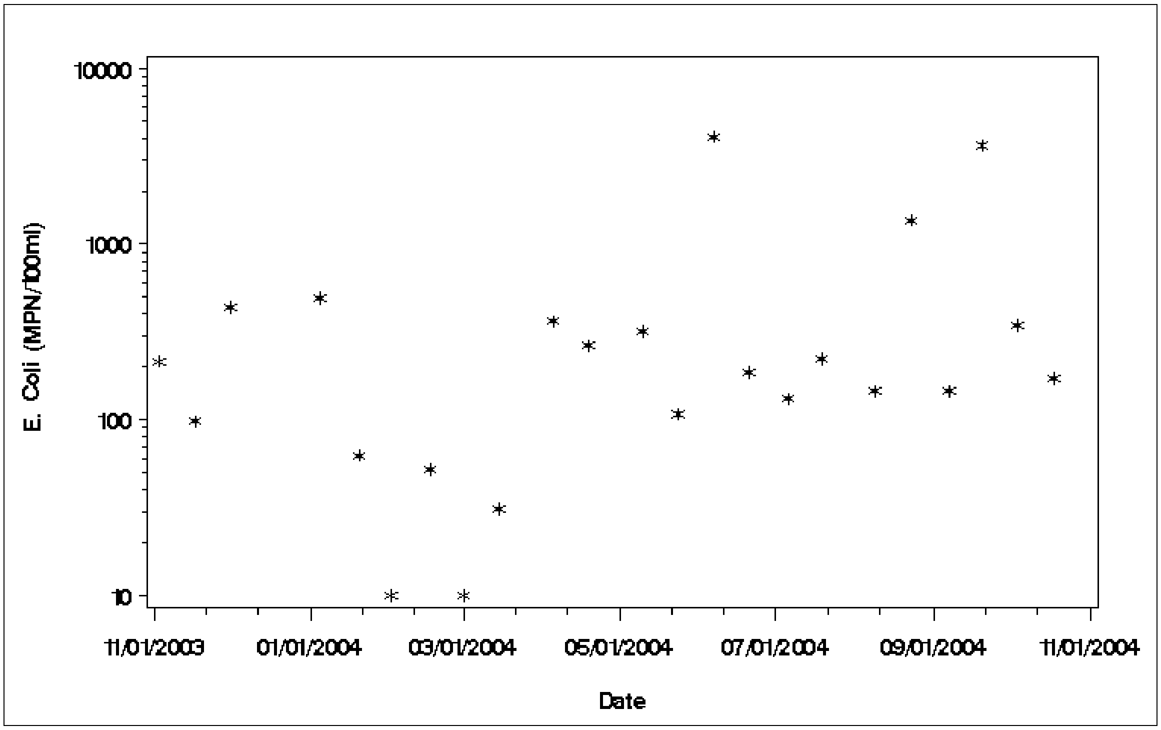

Figure A-6: ***E. coli*** **Concentration vs. Time for MDE Monitoring Station CON0051**

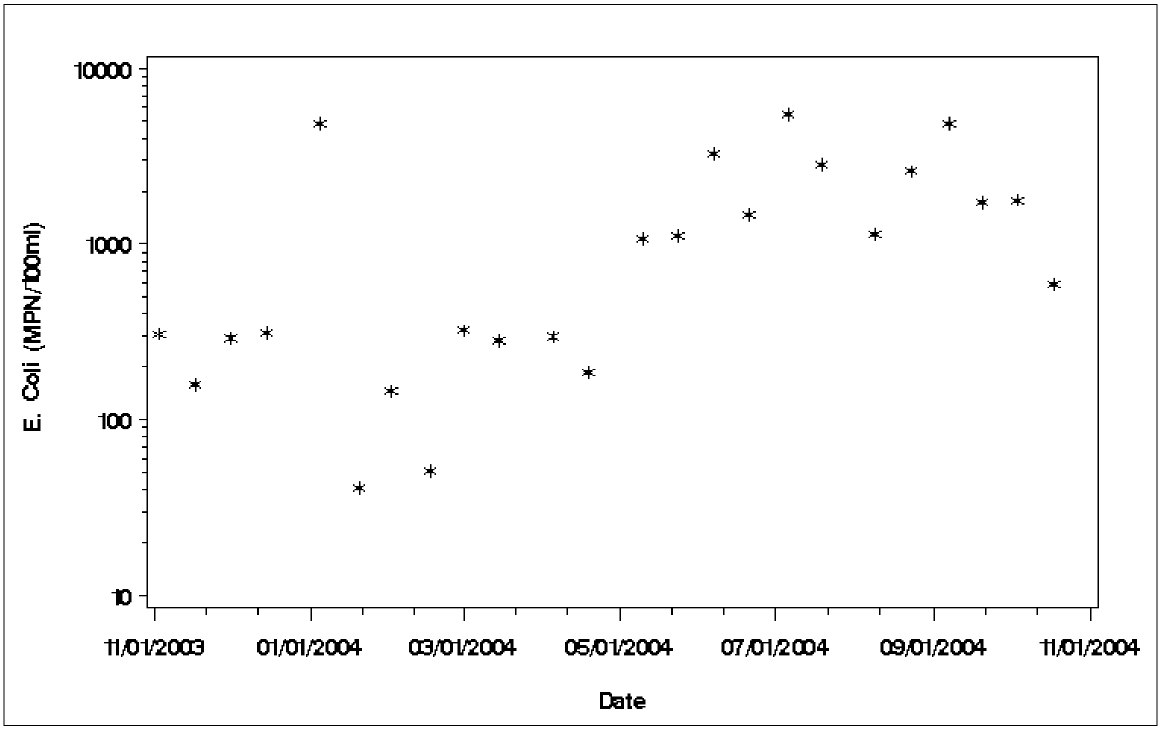

Figure A-7: *E. coli* Concentration vs. Time for MDE Monitoring Station MEA0009

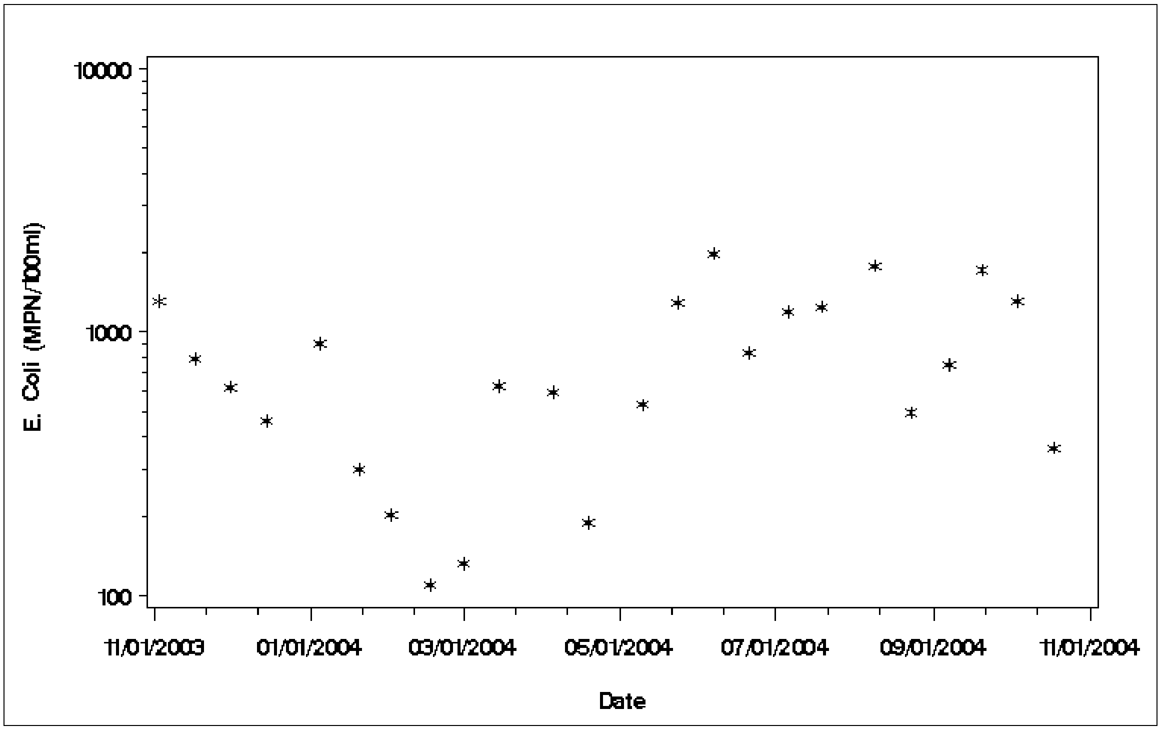

Figure A-8: *E. coli* Concentration vs. Time for MDE Monitoring Station UWR0000

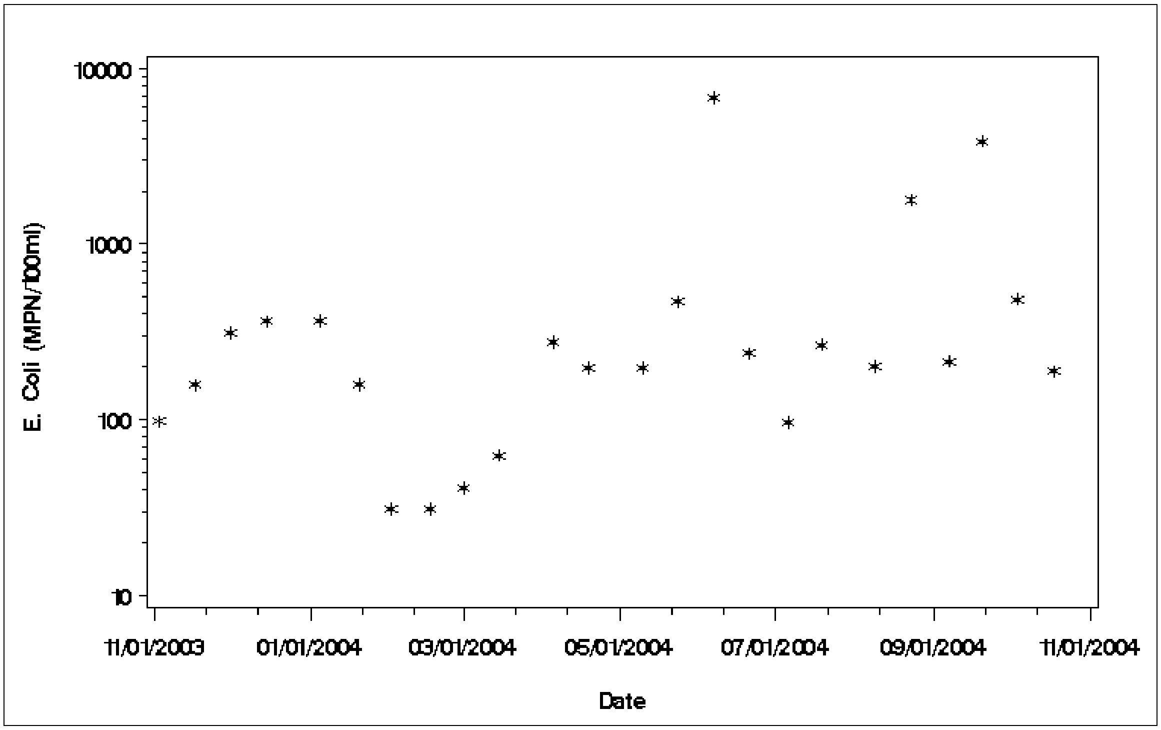

Figure A-9: *E. coli* Concentration vs. Time for MDE Monitoring Station CON0005

Appendix B - Flow Duration Curve Analysis to Define Strata

The Conococheague 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 antecedent soil moisture 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 one active USGS gage station in the Conococheague Creek watershed, station #01614500 Conococheague Creek at Fairview, MD, was used for the analysis. The dates of information used were from October 1, 1982 to September 30, 2007. A flow duration curve for this gage station is presented in Figure B-1.

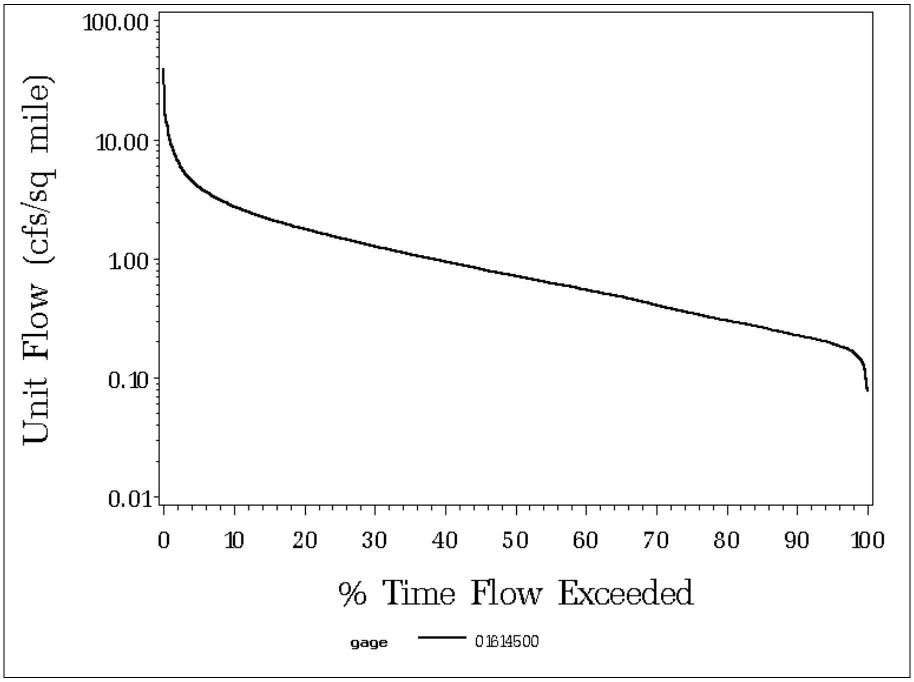

Figure B-1: Flow Duration Curve for USGS Gage 01614500

Based on the flow data from the Conococheague Creek gage station the long-term average daily unit flow is 1.28 cfs/sq. mile, which corresponds to a flow frequency of 29.7%. 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 29.7 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 29.7% and a low flow condition will be defined as occurring when the daily flow duration percentile is greater than 29.7%. Definitions of high and low range flows are presented in Table B-1.

Table B-1: 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-19 show the Conococheague Creek watershed *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 the Conococheague Creek watershed there are sufficient samples in both the high flow and low flow strata to calculate the geometric means for both the annual average and seasonal (May 1st – September 30th) flow conditions.

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-2. 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-19.

Table B-2: Weighting Factors for Estimation of Geometric Mean

Hydrological Condition		Averaging Period	Water Quality Data Used	Fraction High Flow	Fraction Low Flow	Condition Period
Annual	Average	365 days	All	0.297	0.703	Long-Term Average
	Wet (High Flow)	365 days	All	0.739	0.261	Jan. 1996 – Jan. 1997
	Dry (Low Flow)	365 days	All	0.038	0.962	June 2001 – June 2002
Seasonal	Wet (High Flow)	May 1st – Sept. 30th	May 1st – Sept. 30th	0.612	0.388	May – Sept. 1996
	Dry (Low Flow)	May 1st – Sept. 30th	May 1st – Sept. 30th	0	1.000	May – Sept. 2007

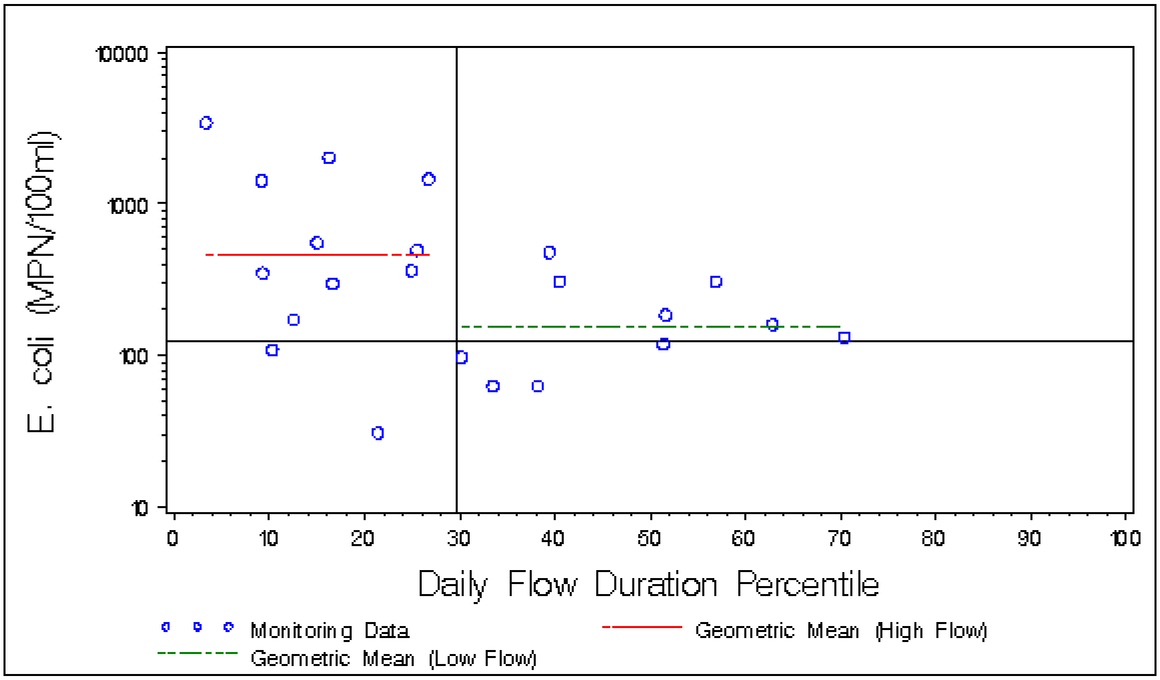

Figure B-2: ***E. coli*** **Concentration vs. Flow Duration for Monitoring Station CON0217 (Annual Condition)**

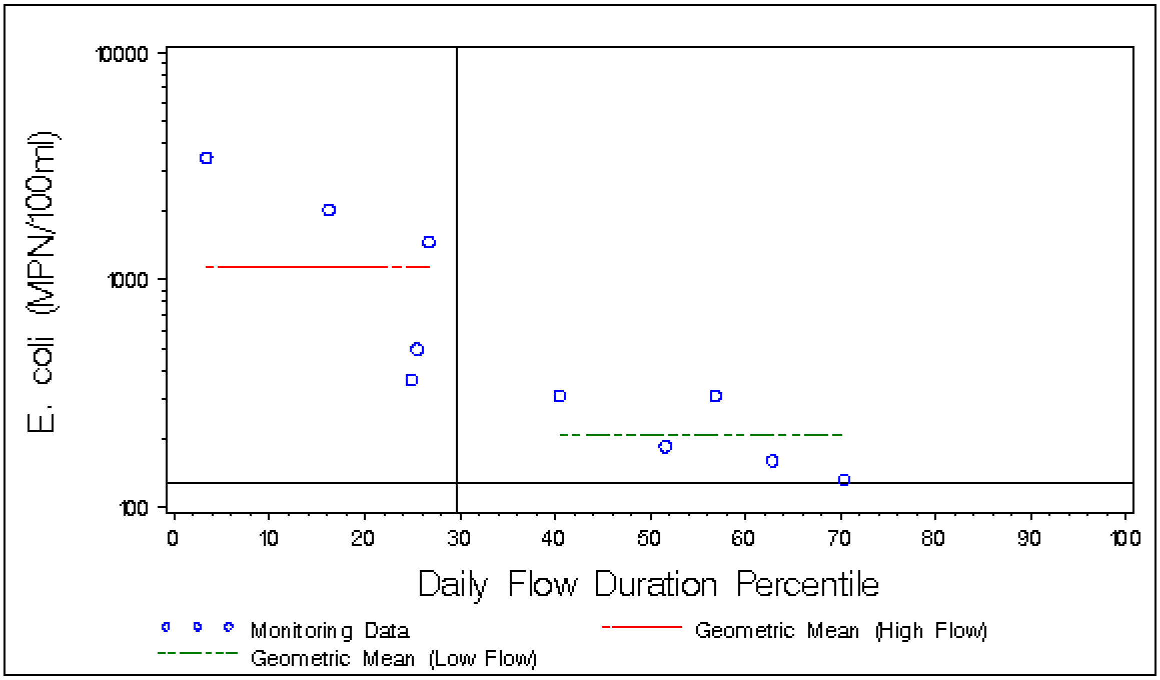

Figure B-3: ***E. coli*** **Concentration vs. Flow Duration for Monitoring Station CON0217 (Seasonal Condition)**

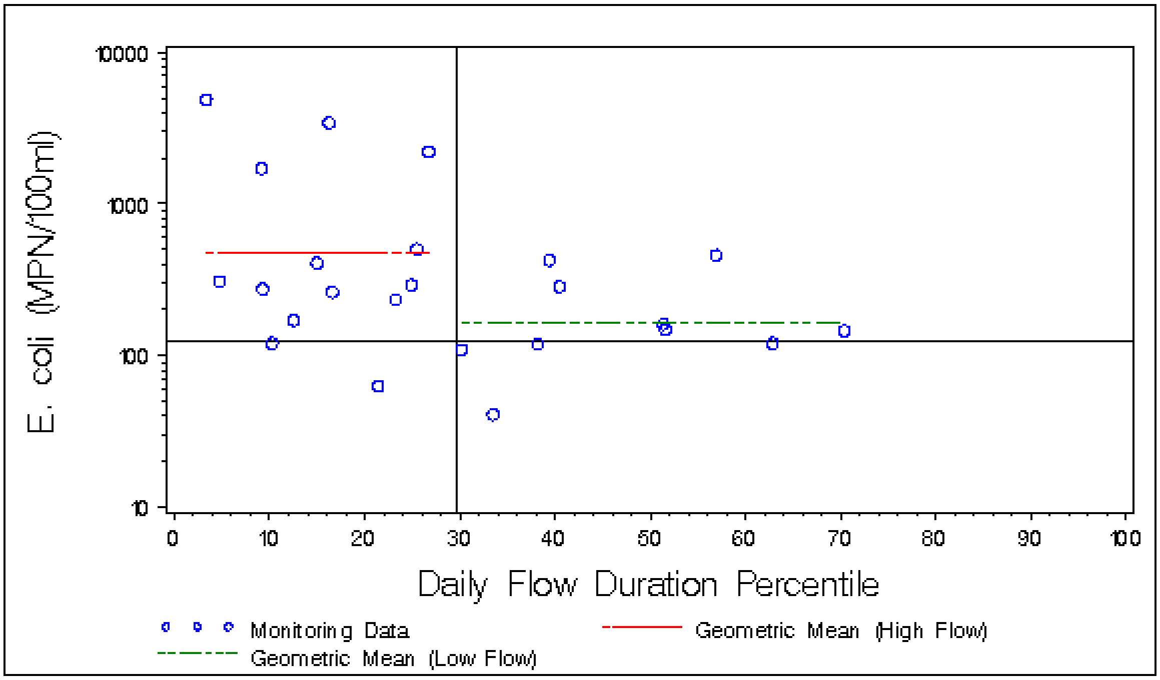

Figure B-4: ***E. coli*** **Concentration vs. Flow Duration for Monitoring Station CON0180 (Annual Condition)**

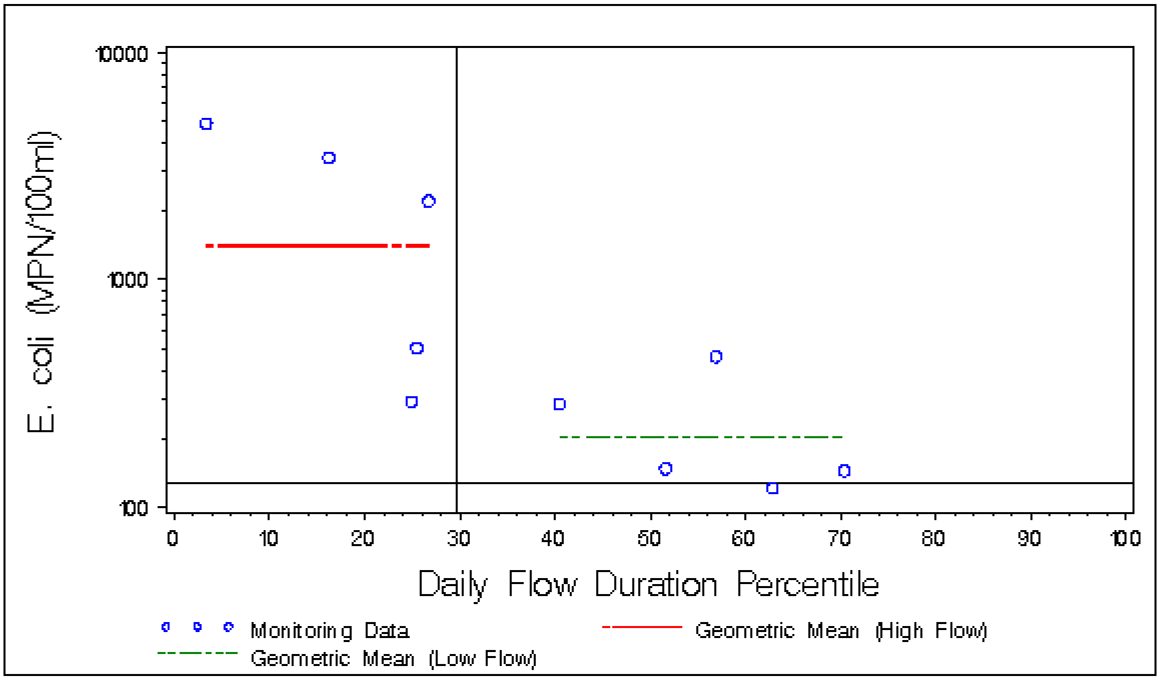

Figure B-5: ***E. coli*** **Concentration vs. Flow Duration for Monitoring Station CON0180 (Seasonal Condition)**

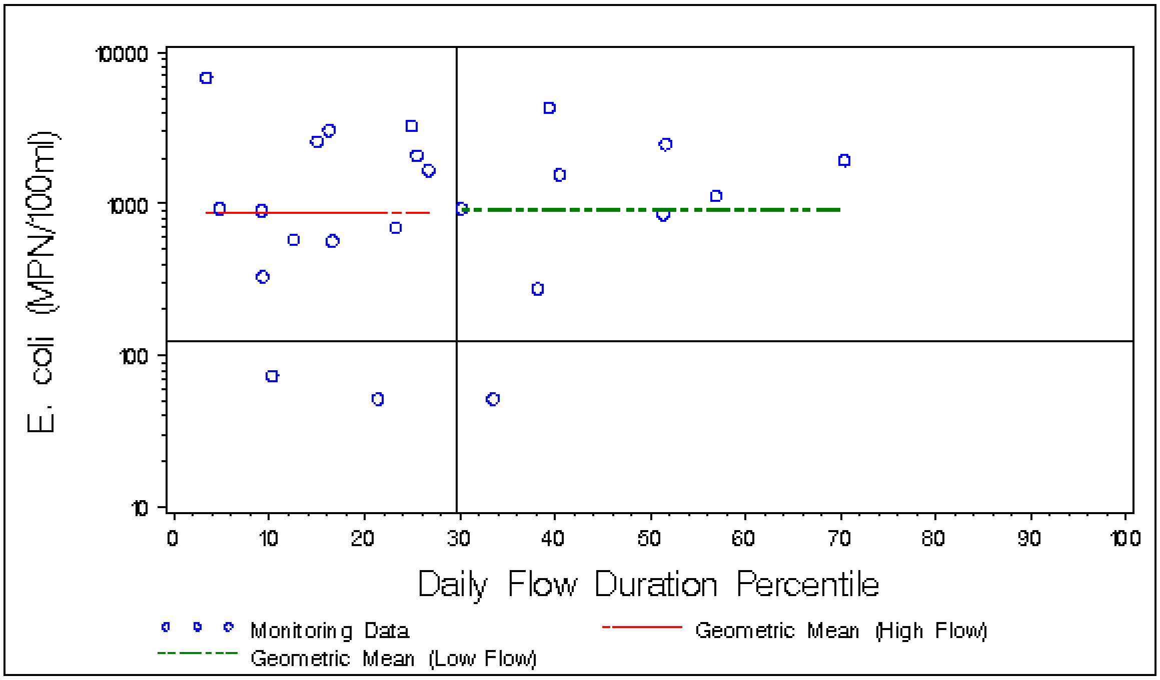

Figure B-6: *E. coli* Concentration vs. Flow Duration for Monitoring Station RKD0006 (Annual Condition)

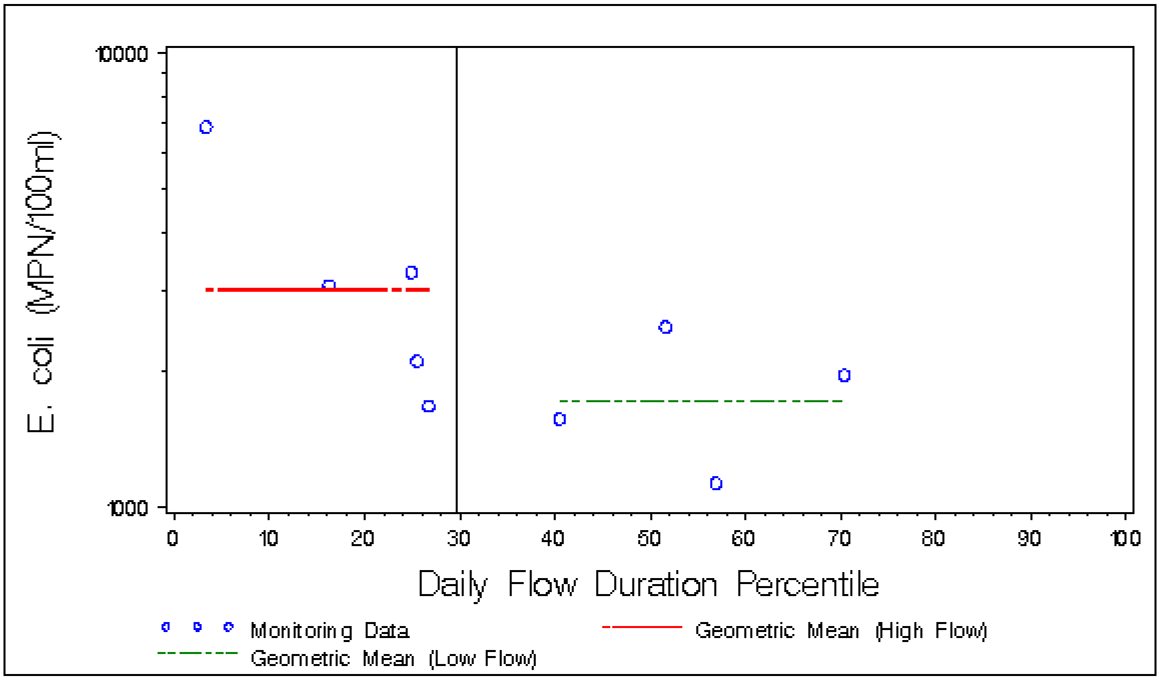

Figure B-7: *E. coli* Concentration vs. Flow Duration for Monitoring Station RKD0006 (Seasonal Condition)

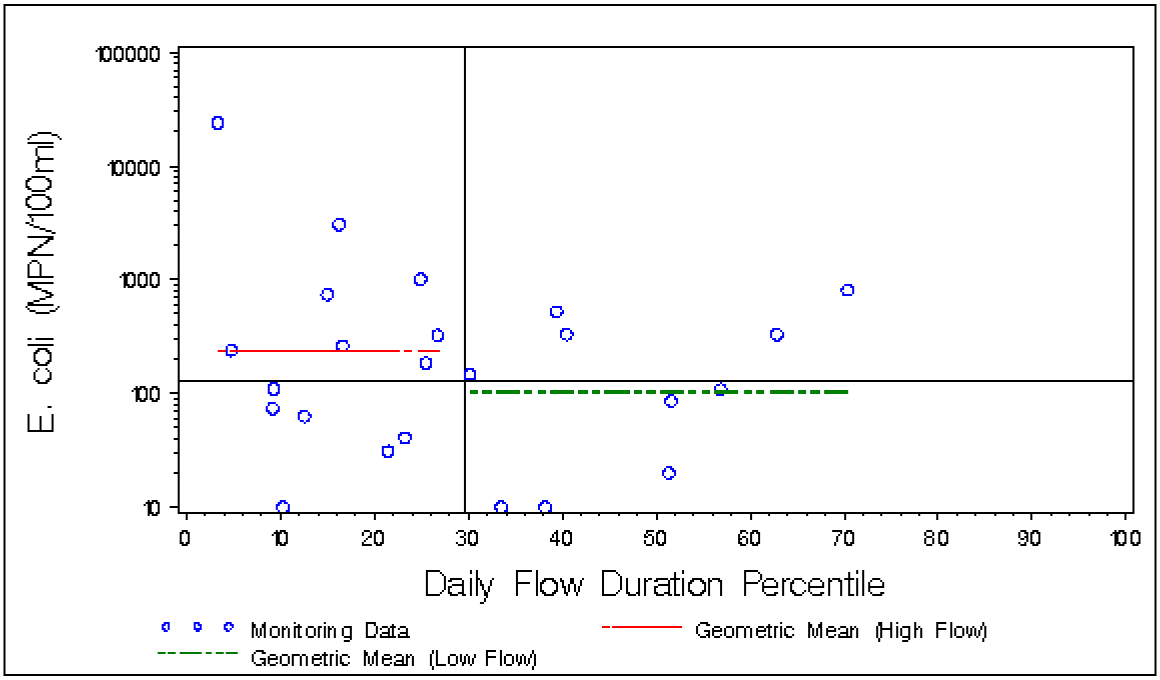

Figure B-8: *E. coli* Concentration vs. Flow Duration for Monitoring Station TMS0006 (Annual Condition)

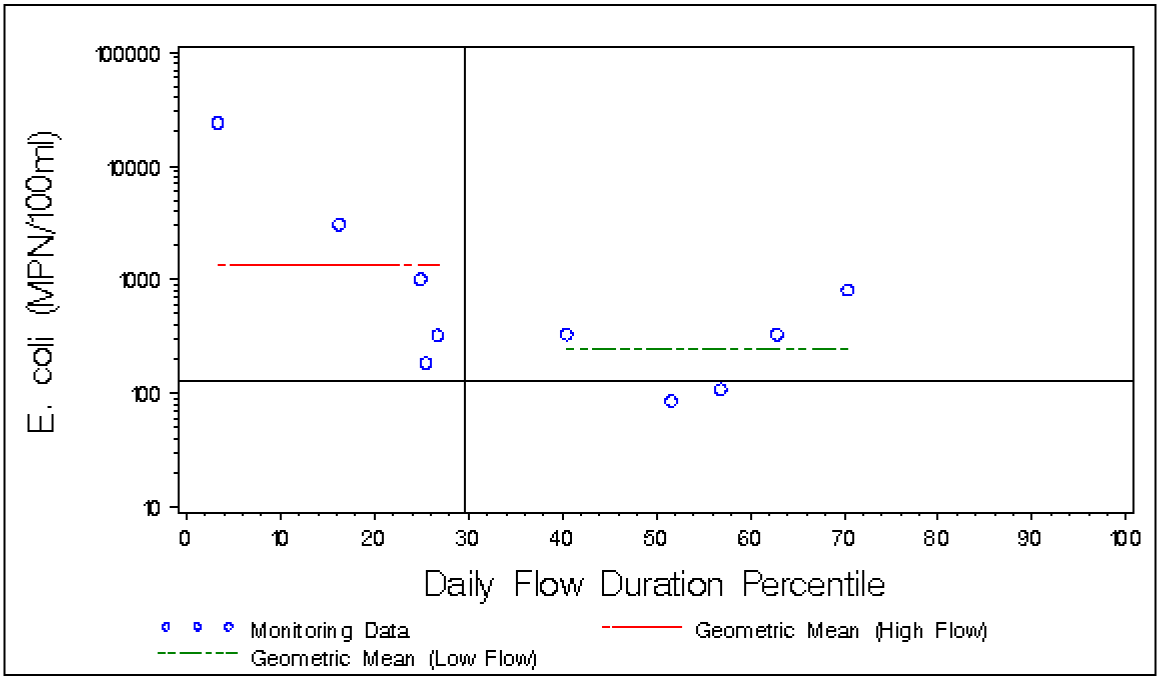

Figure B-9: *E. coli* Concentration vs. Flow Duration for Monitoring Station TMS0006 (Seasonal Condition)

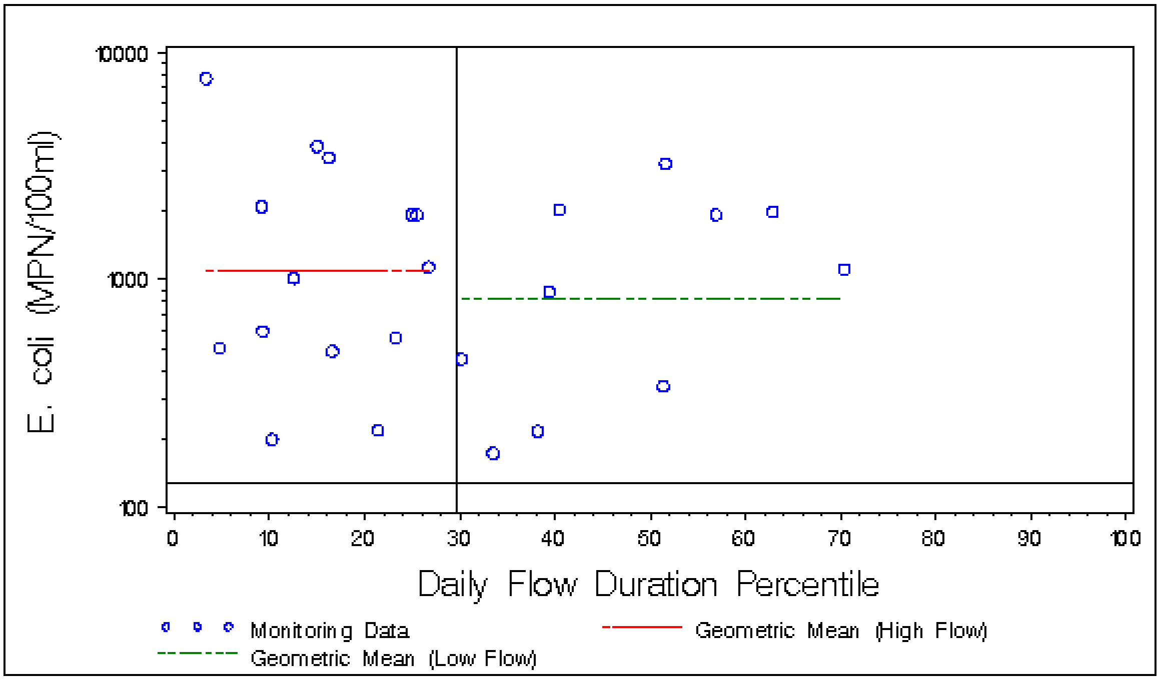

Figure B-10: *E. coli* Concentration vs. Flow Duration for Monitoring Station RUS0005 (Annual Condition)

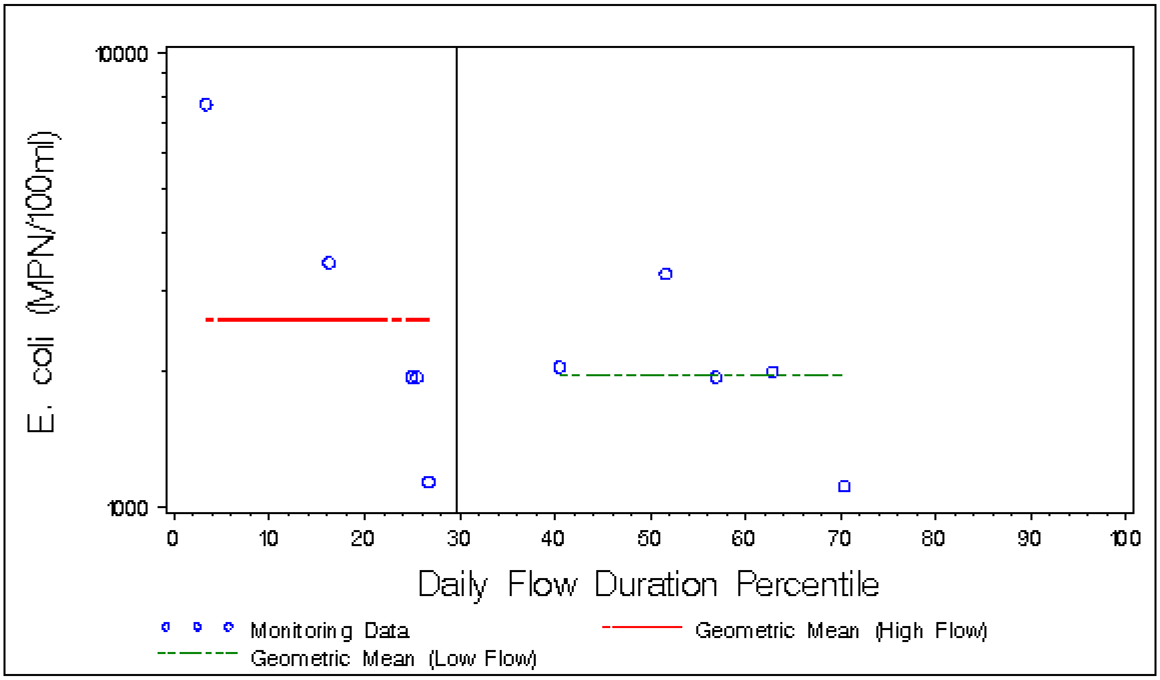

Figure B-11: *E. coli* Concentration vs. Flow Duration for Monitoring Station RUS0005 (Seasonal Condition)

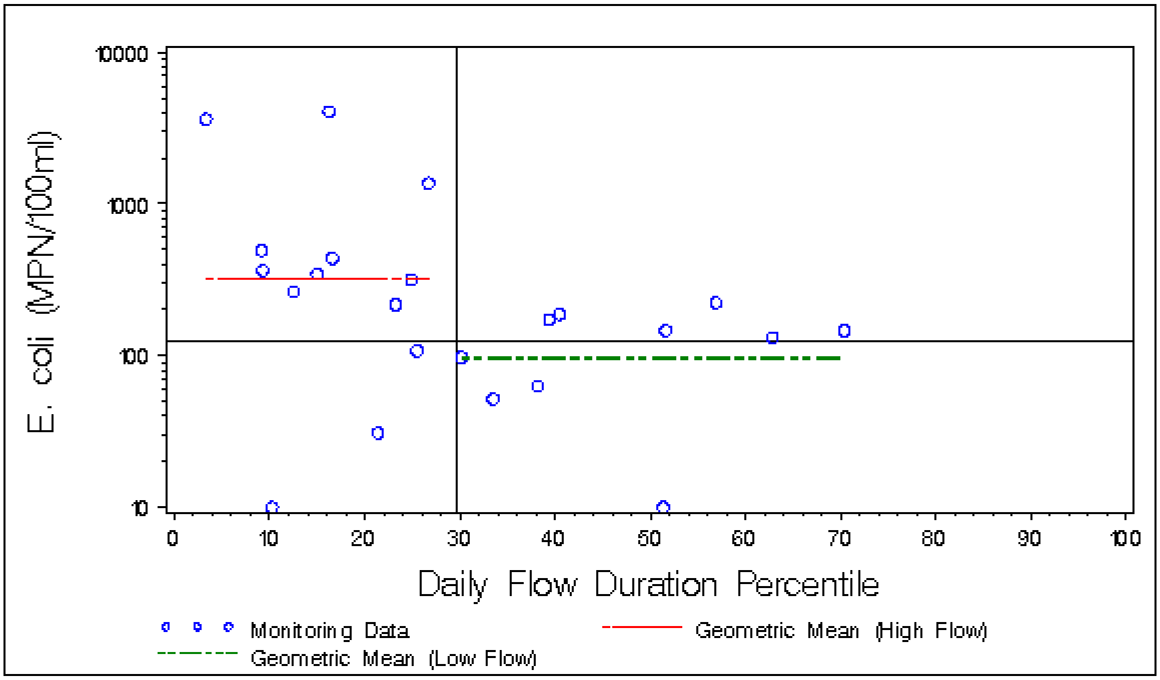

Figure B-12: *E. coli* Concentration vs. Flow Duration for Monitoring Station CON0051 (Annual Condition)

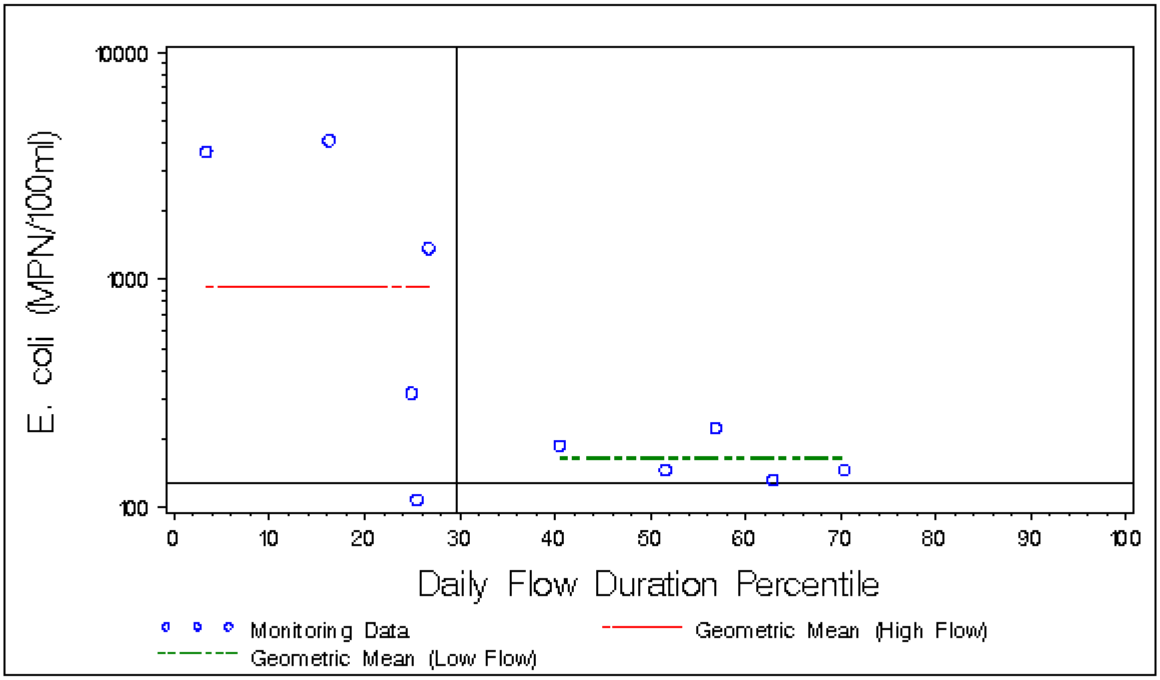

Figure B-13: *E. coli* Concentration vs. Flow Duration for Monitoring Station CON0051 (Seasonal Condition)

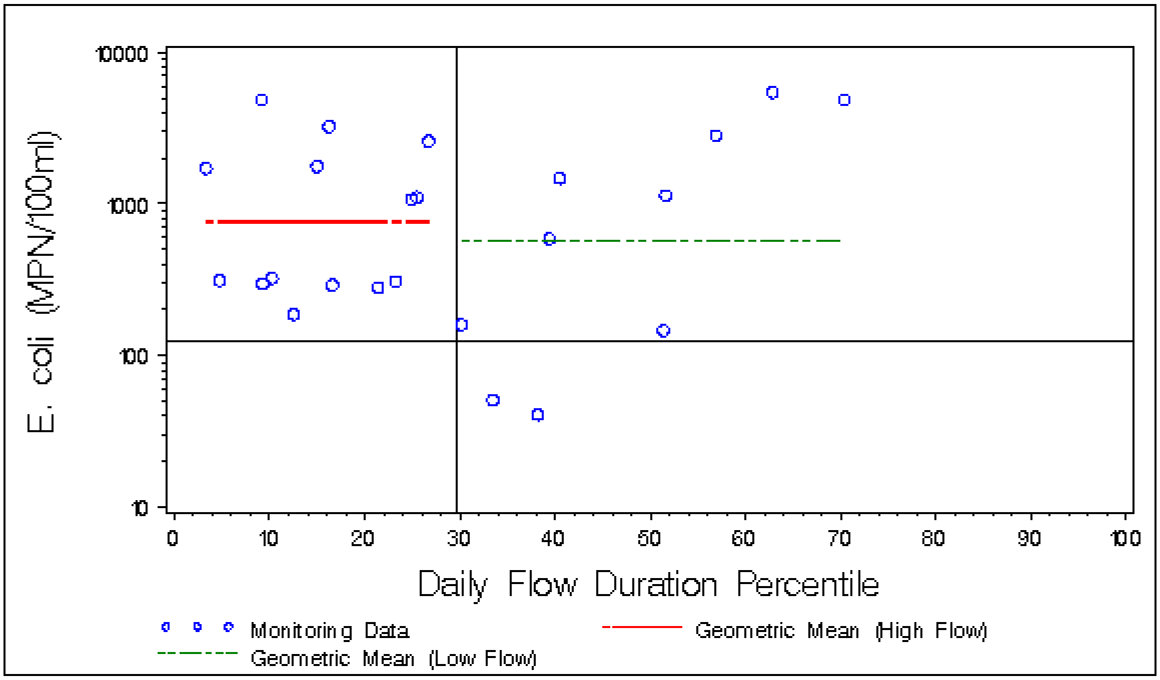

Figure B-14: *E. coli* Concentration vs. Flow Duration for Monitoring Station MEA0009 (Annual Condition)

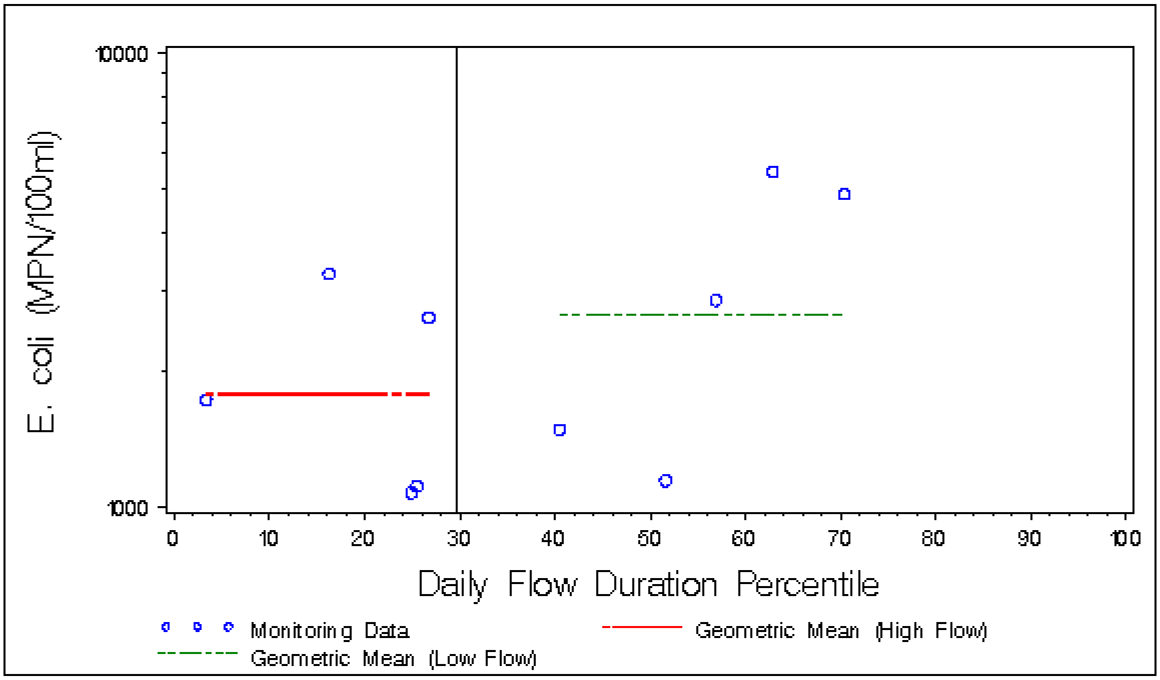

Figure B-15: *E. coli* Concentration vs. Flow Duration for Monitoring Station MEA0009 (Seasonal Condition)

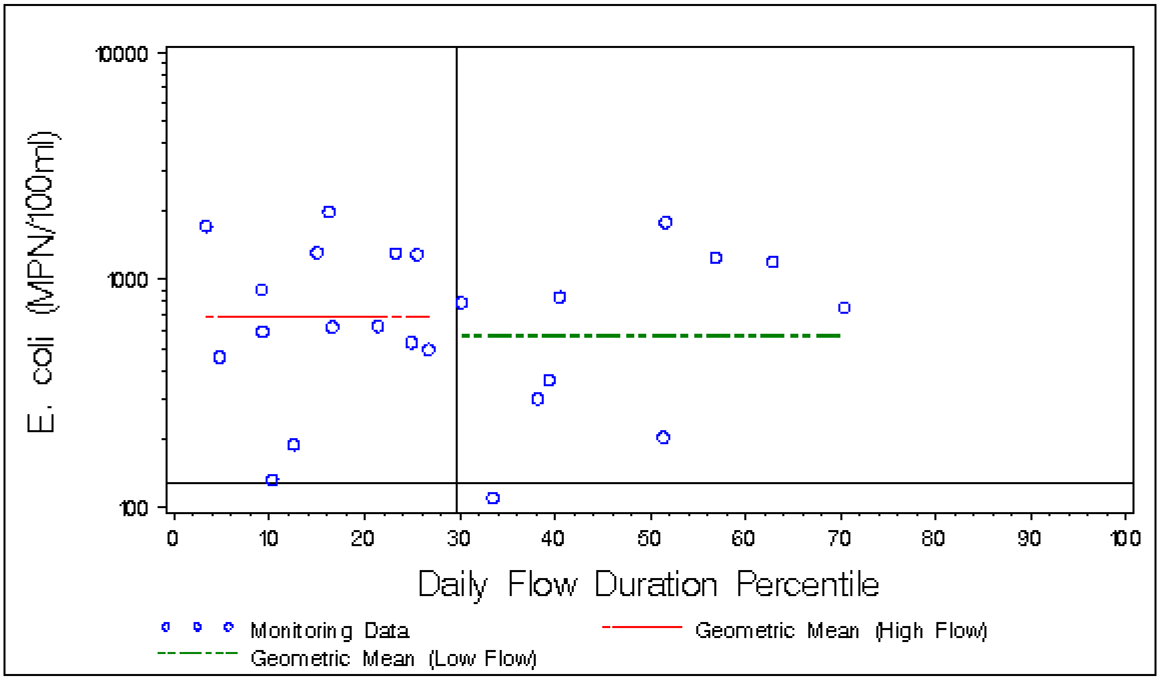

Figure B-16: *E. coli* Concentration vs. Flow Duration for Monitoring Station UWR0000 (Annual Condition)

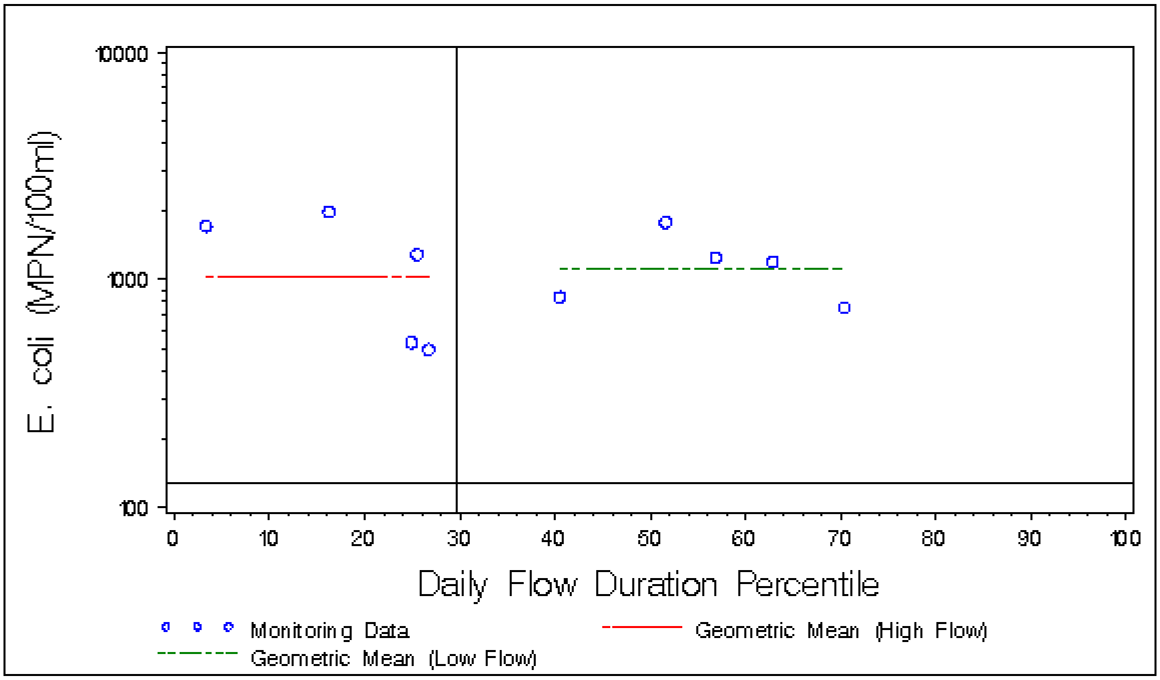

Figure B-17: *E. coli* Concentration vs. Flow Duration for Monitoring Station UWR0000 (Seasonal Condition)

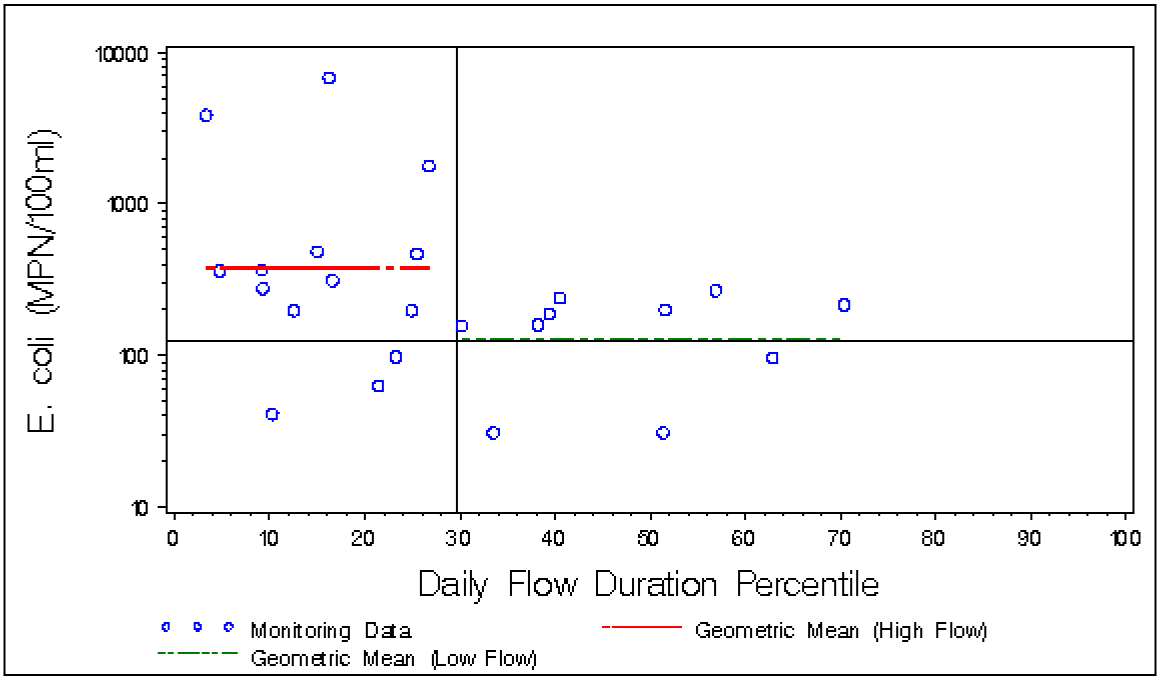

Figure B-18: *E. coli* Concentration vs. Flow Duration for Monitoring Station CON0005 (Annual Condition)

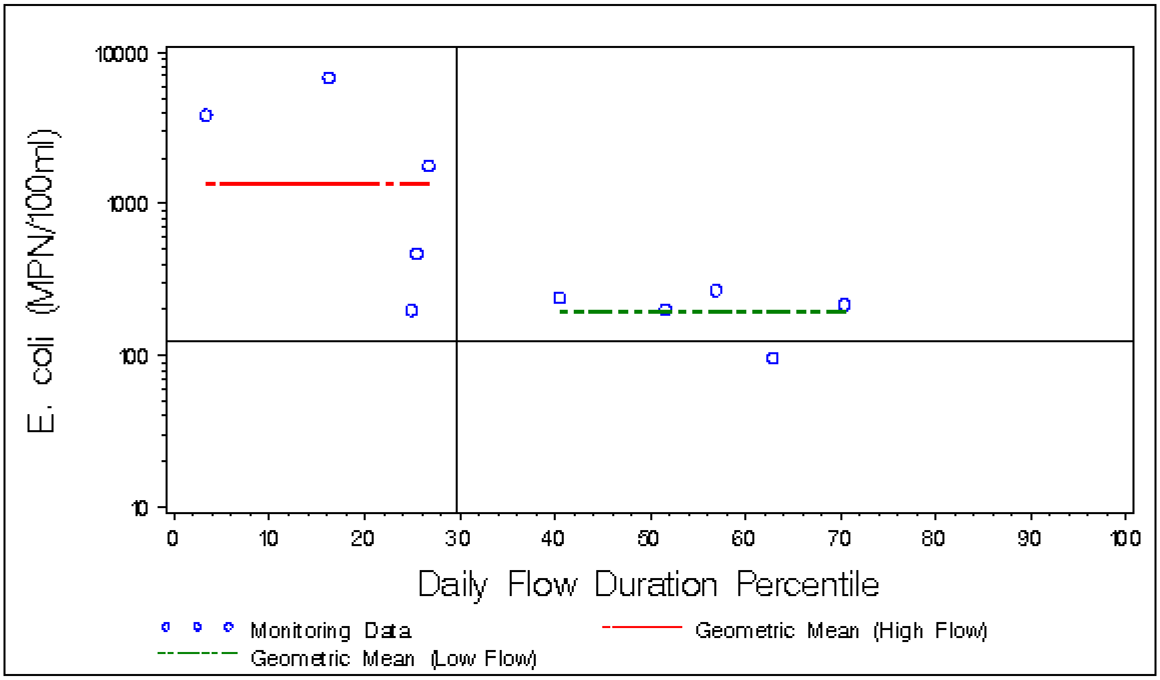

Figure B-19: *E. coli* Concentration vs. Flow Duration for Monitoring Station CON0005 (Seasonal Condition)

Appendix C – BST Report

Maryland Department of the Environment

Identifying Sources of Fecal Pollution in Shellfish and Nontidal Waters in Maryland Watersheds

June 2004 – October 2006

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Department of Biological Sciences and Environmental Health Science
Salisbury University, Salisbury, MD

Final Report
October 31, 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, Conococheague 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.

Conococheague Creek Watershed ARA Results

Known-Source Library. A 1,120 known-source isolate library was constructed that included 567 isolates from sources in the Antietam Creek Watershed combined with the 553 isolates from the Conococheague Creek Watershed. The known sources in the combined library were grouped into four categories: humans, livestock (cows and horses), pets (specifically dogs), and wildlife (deer, fox, goose, rabbit) (Table C-2). The library was analyzed for its ability to take a subset of the library isolates and correctly predict the identity of their host sources when they were treated as unknowns. Average rates of correct classification (ARCC) for the library were found by repeating this analysis using several probability cutoff points, as described above. The number-not-classified for each probability was determined. From these results, the percent unknown and percent correct classification (RCCs) was calculated (Table C-3).

Table C-2: Category, total number, and number of unique patterns in the Conococheague Creek known-source library and the combined Antietam-Conococheague known-source library.

Category	Potential Sources	Total Isolates	Unique Patterns
Conococheague Creek Library:			
human	human	90	56
livestock	cow, horse	177	57
pet	dog	65	34
wildlife	deer, rabbit, goose	221	61
Total		553	208
Combined ANT-CON Library:			
human	human	175	106
livestock	cow, horse	355	121
pet	dog	131	63
wildlife	deer, fox, goose, rabbit	459	101
Total		1120	391

For Conococheague Creek Watershed, a cutoff probability of 0.50 (50%) was shown to yield an ARCC of 70 % (Table C-3). The resulting RCCs for human and pet are a very high 91 % and 94%, respectively, with 76% for wildlife, and 39% for livestock (Table C-4).

Table C-3: Number of isolates not classified, percent unknown, and percent correct for eight (8) cutoff probabilities for Conococheague Creek known-source isolates using the combined Antietam-Conococheague know-source library.

Threshold	0	0.25	0.375	0.5	0.6	0.7	0.8	0.9
% correct	62.7%	62.7%	62.7%	70.2%	71.3%	81.0%	89.3%	98.5%
% unknown	0.0%	0.0%	0.5%	36.3%	53.3%	68.5%	77.9%	88.2%
# not classified	0	0	3	201	295	379	431	488

Figure C-1: Conococheague Creek Classification Model: Percent Correct versus Percent Unknown using a combined Antietam-Conococheague library.

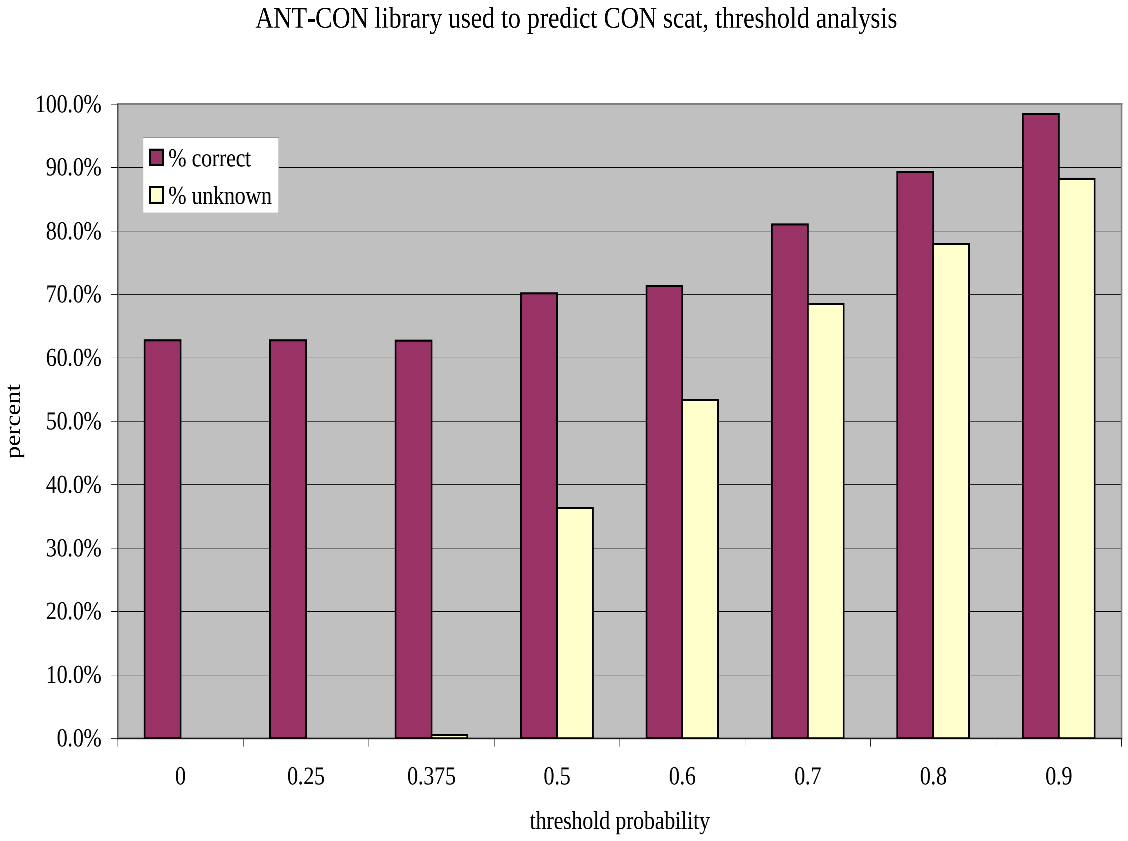


Table C-4: Actual species categories versus predicted categories, at 50% probability cutoff, with rates of correct classification (RCC) for each category.

Actual	Predicted Human	Livestock	Pet	Wildlife	Unknown	Total	RCC*
Human	63	1	5	0	21	90	91.3%
Livestock	18	42	18	30	69	177	38.9%
Pet	0	1	48	2	14	65	94.1%
Wildlife	13	6	11	94	97	221	75.8%
Total	94	50	82	126	201	553	

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

Conococheague Creek Water Samples. Monthly monitoring from eight (8) monitoring stations on Conococheague Creek was the source of water samples (Figure C-2) The maximum number of *Enterococcus i*solates per water sample was 24, although the number of isolates that actually grew was sometimes fewer than 24. A total of 2,181 *Enterococcus* isolates were analyzed by statistical analysis. The BST results by species category, shown in Table 5-CON, indicate that 78% of the water isolates were assigned to a probable host source when using a 0.50 (60%) probability cutoff.

Table C-5: Probable host sources of water isolates by species category, number of isolates, and percent isolates classified at a cutoff probability of 50%.

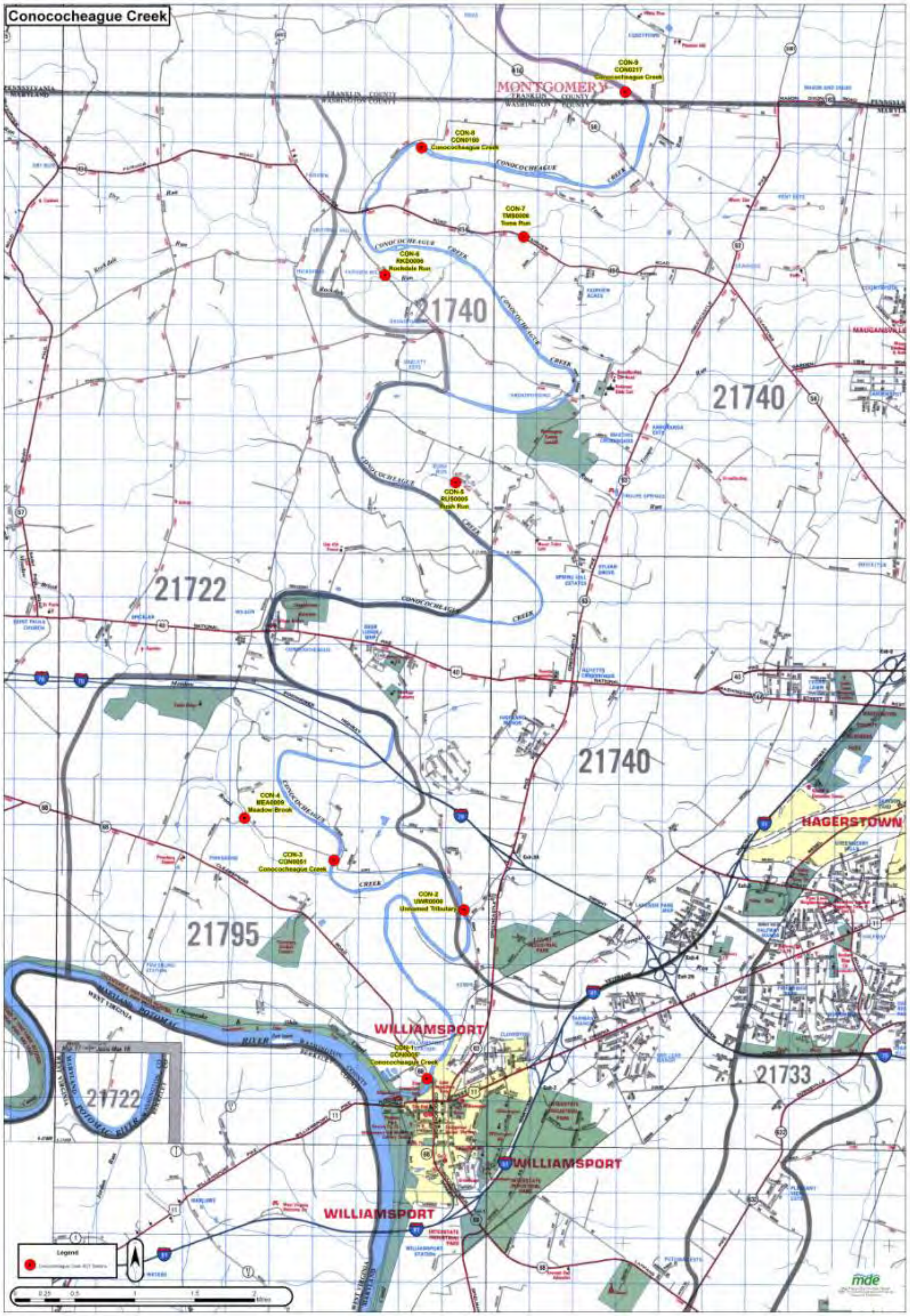
Category	Number	% assigned to category at 50% Prob.	% assigned to category (excluding unknowns)
human	425	19.5%	25.0%
livestock	229	10.5%	13.5%
pet	673	30.9%	39.6%
wildlife	373	17.1%	21.9%
unknown	481	22.1%	0
Missing Data	0	-	0
Total	2181	100.0%	100.0%
% classified	**78 %**		

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

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

	Season				
Station	Spring	Summer	Fall	Winter	Total
CON0005	134	75	121	98	428
CON0180	72	39	61	67	239
CON0217	68	38	59	55	220
MEA0009	72	68	48	61	249
RKD0006	72	66	68	67	273
RUS0005	71	71	57	68	267
TMS0006	72	72	65	38	247
UWR0000	70	62	62	64	258
Total	631	491	541	518	2181

Figure C-2: Map of Conococheague Creek Watershed.
[Dots indicate water monitoring sites.]



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: BST Analysis: Number of Isolates per Station per Date.

		Predicted Source					
Station	Date	Human	Livestock	Pet	Wildlife	Unknown	Total
CON0005	11/17/03	7	2	14	3	11	37
CON0005	12/01/03	9	7	9	6	6	37
CON0005	01/05/04	4	9	7	7	13	40
CON0005	02/02/04	5	0	2	2	6	15
CON0005	03/01/04	12	8	3	6	14	43
CON0005	04/05/04	16	8	6	10	7	47
CON0005	05/10/04	14	4	9	5	7	39
CON0005	06/07/04	4	9	22	5	8	48
CON0005	07/06/04	0	0	2	3	1	6
CON0005	08/09/04	1	0	7	12	6	26
CON0005	09/07/04	4	2	9	15	13	43
CON0005	10/04/04	8	2	25	9	3	47
CON0180	11/17/03	12	1	4	0	2	19
CON0180	12/01/03	3	1	6	4	7	21
CON0180	01/05/04	5	3	6	3	3	20
CON0180	02/02/04	12	4	2	6	0	24
CON0180	03/01/04	2	4	4	4	9	23
CON0180	04/05/04	7	6	5	3	3	24
CON0180	05/10/04	1	2	11	2	8	24
CON0180	06/07/04	2	1	16	2	3	24
CON0180	07/06/04	0	1	2	1	3	7
CON0180	08/09/04	3	0	1	5	3	12
CON0180	09/07/04	0	1	12	0	7	20
CON0180	10/04/04	8	1	3	2	7	21
CON0217	11/17/03	3	2	3	0	11	19
CON0217	12/01/03	1	2	4	4	9	20
CON0217	01/05/04	2	3	2	4	10	21
CON0217	02/02/04	6	0	1	0	6	13
CON0217	03/01/04	6	4	4	3	4	21
CON0217	04/05/04	7	5	0	9	3	24
CON0217	05/10/04	2	2	7	8	1	20
CON0217	06/07/04	7	2	14	0	1	24
CON0217	07/06/04	0	0	0	4	1	5
CON0217	08/09/04	2	2	2	6	2	14
CON0217	09/07/04	1	0	14	1	3	19
CON0217	10/04/04	2	4	6	4	4	20
MEA0009	11/17/03	0	1	8	1	9	19
MEA0009	12/01/03	0	0	5	0	0	5
MEA0009	01/05/04	5	5	5	1	5	21

Table C-7: BST Analysis: Number of Isolates per Station per Date (continued).

		Predicted Source					
Station	Date	Human	Livestock	Pet	Wildlife	Unknown	Total
MEA0009	02/02/04	4	0	4	5	7	20
MEA0009	03/01/04	3	0	5	4	8	20
MEA0009	04/05/04	3	4	4	5	8	24
MEA0009	05/10/04	12	2	3	2	5	24
MEA0009	06/07/04	6	0	16	1	1	24
MEA0009	07/06/04	5	0	14	1	4	24
MEA0009	08/09/04	2	3	2	9	8	24
MEA0009	09/07/04	3	3	8	6	0	20
MEA0009	10/04/04	15	0	2	2	5	24
RKD0006	11/17/03	4	1	8	1	6	20
RKD0006	12/01/03	8	2	7	0	7	24
RKD0006	01/05/04	3	4	3	4	5	19
RKD0006	02/02/04	12	3	5	3	1	24
RKD0006	03/01/04	17	3	0	1	3	24
RKD0006	04/05/04	4	1	7	9	3	24
RKD0006	05/10/04	6	3	11	1	3	24
RKD0006	06/07/04	1	2	9	6	6	24
RKD0006	07/06/04	4	0	13	5	2	24
RKD0006	08/09/04	6	2	6	6	4	24
RKD0006	09/07/04	1	2	3	7	5	18
RKD0006	10/04/04	6	4	12	1	1	24
RUS0005	11/17/03	0	3	6	0	7	16
RUS0005	12/01/03	4	3	3	3	6	19
RUS0005	01/05/04	1	12	4	1	4	22
RUS0005	02/02/04	6	2	4	11	0	23
RUS0005	03/01/04	6	0	9	3	5	23
RUS0005	04/05/04	4	4	4	6	6	24
RUS0005	05/10/04	3	4	10	4	2	23
RUS0005	06/07/04	3	3	9	3	6	24
RUS0005	07/06/04	3	2	10	3	5	23
RUS0005	08/09/04	4	4	4	6	6	24
RUS0005	09/07/04	2	4	10	5	3	24
RUS0005	10/04/04	3	1	6	4	8	22
TMS0006	11/17/03	4	3	7	1	6	21
TMS0006	12/01/03	5	4	6	2	5	22
TMS0006	01/05/04	4	1	8	5	5	23
TMS0006	02/02/04	0	0	0	1	5	6
TMS0006	03/01/04	2	0	1	2	4	9
TMS0006	04/05/04	0	2	2	9	11	24
TMS0006	05/10/04	2	4	10	5	3	24
TMS0006	06/07/04	6	1	14	0	3	24
TMS0006	07/06/04	0	0	12	5	7	24

Table C-7: BST Analysis: Number of Isolates per Station per Date (continued).

		Predicted Source					
Station	Date	Human	Livestock	Pet	Wildlife	Unknown	Total
TMS0006	08/09/04	0	0	16	6	2	24
TMS0006	09/07/04	7	0	14	1	2	24
TMS0006	10/04/04	1	1	6	7	7	22
UWR0000	11/17/03	5	3	2	0	4	14
UWR0000	12/01/03	4	3	11	1	5	24
UWR0000	01/05/04	3	3	12	1	4	23
UWR0000	02/02/04	7	6	1	3	3	20
UWR0000	03/01/04	1	0	1	4	15	21
UWR0000	04/05/04	8	3	1	12	0	24
UWR0000	05/10/04	5	2	5	3	7	22
UWR0000	06/07/04	4	1	18	1	0	24
UWR0000	07/06/04	2	0	22	0	0	24
UWR0000	08/09/04	4	0	8	5	6	23
UWR0000	09/07/04	1	3	5	1	5	15
UWR0000	10/04/04	3	0	8	10	3	24
Total		425	229	673	373	481	2181

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

		Predicted Source					
Station	Date	Human	Livestock	Pet	Wildlife	Unknown	Total
CON0005	11/17/03	19%	5%	38%	8%	30%	100%
CON0005	12/01/03	24%	19%	24%	16%	16%	100%
CON0005	01/05/04	10%	23%	18%	18%	33%	100%
CON0005	02/02/04	33%	0%	13%	13%	40%	100%
CON0005	03/01/04	28%	19%	7%	14%	33%	100%
CON0005	04/05/04	34%	17%	13%	21%	15%	100%
CON0005	05/10/04	36%	10%	23%	13%	18%	100%
CON0005	06/07/04	8%	19%	46%	10%	17%	100%
CON0005	07/06/04	0%	0%	33%	50%	17%	100%
CON0005	08/09/04	4%	0%	27%	46%	23%	100%
CON0005	09/07/04	9%	5%	21%	35%	30%	100%
CON0005	10/04/04	17%	4%	53%	19%	6%	100%
CON0180	11/17/03	63%	5%	21%	0%	11%	100%
CON0180	12/01/03	14%	5%	29%	19%	33%	100%
CON0180	01/05/04	25%	15%	30%	15%	15%	100%
CON0180	02/02/04	50%	17%	8%	25%	0%	100%
CON0180	03/01/04	9%	17%	17%	17%	39%	100%

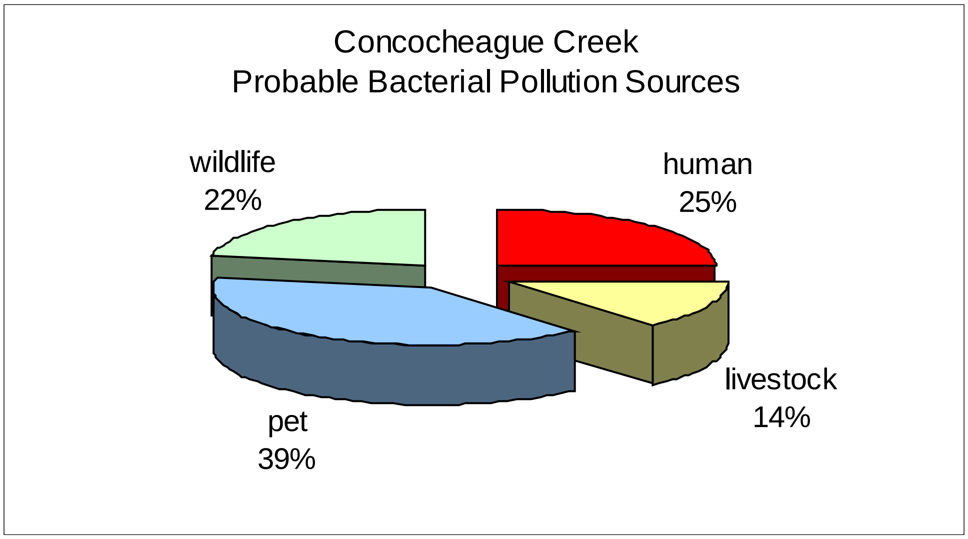
Table C-8: BST Analysis: Percentage of Sources per Station per Date (continued).

		Predicted Source					
Station	Date	Human	Livestock	Pet	Wildlife	Unknown	Total
CON0180	04/05/04	29%	25%	21%	13%	13%	100%
CON0180	05/10/04	4%	8%	46%	8%	33%	100%
CON0180	06/07/04	8%	4%	67%	8%	13%	100%
CON0180	07/06/04	0%	14%	29%	14%	43%	100%
CON0180	08/09/04	25%	0%	8%	42%	25%	100%
CON0180	09/07/04	0%	5%	60%	0%	35%	100%
CON0180	10/04/04	38%	5%	14%	10%	33%	100%
CON0217	11/17/03	16%	11%	16%	0%	58%	100%
CON0217	12/01/03	5%	10%	20%	20%	45%	100%
CON0217	01/05/04	10%	14%	10%	19%	48%	100%
CON0217	02/02/04	46%	0%	8%	0%	46%	100%
CON0217	03/01/04	29%	19%	19%	14%	19%	100%
CON0217	04/05/04	29%	21%	0%	38%	13%	100%
CON0217	05/10/04	10%	10%	35%	40%	5%	100%
CON0217	06/07/04	29%	8%	58%	0%	4%	100%
CON0217	07/06/04	0%	0%	0%	80%	20%	100%
CON0217	08/09/04	14%	14%	14%	43%	14%	100%
CON0217	09/07/04	5%	0%	74%	5%	16%	100%
CON0217	10/04/04	10%	20%	30%	20%	20%	100%
MEA0009	11/17/03	0%	5%	42%	5%	47%	100%
MEA0009	12/01/03	0%	0%	100%	0%	0%	100%
MEA0009	01/05/04	24%	24%	24%	5%	24%	100%
MEA0009	02/02/04	20%	0%	20%	25%	35%	100%
MEA0009	03/01/04	15%	0%	25%	20%	40%	100%
MEA0009	04/05/04	13%	17%	17%	21%	33%	100%
MEA0009	05/10/04	50%	8%	13%	8%	21%	100%
MEA0009	06/07/04	25%	0%	67%	4%	4%	100%
MEA0009	07/06/04	21%	0%	58%	4%	17%	100%
MEA0009	08/09/04	8%	13%	8%	38%	33%	100%
MEA0009	09/07/04	15%	15%	40%	30%	0%	100%
MEA0009	10/04/04	63%	0%	8%	8%	21%	100%
RKD0006	11/17/03	20%	5%	40%	5%	30%	100%
RKD0006	12/01/03	33%	8%	29%	0%	29%	100%
RKD0006	01/05/04	16%	21%	16%	21%	26%	100%
RKD0006	02/02/04	50%	13%	21%	13%	4%	100%
RKD0006	03/01/04	71%	13%	0%	4%	13%	100%
RKD0006	04/05/04	17%	4%	29%	38%	13%	100%
RKD0006	05/10/04	25%	13%	46%	4%	13%	100%
RKD0006	06/07/04	4%	8%	38%	25%	25%	100%
RKD0006	07/06/04	17%	0%	54%	21%	8%	100%
RKD0006	08/09/04	25%	8%	25%	25%	17%	100%
RKD0006	09/07/04	6%	11%	17%	39%	28%	100%

Table C-8: BST Analysis: Percentage of Sources per Station per Date (continued).

		Predicted Source					
Station	Date	Human	Livestock	Pet	Wildlife	Unknown	Total
RKD0006	10/04/04	25%	17%	50%	4%	4%	100%
RUS0005	11/17/03	0%	19%	38%	0%	44%	100%
RUS0005	12/01/03	21%	16%	16%	16%	32%	100%
RUS0005	01/05/04	5%	55%	18%	5%	18%	100%
RUS0005	02/02/04	26%	9%	17%	48%	0%	100%
RUS0005	03/01/04	26%	0%	39%	13%	22%	100%
RUS0005	04/05/04	17%	17%	17%	25%	25%	100%
RUS0005	05/10/04	13%	17%	43%	17%	9%	100%
RUS0005	06/07/04	13%	13%	38%	13%	25%	100%
RUS0005	07/06/04	13%	9%	43%	13%	22%	100%
RUS0005	08/09/04	17%	17%	17%	25%	25%	100%
RUS0005	09/07/04	8%	17%	42%	21%	13%	100%
RUS0005	10/04/04	14%	5%	27%	18%	36%	100%
TMS0006	11/17/03	19%	14%	33%	5%	29%	100%
TMS0006	12/01/03	23%	18%	27%	9%	23%	100%
TMS0006	01/05/04	17%	4%	35%	22%	22%	100%
TMS0006	02/02/04	0%	0%	0%	17%	83%	100%
TMS0006	03/01/04	22%	0%	11%	22%	44%	100%
TMS0006	04/05/04	0%	8%	8%	38%	46%	100%
TMS0006	05/10/04	8%	17%	42%	21%	13%	100%
TMS0006	06/07/04	25%	4%	58%	0%	13%	100%
TMS0006	07/06/04	0%	0%	50%	21%	29%	100%
TMS0006	08/09/04	0%	0%	67%	25%	8%	100%
TMS0006	09/07/04	29%	0%	58%	4%	8%	100%
TMS0006	10/04/04	5%	5%	27%	32%	32%	100%
UWR0000	11/17/03	36%	21%	14%	0%	29%	100%
UWR0000	12/01/03	17%	13%	46%	4%	21%	100%
UWR0000	01/05/04	13%	13%	52%	4%	17%	100%
UWR0000	02/02/04	35%	30%	5%	15%	15%	100%
UWR0000	03/01/04	5%	0%	5%	19%	71%	100%
UWR0000	04/05/04	33%	13%	4%	50%	0%	100%
UWR0000	05/10/04	23%	9%	23%	14%	32%	100%
UWR0000	06/07/04	17%	4%	75%	4%	0%	100%
UWR0000	07/06/04	8%	0%	92%	0%	0%	100%
UWR0000	08/09/04	17%	0%	35%	22%	26%	100%
UWR0000	09/07/04	7%	20%	33%	7%	33%	100%
UWR0000	10/04/04	13%	0%	33%	42%	13%	100%

Figure C-3. Conococheague Creek Watershed relative contributions by probable sources of *Enterococcus* contamination.



Conococheague Creek Summary

The use of ARA was successful for identification of *Enterococcus* sources in the Conococheague Creek Watershed for source categories in the library. In this watershed, the RCCs ran as high as 94%. When water isolates were compared to the library and potential sources predicted, 78% of the isolates were classified by statistical analysis. The largest category of potential sources in the watershed as a whole was pet (40% of classified water isolates), followed by human and wildlife (25% and 22% of classified isolates, respectively). The potential contribution by livestock was low and made up only 14% of classified isolates.

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BST Adjustment

The current BST methodology produces significant inaccuracies. This is seen in Table C-4, which shows results of the analysis of samples from known sources. For example out of 90 isolates known to be of human source only 63 were classified by the analysis to be human. One isolate was classified as livestock, 5 as pet and 21 as unknown. Taking another view, a total of 94 of all isolates were classified as human of which only 63 were actually known to be of human source. The remainder of those 94 isolates comprised of 18 known livestock isolates and 13 known wildlife isolates.

The results provided by the BST methodology can be adjusted based on the known source classification results provided in Table C-4 to account for the inaccuracies of the BST analysis.

Example:

The current BST methodology provides the following source percentages for station CON0217 during high flow conditions:

Domestic animals: 25.67 %
Human: 17.23
Livestock: 14.33
Wildlife: 20.79
Unknown: 21.98

To get the correct human source percentage we redistribute the above percentages as follows.

Correct Human Source Percentage	= (5/82) x 25.67	<=	82 known isolates were predicted as pet, of which 5 are known to be of human source
	+ (63/94) x 17.23	<=	94 known isolates were predicted as human, of which 63 are known to be of human source
	+ (1/50) x 14.33	<=	50 known isolates were predicted as livestock, of which 1 is known to be of human source
	+ (0/126) x 20.79	<=	126 known isolates were predicted as wildlife, of which 0 are known to be of human source
	+ (21/201) x 21.98	<=	201 known isolates were classified as unknown, of which 21 are known to be of human source
	= 15.70		

Thus the correct human source percentage, the value used in the TMDL analysis, is 15.70% and not 17.23%. Corrected percentages are also calculated as above for domestic animal, livestock and wildlife sources. The classification of unknown is eliminated in the process as all known isolates are of known source. For station CON0217 during high flow condition the corrected source percentages are as follows:

Domestic animals: 17.2 %
Human: 15.7
Livestock: 33.5
Wildlife: 33.7

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 the Conococheague Creek watershed. The approach builds upon the TMDL analysis that was conducted to ensure that compliance with the annual average target will result in compliance with the applicable water quality standards. The annual average loading target was converted into allowable *daily* values by using the loadings developed from the TMDL analysis. The approach is consistent with available EPA guidance on generating daily loads for TMDLs.

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

Level of Resolution

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

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

Probability Level

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

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

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

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

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

To calculate the Conococheague Creek watershed MDL for non-point sources and MS4s, 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 the two flow strata, with an upper bound percentile that accounts for the variability of daily loads. The upper bound percentile and the maximum daily loads were estimated following EPA's "Technical Support Document for Water Quality-Based Toxics Control" (1991 TSD) (EPA 1991); and "Approaches For Developing a Daily Load Expression for TMDLs Computed for Longer Term Averages" (EPA 2006).

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

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

and,

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

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)

σ^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 nine monitoring stations of the Conococheague Creek watershed. 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©.

$$Z = [\log_{10}(MOC) - \log(AM) + 0.5\sigma^2]/\sigma \qquad \text{(D3)}$$

where,

Z = z-score associated with upper bound percentile
MOC = maximum observed bacteria concentration (MPN/100ml)
AM = arithmetic mean observed bacteria concentrations (MPN/100ml)
σ^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. In the case of the Conococheague Creek watershed, a value measured during high-flow conditions at the TMS0006 station resulted in the highest percentile of both strata of the nine stations. This value translates to the 99.0th 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

Subwatershed	Flow Stratum	Maximum Observed *E. coli* Concentration (MPN/100ml)	Percentile (%)
CON0217[1]	High	3,448	93.4
	Low	479	95.1
CON0180sub[1]	High	4,884	96.4
	Low	460	92.8
RKD0006[1]	High	6,867	93.0
	Low	4,352	88.2
TMS0006[1]	High	24,192	99.0
	Low	813	90.0
RUS0005	High	7,701	96.4
	Low	3,255	90.7
CON0051sub[1]	High	4,106	93.6
	Low	223	82.1
MEA0009	High	4,884	95.4
	Low	5,475	89.2
UWR0000	High	1,989	91.3
	Low	1,789	90.1
CON0005sub	High	6,867	97.7
	Low	269	82.1

[1] Subwatersheds partially located in Pennsylvania

The 99.0th percentile value results in a maximum daily load that would not be exceeded 99.0% 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,

$$L_b{*}(1\text{-}R) = Q_H{*}C_H{*}F_{1H}{*}W_H{*}(1\text{-}R) + Q_L{*}C_L{*}F_{1L}{*}W_L{*}(1\text{-}R) \qquad \text{(D4)}$$

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:

$$C_{LTA\text{-}H} = C_{b\text{-}H}{*}(1\text{-}R_H) \qquad \text{(D5)}$$

$$C_{LTA\text{-}L} = C_{b\text{-}L}{*}(1\text{-}R_L) \qquad \text{(D6)}$$

The TMDL concentrations estimated as explained above are shown in Table D-2.

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

Subwatershed	**Flow Stratum**	**LTA Geometric Mean *E. coli* Concentration** (MPN/100ml)	**LTA Arithmetic Mean* *E. coli* Concentration** (MPN/100ml)
CON0217[1]	High	107	260
	Low	36	45
CON0180sub[1]	High	87	202
	Low	30	39
RKD0006[1]	High	42	112
	Low	44	105
TMS0006[1]	High	49	367
	Low	21	79
RUS0005	High	59	108
	Low	45	77
CON0051sub[1]	High	90	368
	Low	27	42
MEA0009	High	34	62
	Low	25	134
UWR0000	High	77	105
	Low	64	95
CON0005sub	High	80	227
	Low	27	37

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

The next step is to calculate the 99.0th 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 pollutant concentrations does not change after these concentrations have been reduced or controlled by a fixed proportion (Ott 1995). Therefore, the coefficient of variation estimated using the monitoring data concentrations does not change, and it can be used to estimate the 99.0th 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

Subwatershed	Flow Stratum	Coefficient of Variation	MDL *E. coli* Concentration (MPN/100ml)
CON0217[1]	High	2.22	2,324
	Low	0.77	174
CON0180sub[1]	High	2.11	1,753
	Low	0.81	155
RKD0006[1]	High	2.46	1,061
	Low	2.18	930
TMS0006[1]	High	7.47	5,054
	Low	3.53	891
RUS0005	High	1.51	735
	Low	1.39	494
CON0051sub[1]	High	3.95	4,344
	Low	1.15	228
MEA0009	High	1.54	431
	Low	5.18	1,713
UWR0000	High	0.93	474
	Low	1.11	502
CON0005sub	High	2.67	2,262
	Low	0.95	172

[1] Subwatersheds partially located in Pennsylvania

With the 99.0th 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 non-point sources for each subwatershed can be now estimated as:

$$\begin{aligned} Daily\ TMDL\ (MPN/day) = {} & Q_H*(99.0^{th}C_{LTA\text{-}H})*F_{1H}*W_H \\ & + Q_L*(99.0^{th}C_{LTA\text{-}L})*F_{1L}*W_L \end{aligned} \qquad \text{(D7)}$$

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

$$WWTP\text{-}WLA\ MDL_{\ (billion\ MPN/day)} = [WWTP\text{-}WLA_{\ (billion\ MPN/year)}]*(3.11/365) \quad \text{(D8)}$$

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

Table D-4: Maximum Daily Loads Summary

Subwatershed	Flow Stratum	Maximum Daily Load (Billion *E. coli* MPN/day)	
		by Stratum	Weighted by Stratum
CON0217[1]	High Low	84,987 1,162	26,058
CON0180sub[1]	High Low	478 8	147
RKD0006[1]	High Low	806 129	330
TMS0006[1]	High Low	1,746 56	558
RUS0005	High Low	558 68	214
CON0051sub[1]	High Low	5,061 49	1,537
MEA0009	High Low	251 182	202
UWR0000	High Low	273 53	118
CON0005sub	High Low	1,743 24	535

[1] Subwatersheds partially located in Pennsylvania

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). The maximum daily load allocations for the Conococheague Creek watershed are presented in Table D-5.

Table D-5: Conococheague Creek Watershed Maximum Daily Loads in MD

Subwatershed	**Total Allocation**	**LA**	**SW-WLA**	**WWTP-WLA**
	(Billion MPN *E. coli* /day)			
CON0217[1]	47	44	3	0
CON0180sub[1]	57	53	4	0
RKD0006[1]	227	178	49	0
TMS0006[1]	498	427	70	0
RUS0005	214	163	50	0
CON0051sub[1]	1,537	1,347	189	0.04
MEA0009	202	157	45	0.15
UWR0000	118	93	25	0
CON0005sub	535	260	214	61
Total	**3,433**	**2,722**	**650**	**61**

[1] MD portion of the subwatershed only.

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