Total Maximum Daily Loads of Fecal Bacteria for the Prettyboy Reservoir Basin in Baltimore and Carroll Counties, Maryland

FINAL

MARYLAND
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Submitted to:

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List of Abbreviations

ARCC	Average rates of correct classification
ARA	Antibiotic Resistance Analysis
BMP	Best Management Practice
BST	Bacteria Source Tracking
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 Prettyboy Reservoir watershed (MD basin number 02-13-08-06). Section 303(d) of the federal Clean Water Act (CWA) and the EPA's implementing regulations direct each state to identify and list waters, known as water quality limited segments (WQLSs), in which current required controls of a specified substance are inadequate to achieve water quality standards. For each WQLS, states are required to either establish a Total Maximum Daily Load (TMDL) of the specified substance that the waterbody can receive without violating water quality standards or demonstrate that water quality standards are being met.

The Maryland Department of the Environment (MDE) has identified the tributaries of Prettyboy Reservoir in the State of Maryland's 303(d) List as impaired by fecal bacteria (listed in 2002) and impacts to biological communities (listed in 2002 and 2004). The reservoir itself is not listed as impaired by fecal bacteria. The Prettyboy Reservoir and all its tributaries have been designated as Use III-P (Nontidal Cold Water and Public Water Supply). See Code of Maryland Regulations (COMAR) 26.08.02.08J. This document proposes to establish a TMDL for fecal bacteria in the Prettyboy Reservoir watershed that will allow for attainment of the beneficial use designation of water contact recreation. The listings for impacts to biological communities will be addressed in a separate TMDL document. TMDLs for the impoundment were developed for mercury in 2002 and nutrients in 2006, and approved by EPA in 2004 and 2007, respectively. MDE monitored the Prettyboy Reservoir 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. To account for portions of subwatersheds located in Pennsylvania (PA), an upstream load allocation (LA_{PA}), determined to be necessary in order to meet MD water quality standards in the MD portion of the watershed, is also included in this TMDL.

For this TMDL analysis, the Prettyboy Reservoir watershed has been divided into four subwatersheds. For convenience, three of the four subwatersheds will be referenced by the downstream bacteria monitoring station's name and location: GUN0476 (Gunpowder Falls at Gunpowder Run), GRG0013 (Grave Run) and GOB0042 (Georges Run). The fourth subwatershed encompasses all unmonitored areas downstream of the three stations, excepting the impoundment, and will be referred to as the "Downstream Subwatershed." The pollutant loads set forth in this document are for these four 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 three representative stations in the Prettyboy Reservoir 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

Prettyboy Reservoir watershed is established after considering three different hydrological conditions: high flow and low flow annual conditions, and an average seasonal condition (the period between May 1st and September 30th when water contact recreation is more prevalent). 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 two of the four subwatersheds, it was estimated that water quality standards could not be attained with MPRs; thus, higher maximum reductions were applied.

The MD 8-digit Prettyboy Reservoir Total Baseline Load consists of upstream loads generated outside the MD 8-digit watershed assessment unit: a Pennsylvania Upstream Baseline Load (BL_{PA}), plus loads generated within the assessment unit: a MD 8-digit Prettyboy Reservoir Baseline Load (BL_{PR}) Contribution. The baseline loads are summarized in the following table:

MD 8-Digit Prettyboy Reservoir Fecal Bacteria Baseline Loads (Billion MPN *E. coli*/year)								
Total Baseline Load	=	**Upstream Baseline Load**[1]	+	**MD 8-digit Prettyboy Reservoir Baseline Load Contribution**				
		BL_{PA}		**Nonpoint Source BL_{PR}**	+	**NPDES Stormwater BL_{PR}**	+	**WWTP BL_{PR}**
745,438	=	77,136	+	625,714	+	41,718	+	870

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

The MD 8-digit Prettyboy Reservoir 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 Prettyboy Reservoir TMDL Contribution.

The MD 8-digit Prettyboy Reservoir TMDL Contribution, representing the sum of individual TMDLs for the four subwatersheds or portions thereof within MD, is distributed between a load allocation (LA_{PR}) for nonpoint sources and waste load allocations (WLA_{PR}) for point sources. Point sources include any 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 Prettyboy Reservoir TMDL of fecal bacteria is presented in the following table:

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

TMDL	=	**LA**			+	**WLA**			+	**MOS**
		LA_{PA}[1]	+	**LA_{PR}**		**SW WLA_{PR}**	+	**WWTP WLA_{PR}**		
217,931	=	11,494	+	199,917	+	5,650	+	870	+	Incorpo-rated

Upstream Load Allocation

MD 8-digit Prettyboy Reservoir TMDL Contribution (206,437)

[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 8-digit Prettyboy Reservoir watershed. The LA_{PA} represents a reduction of approximately 85% from the PA baseline load of 77,136 billion MPN *E. coli*/year. The MD 8-digit TMDL Contribution (206,437 billion MPN *E. coli*/year) represents a reduction of approximately 69% from the MD 8-digit Baseline Load Contribution of 668,302 billion MPN *E. coli*/year.

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

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

MDL	=	**LA**			+	**WLA**			+	**MOS**
		LA_{PA}[1]	+	**LA_{PR}**		**SW WLA_{PR}**	+	**WWTP WLA_{PR}**		
6,760	=	374	+	6,164	+	215	+	7	+	Incorpo-rated

Upstream MDL

MD 8-digit Prettyboy Reservoir MDL Contribution (6,386)

Once EPA has approved a TMDL, MDE intends for the required reductions to be implemented in an iterative process that first addresses those sources with the largest impacts to water quality and creating the greatest risks to human health, with consideration given to ease and cost of implementation. In addition, follow-up monitoring plans will be established to track progress and to assess the implementation efforts. As previously stated, water quality standards cannot be attained in two of the four 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 Prettyboy Reservoir watershed (MD basin number 02-13-08-06). Section 303(d)(1)(C) of the federal Clean Water Act (CWA) and the U.S. Environmental Protection Agency's (EPA) implementing regulations direct each state to develop a TMDL for each impaired water quality limited segment (WQLS) on the Section 303(d) List, taking into account seasonal variations and a protective margin of safety (MOS) to account for uncertainty. A TMDL reflects the total pollutant loading of the impairing substance a waterbody can receive and still meet water quality standards.

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

The Maryland Department of the Environment (MDE) has identified the tributaries of Prettyboy Reservoir in the State of Maryland's 303(d) List as impaired by fecal bacteria (listed in 2002) and impacts to biological communities (listed in 2002 and 2004). The reservoir itself is not listed as impaired by fecal bacteria. The Prettyboy Reservoir and all its tributaries have been designated as Use III-P (Nontidal Cold Water and Public Water Supply). See Code of Maryland Regulations (COMAR) 26.08.02.08J. This document proposes to establish a TMDL for fecal bacteria in the Prettyboy Reservoir watershed that will allow for attainment of the beneficial use designation of water contact recreation. The listings for impacts to biological communities will be addressed in a separate TMDL document. TMDLs were developed for mercury in 2002 and nutrients in 2006, and approved by EPA in 2004 and 2007, respectively. MDE monitored the Prettyboy Reservoir 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. To account for portions of subwatersheds located in Pennsylvania (PA), an upstream load allocation (LA_{PA}), determined to be necessary in order to meet MD water quality standards in the MD portion of the watershed, is also included in this TMDL.

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 Prettyboy Reservoir TMDL analysis was *E. coli*.

2.0 SETTING AND WATER QUALITY DESCRIPTION

2.1 General Setting

<u>Location</u>

The Prettyboy Reservoir watershed is located in both Maryland (MD) and Pennsylvania (PA) with a drainage area of 79.8 square miles (51,062 acres). The majority of the watershed is in MD (in Baltimore and Carroll counties) with a portion in York County, PA (see Figure 2.1.1).

The watershed includes the towns of Manchester and Hampstead in the west, and Rayville and Middletown to the east. The headwaters of the Gunpowder Falls begin in PA north of Lineboro, MD. The tributaries to the reservoir include Gunpowder Falls, Dykes Creek, Poplar Run, Grave Run, Compass Run, Georges Run and Prettyboy Branch. See Figure 2.1.1.

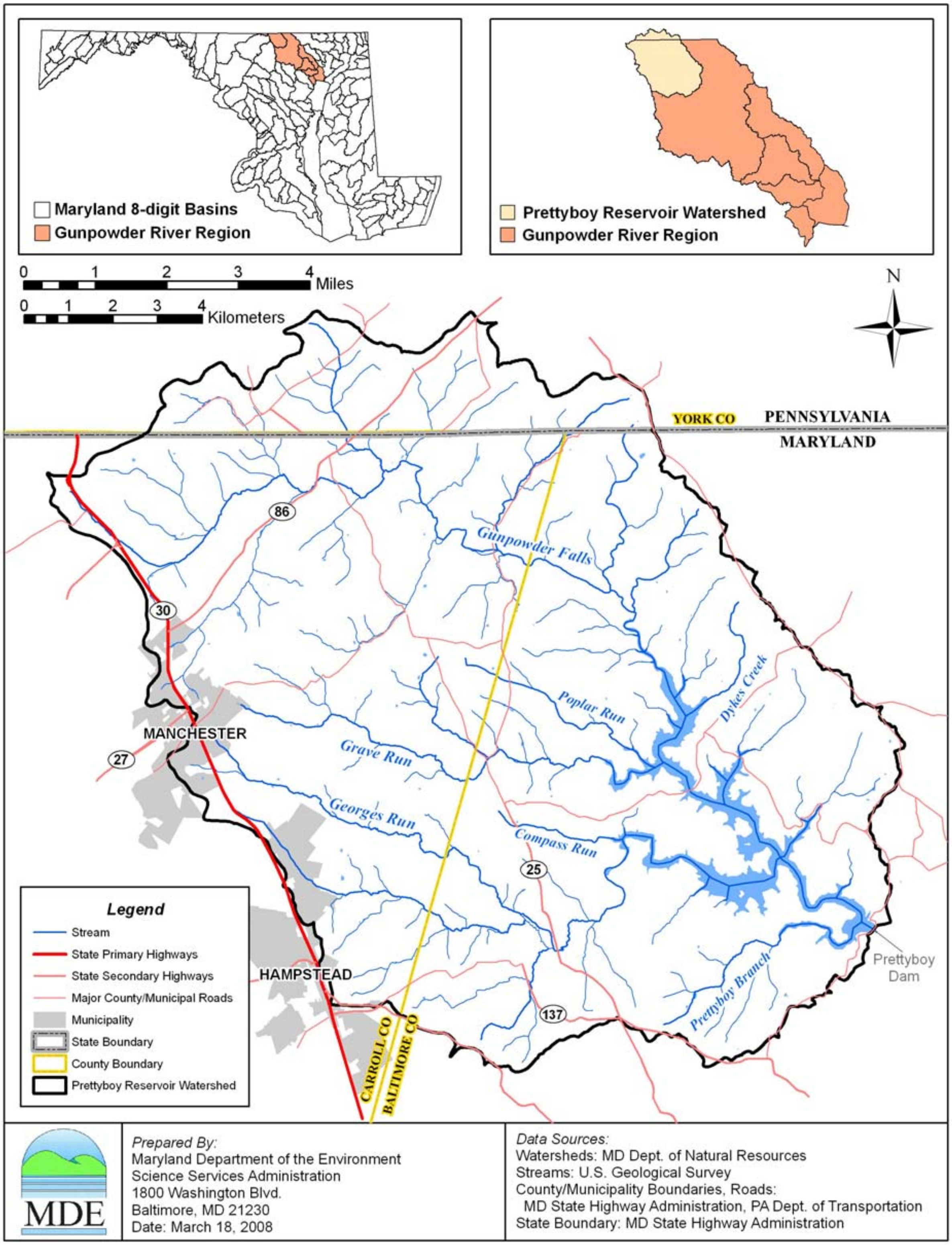


Figure 2.1.1: Location Map of the Prettyboy Reservoir Watershed

Land Use

The Prettyboy Reservoir watershed covers an area of 51,062 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 can be characterized as primarily agricultural and forest land. 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 pasture and forest.

The forested areas are mainly surrounding the reservoir. The major urban areas of the watershed are Manchester and Hampstead.

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 2.1.2. Table 2.1.2 shows the land use percentage distribution for each of the four subwatersheds considered in the analysis. Note that the subwatersheds are identified by the MDE monitoring stations located in the mainstem of the river and it's main tributaries, and are listed by flow from upstream to downstream. The fourth subwatershed encompasses all unmonitored areas downstream of the three monitoring stations, excepting the impoundment, and is identified as the Downstream Subwatershed.

Table 2.1.1: Land Use Percentage Distribution for the Prettyboy Reservoir Watershed

Land Type	Maryland Area		Pennsylvania Area		*Total*	
	Acres	%	Acres	%	Acres	%
Agricultural	17,378	37.4	825	18.0	18,204	35.7
Forest	17,016	36.6	1,398	30.4	18,414	36.1
Urban	6,943	14.9	264	5.7	7,207	14.1
Pasture	3,621	7.8	2,108	45.9	5,729	11.2
Water	1,508	3.2	0	0	1,508	3.0
Total	**46,467**	**100**	**4,595**	**100**	**51,062**	**100**

Table 2.1.2: Land Use Percentage Distribution for the Prettyboy Reservoir Watershed

Station / Subwatershed	Land Use Area (%)				
	Agricultural	Forest	Urban	Pasture	Water
GUN0476 / Gunpowder Falls	36.3	31.0	13.7	19.0	0.01
GRG0013 / Grave Run	45.7	34.0	13.2	7.2	0.00
GOB0042 / Georges Run	50.1	18.9	21.8	9.2	0.02
Downstream Subwatershed	24.5	50.8	10.6	6.1	8.1

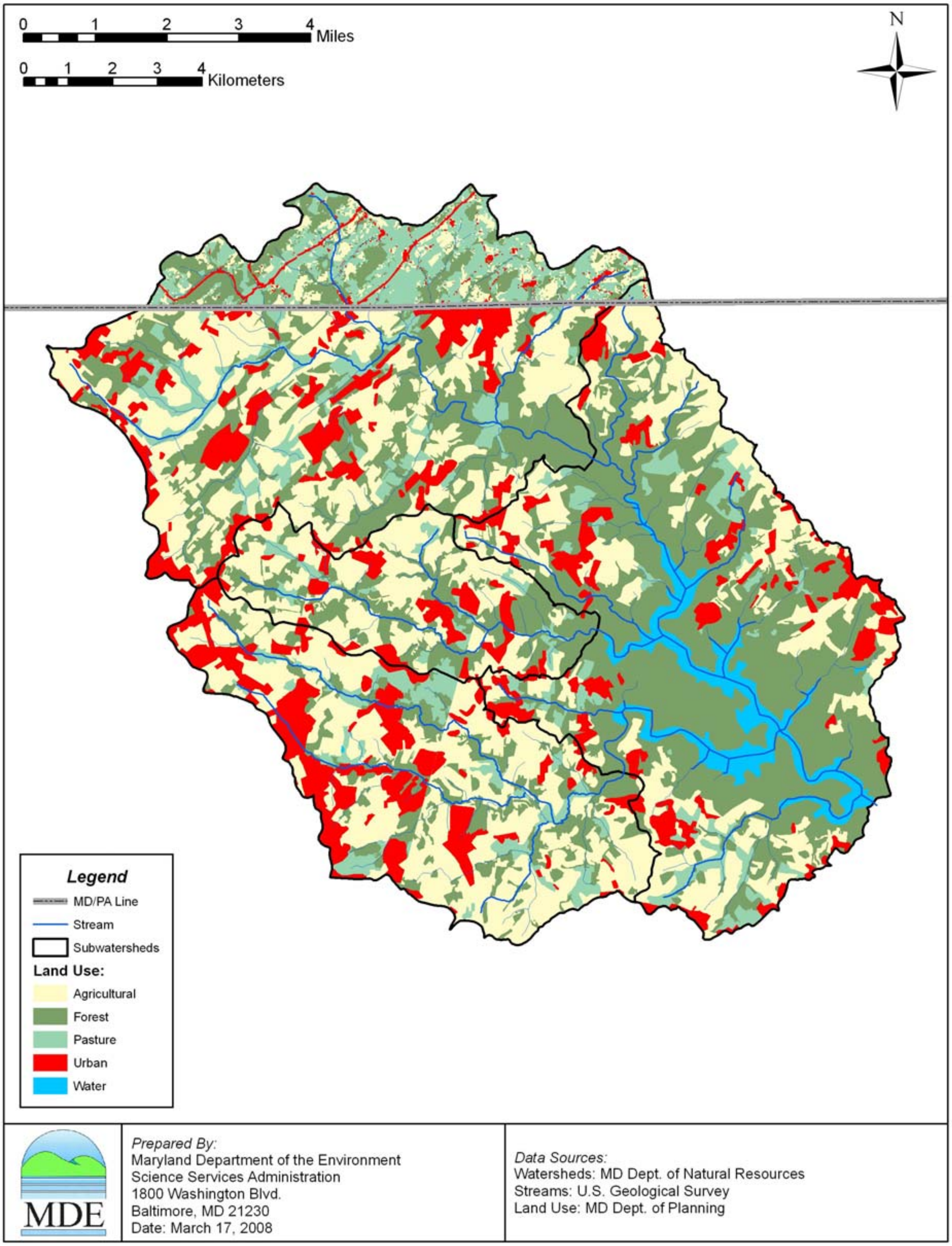


Figure 2.1.2: Land Use of the Prettyboy Reservoir Watershed

Population

The total population in the Prettyboy Reservoir watershed is estimated to be 14,971 people. Figure 2.1.3 illustrates the population density in the watershed. The human population and the number of households were estimated based on a weighted average from the 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.

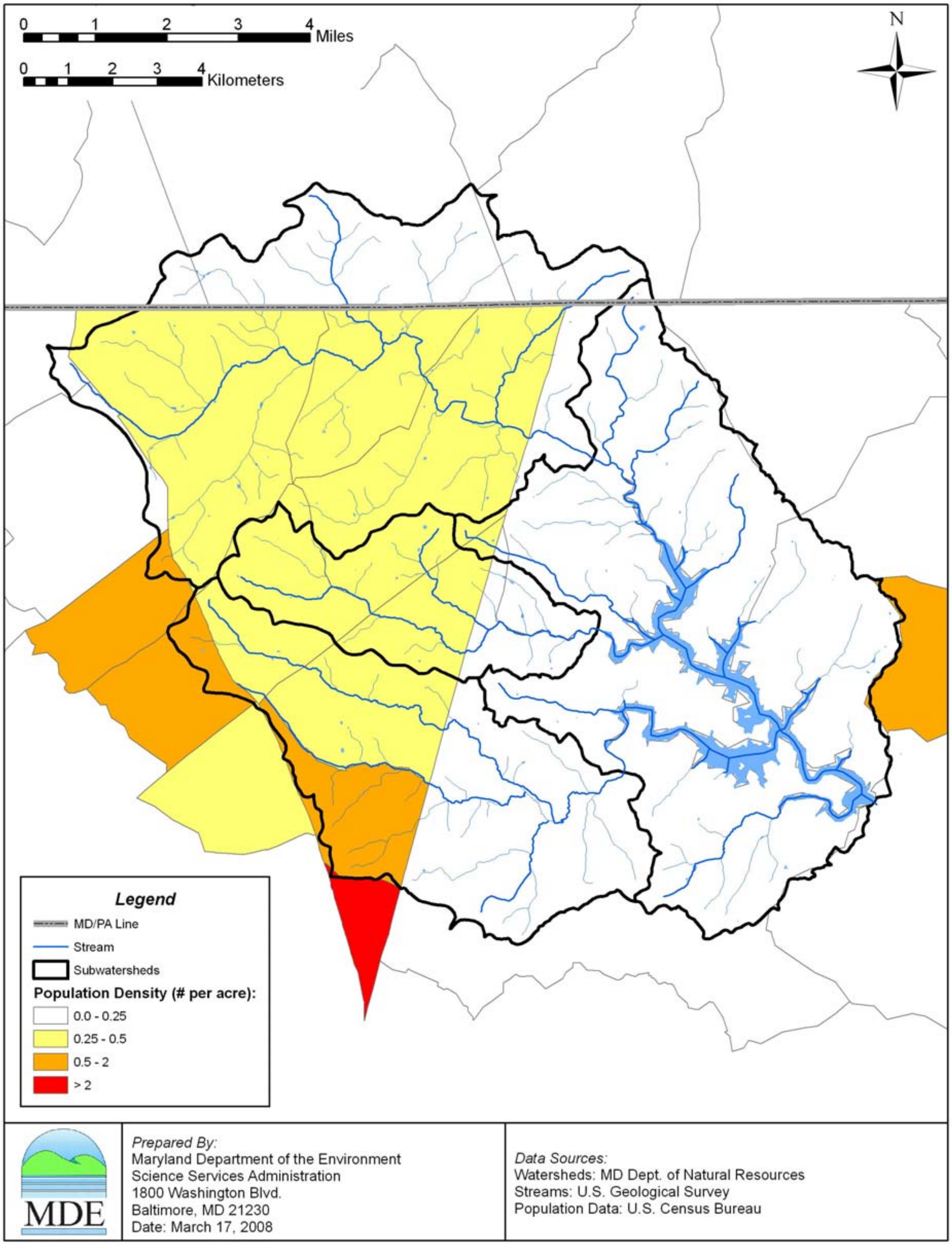
Table 2.1.3: Number of Dwellings Per Acre

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 Prettyboy Reservoir Watershed

Station / Subwatershed	Population
GUN0476 / Gunpowder Falls	5,642
GRG0013 / Grave Run	1,173
GOB0042 / Georges Run	5,219
Downstream Subwatershed	2,937
Total	**14,971**



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Date: March 17, 2008

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

Figure 2.1.3: Population Density in the Prettyboy Reservoir Watershed

2.2 Water Quality Characterization

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

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

Bacteria Monitoring

Table 2.2.1 lists the historical monitoring data for the Prettyboy Reservoir watershed. MDE conducted monitoring sampling at three stations in the Prettyboy Reservoir watershed from November 2003 through October 2004. Three United States Geological Survey (USGS) gage stations were used in deriving the surface water flow and a fourth was used in evaluating long-term hydrological conditions. 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 three 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 three stations ranged between 10 and 15,530 MPN/100 ml.

Table 2.2.1: Historical Monitoring Data in the MD 8-Digit Prettyboy Reservoir Watershed

Organization	Date	Design	Summary
DNR	01/1986 through 12/2003	Fecal Coliform*	1 station 1 sample per month
MDE	11/2003 through 10/2004	*E. coli*	3 stations 2 samples per month
MDE	11/2003 through 10/2004	BST (*Enterococcus)*	3 stations 1 sample per month

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

Table 2.2.2: Location of DNR Core Station in the MD 8-Digit Prettyboy Reservoir Watershed

Station	Tributary	Latitude (Decimal Degrees)	Longitude (Decimal Degrees)
GUN0476	Gunpowder Falls	39.689	-76.780

Table 2.2.3: Locations of MDE Monitoring Stations in the MD 8-Digit Prettyboy Reservoir Watershed

Tributary	Station	Observation Period	Total Observations	Latitude (Decimal Degrees)	Longitude (Decimal Degrees)
Gunpowder Falls	GUN0476	2003 - 2004	24	39.689	-76.781
Grave Run	GRG0013	2003 - 2004	24	39.655	-76.779
Georges Run	GOB0042	2003 - 2004	24	39.626	-76.773

Table 2.2.4: Location of USGS Gauging Stations in the MD 8-Digit Prettyboy Reservoir Watershed

Site Number	Observation Period Used	Total Observations	Latitude	Longitude
01581810	2003-2004	24	39.690	-76.781
01581830	2003-2004	24	39.655	-76.781
01581870	2003-2004	24	39.626	-76.773
01582000	1982-2007	9,131	39.604	-76.620

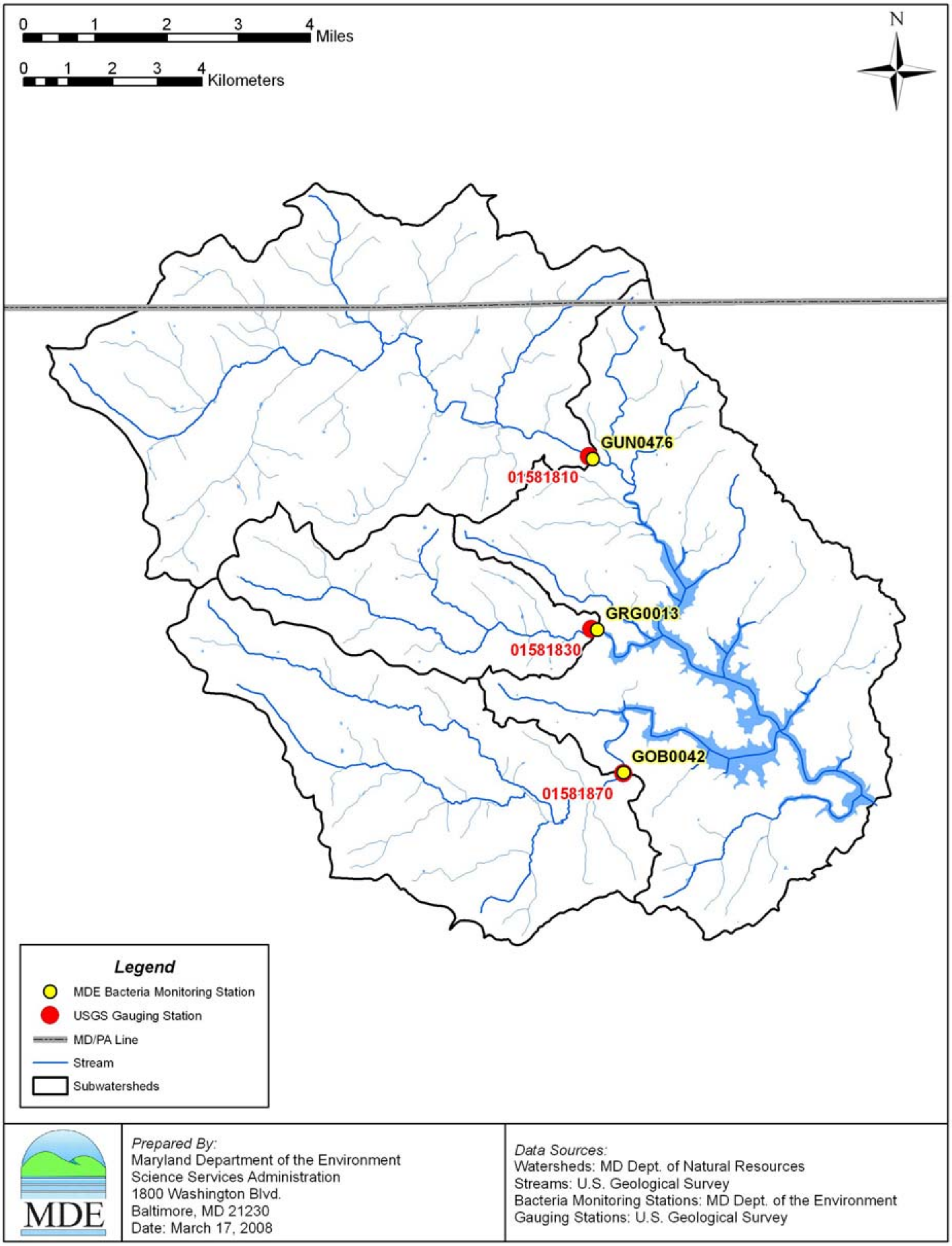


Figure 2.2.1: Monitoring Stations and Subwatersheds in the MD 8-digit Prettyboy Reservoir Watershed

2.3 Water Quality Impairment

Designated Uses and Water Quality Standard

The Maryland water quality standards Surface Water Use Designation for Prettyboy Reservoir and its tributaries is Use III-P (Nontidal Cold Water and Public Water Supply). (COMAR 26.08.02.08J) The Prettyboy Reservoir 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 GUN0476, which showed a geometric mean of 407 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 the Prettyboy Reservoir watershed 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 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 Prettyboy Reservoir 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.

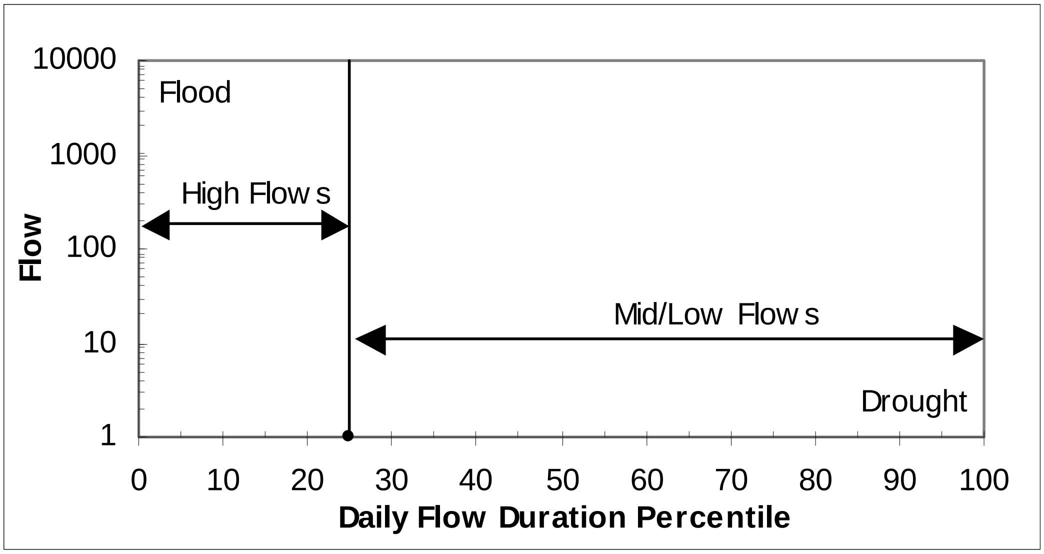


Figure 2.3.1: Conceptual Diagram of Flow Duration Zones

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 01582000 it was determined that the long-term average daily flow corresponds to a daily flow duration of 35.5%. Hence for this analysis it is defined that flows greater than the 35.5 percentile flow represent high flows, and flows lesser than the 35.5 percentile flow represent mid/low flows. A detailed method of how the flow strata were defined is presented in Appendix B.

Factors for estimating a steady-state geometric mean are based on the frequency of each flow stratum. The weighting factor accounts for the proportion of time that each flow stratum represents. The weighting factors for an average hydrological year used in the Prettyboy Reservoir 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 Prettyboy Reservoir Watershed

Flow Duration Zone	Duration Interval	Weighting Factor
High Flows	0 – 35.5%	0.355
Mid/Low Flows	35.5 – 100%	0.645

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 Prettyboy Reservoir subwatersheds for the annual and seasonal (May 1st –September 30th) periods. For the seasonal period, insufficient samples fell in the high flow zone. As such, for the seasonal analysis, only the overall geometric mean for the period was applied. For the downstream subwatershed the average high and low flow geometric mean concentrations of the three upstream watersheds were applied to account for the unmonitored streams.

Table 2.3.3: Prettyboy Reservoir 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)
GUN0476 Gunpowder Falls	**High**	14	20	9,210	185	403
	Low	10	210	5,200	618	
GRG0013 Grave Run	**High**	14	20	4,880	97	101
	Low	10	10	460	104	
GOB0042 Georges Run	**High**	14	20	15,530	139	182
	Low	10	100	930	212	
Downstream Subwatershed	**High**	N/A			140	234
	Low				311	

Table 2.3.4: Prettyboy Reservoir Watershed Seasonal Period (May 1 - September 30) Steady-State Geometric Means per Subwatershed

Station / Tributary	Number of Samples	*E. coli* Minimum Concentration (MPN/100ml)	*E. coli* Maximum Concentration (MPN/100ml)	Seasonal Steady State Geometric Mean (MPN/100ml)
GUN0476 Gunpowder Falls	10	340	5,200	751
GRG0013 Grave Run	10	10	460	134
GOB0042 Georges Run	10	110	930	287
Downstream Subwatershed	N/A			391

2.4 Source Assessment

Nonpoint Source Assessment

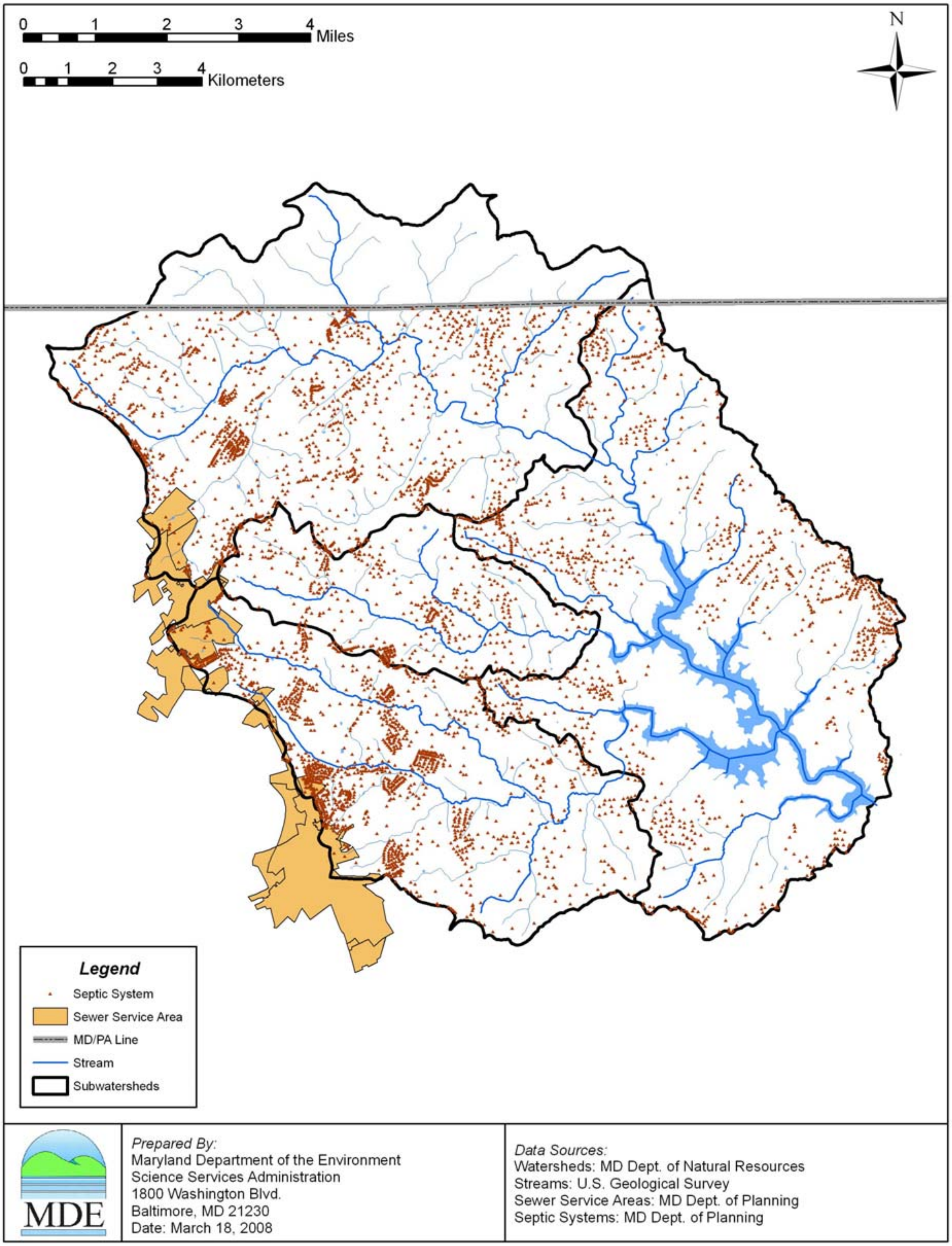
Nonpoint sources of fecal bacteria do not have one discharge point but occur over the entire length of a stream or waterbody. During rain events, surface runoff transports water and fecal bacteria over the land surface and discharges to the stream system. This transport is dictated by rainfall, soil 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 MD Prettyboy Reservoir watershed is serviced by both sewer systems and septic systems. Sewer systems are present in the towns of Manchester and Hampstead. Wastewater collected by the Manchester WWTP is treated and discharged into Georges Run. Wastewater collected by the Hampstead WWTP is treated and discharged in the Loch Raven Reservoir watershed.

On-site disposal (septic) systems are located throughout the Prettyboy Reservoir watershed. Table 2.4.1 presents the number of septic systems per subwatershed in MD. 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 Per Subwatershed in the MD 8-Digit Prettyboy Reservoir Watershed

Station / Subwatershed	Septic Systems
GUN0476 / Gunpowder Falls	1,300
GRG0013 / Grave Run	416
GOB0042 / Georges Run	1,391
Downstream Subwatershed	1,047
Total	**4,154**



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Date: March 18, 2008

Data Sources:
Watersheds: MD Dept. of Natural Resources
Streams: U.S. Geological Survey
Sewer Service Areas: MD Dept. of Planning
Septic Systems: MD Dept. of Planning

Figure 2.4.1: Sanitary Sewer Service Areas and Septic Locations in the MD 8-digit Prettyboy Reservoir 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 and other NPDES regulated stormwater discharges 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 Prettyboy Reservoir watershed is located in Baltimore and Carroll Counties, which both have individual Phase I NPDES MS4 permits. The municipalities of Hampstead and Manchester are also covered by general Phase II NPDES MS4 permits. Statements and information provided to MDE by the two Counties characterize the Prettyboy Reservoir watershed as essentially outside the reach of each County's stormwater system management plan (with the exception of the Hampstead and Manchester Phase II areas):

> "The Prettyboy Reservoir serves as a drinking water reservoir for the Baltimore Metropolitan region. Predominate land uses for the Baltimore County portion of the Prettyboy Reservoir watershed are agriculture and forest. As such, an NPDES urban stormwater management plan is not required. Current zoning and reforestation activities will maintain Prettyboy Reservoir watershed's undeveloped status." (Baltimore County, MD 2006)
>
> "The Prettyboy Reservoir serves as a drinking water reservoir for the Baltimore metropolitan region. The upper reach of the Gunpowder system that feeds the Prettyboy system is located in Carroll County. The predominate zoning and land use in the watershed is agriculture and as such, is not served by an organized storm sewer system. There is one area of urban development in the Prettyboy Watershed, represented by the Incorporated Towns of Manchester and Hampstead. Those two towns are located along MD Rt. 30 and are covered under the MS4 Phase II General Permit. As Rt. 30 essentially represents the western boundary of the watershed, land within the Town boundaries located east of Rt. 30 is in the Prettyboy watershed…however, the predominate use of land in the watershed is agriculture and is expected to remain so. As such, an NPDES urban stormwater management plan is not required." (Carroll County, MD 2008)

MDE's Water Management Administration (WMA) has confirmed these characterizations of the watershed. Carroll County's Department of Planning has provided MDE with data and GIS files delineating the reach of their Phase II stormwater areas in Manchester and Hampstead. Additionally, there are two industrial stormwater permits in the watershed outside of the towns' Phase II areas. Potential fecal bacteria loads from these facilities are considered to be insignificant relative to the overall load contribution and therefore are not included in the TMDL analysis.

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 not any SSOs reported to MDE between November 2003 and October 2004 in the Prettyboy Reservoir 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 is one active municipal NPDES permitted point source facility with permits regulating the discharge of fecal bacteria in the Prettyboy Reservoir watershed. This facility, Manchester WWTP, treats approximately 0.24 MGD (million gallons per day). Manchester WWTP only discharges to the stream during the months of December, January, and February. From March through November spray fields are utilized. There are no industrial facilities in the Prettyboy Reservoir watershed with NPDES permits regulating the discharge of fecal bacteria. Table 2.4.2 lists these facilities and Figure 2.4.2 shows their location in the watershed.

Table 2.4.2: NPDES Permitted Facilities Regulated for Fecal Bacteria Discharge in the MD 8-Digit Prettyboy Reservoir Watershed

Facility	NPDES Permit No.	County	Average Flow (MGD)	Fecal Coliform Concentration Annual AVG (MPN/100ml)	Fecal Coliform Load (Billion MPN/day)
Manchester WWTP	MD0022578	Carroll	0.244	4,420	40.9

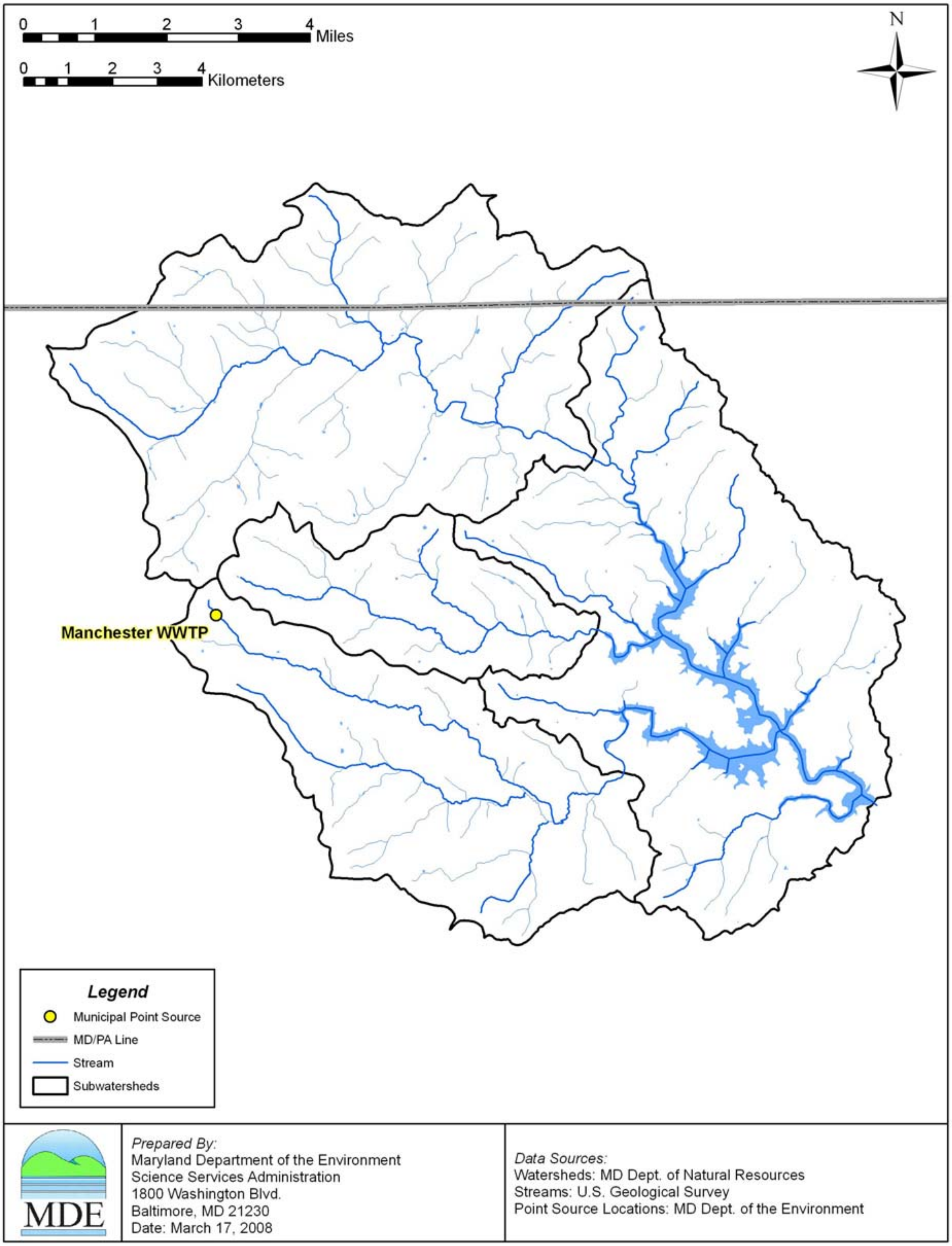

Figure 2.4.2: Permitted Point Sources Discharging Fecal Bacteria in the MD 8-digit Prettyboy Reservoir Watershed

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 three stations in the Prettyboy Reservoir 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. For the downstream subwatershed averages of the three upstream source percentages were used.

In the seasonal period, only two bacteria samples fell in the high flow category for all stations; therefore, a distribution by flow stratum was not calculated due to an insufficient number of samples. For the seasonal analysis, a distribution of all samples was calculated and applied.

Table 2.4.3: Distribution of Fecal Bacteria Source Loads in the Prettyboy Reservoir Watershed for the Average Annual Period

Station	Flow Stratum	% Domestic Animals	% Human	% Livestock	% Wildlife
GUN0476	**High**	17.0	30.1	32.7	20.2
	Low	23.3	24.2	28.6	23.9
	Weighted	21.1	26.3	30.1	22.6
GRG0013	**High**	15.8	22.1	35.6	26.4
	Low	32.9	15.0	22.4	29.7
	Weighted	26.8	17.6	27.1	28.6
GOB0042	**High**	14.6	22.5	43.4	19.5
	Low	28.9	10.8	32.0	28.3
	Weighted	23.8	14.9	36.1	25.2
Downstream Subwatershed	**High**	15.8	24.9	37.2	22.1
	Low	28.3	16.7	27.7	27.3
	Weighted	23.9	19.6	31.1	25.5

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

Station	% Domestic Animals	% Human	% Livestock	% Wildlife
GUN0476	19.3	26.8	29.1	24.8
GRG0013	30.7	20.0	23.8	25.5
GOB0042	25.9	14.4	33.9	25.9
Downstream Subwatershed	25.3	20.4	29.0	25.4

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 Prettyboy Reservoir 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 non point sources and natural background sources. A margin of safety (MOS) is also included and accounts for the uncertainty in the analytical procedures used for water quality modeling, 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.

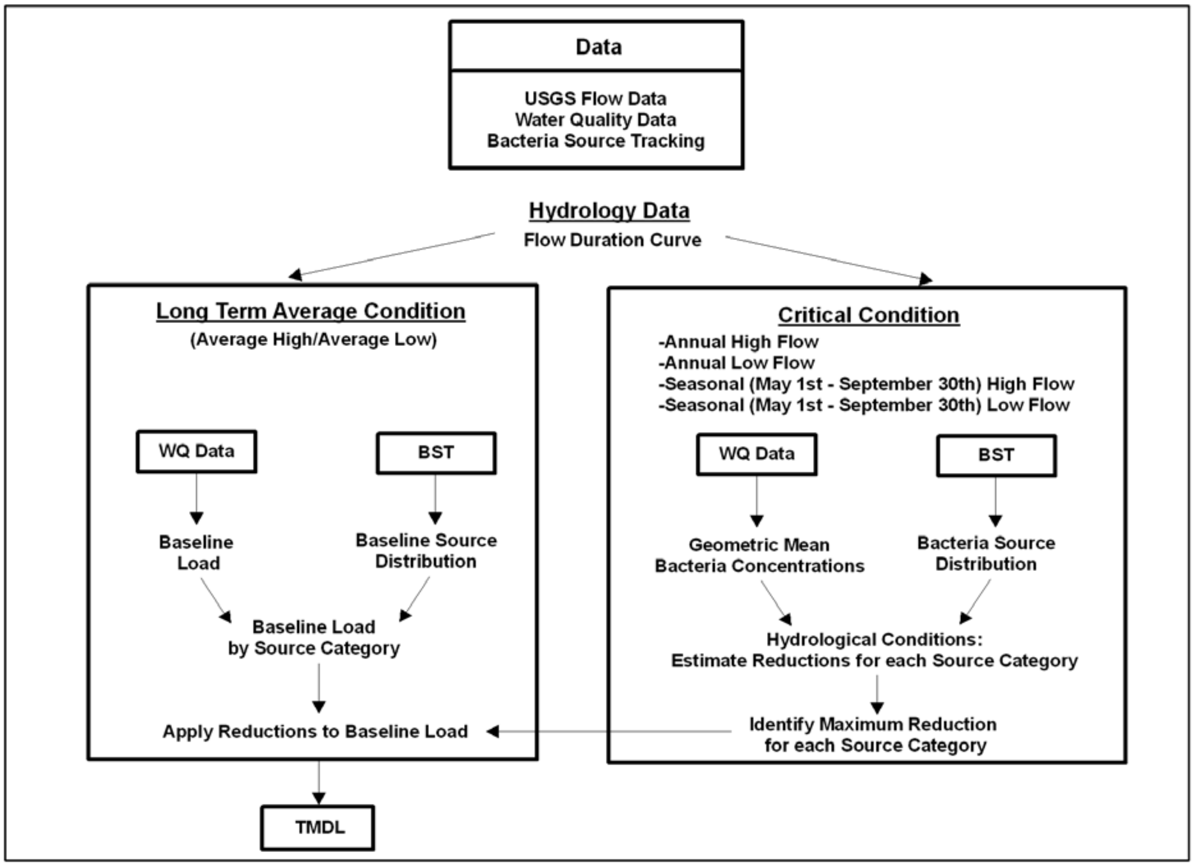

Figure 4.2.1: Diagram of the Non-tidal Bacteria TMDL Analysis Framework

4.3 Estimating Baseline Loads

Baseline loads are estimated for all subwatersheds of Prettyboy Reservoir, 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 Prettyboy Reservoir watershed, weighting factors of 0.355 for high flow and 0.645 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 are subdivided into unique watershed segments, thus allowing individual load and reduction targets to be determined for each. In the

Prettyboy Reservoir watershed the portion of the watershed downstream of the three monitoring stations, as listed in Table 4.3.1, is referred to as the Downstream Subwatershed. This identification represents only the area and load downstream of the three stations.

Table 4.3.1: Subdivided Watersheds in the Prettyboy Reservoir Watershed

Subwatershed	Upstream Station(s)
Downstream Subwatershed	GUN0476, GRG0013, GOB0042

Bacteria loads from this subwatershed are joined by loads from the upstream subwatersheds to result in the concentration that would be measured downstream. However, for the purposes of this TMDL, the downstream bacteria concentration is assigned as the average of the three upstream concentrations and is assumed to be representative of the downstream subwatershed. The bacteria source distribution for the downstream subwatershed is also assigned as the average of the BST analysis results of the three upstream 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		Low Flow		Baseline *E. coli* Load (Billion MPN/year)
		Average Flow (cfs)	*E. coli* Concentration. (MPN/100ml)	Average Flow (cfs)	*E. coli* Concentration (MPN/100ml)	
GUN0476[1]	27.4	64.5	185	19.8	618	295,349
GRG0013	7.6	18.8	97	6.5	104	32,293
GOB0042	15.8	37.0	139	12.3	212	168,437
Downstream Subwatershed[1]	29.0	69.2	140	22.7	311	249,359

[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 668,302 billion MPN *E.coli*/year. The total baseline load for the portions of subwatersheds located in PA is 77,136 billion MPN E. coli/year.

Table 4.3.3: Prettyboy Reservoir Baseline Loads Summary

MD 8-Digit Prettyboy Reservoir Fecal Bacteria Baseline Loads (Billion MPN *E. coli*/year)								
Total Baseline Load	=	**Upstream Baseline Load**[1]	+	**MD 8-digit Prettyboy Reservoir Baseline Load Contribution**				
		BL_{PA}		**Nonpoint Source BL_{PR}**	+	**NPDES Stormwater BL_{PR}**	+	**WWTP BL_{PR}**
745,438	=	77,136	+	625,714	+	41,718	+	870

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

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 35.5% high flow and 64.5% 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 35.5% and a low flow condition as occurring when the daily flow duration interval is greater than 35.5%, 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 01582000, critical condition and seasonality has been determined by assessing various hydrological conditions to account for seasonal and annual averaging periods. The four conditions listed in Table 4.4.1 were used to account for the critical condition.

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

Hydrological Condition		Averaging Period	Water Quality Data Used	Fraction High Flow	Fraction Low Flow	Condition Period
Annual	Average	365 days	All	0.355	0.645	Long-Term Average
	Wet (High Flow)	365 days	All	0.951	0.049	Aug. 2003 – Aug. 2004
	Dry (Low Flow)	365 days	All	0.016	0.984	Aug. 2001 – Aug. 2002
Seasonal	Average	May 1st – Sept. 30th	May 1st – Sept. 30th	N/A	N/A	Long-Term Average For May – Sept. Period

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

The bacteria monitoring data for all stations located in the Prettyboy Reservoir watershed cover a sufficient temporal span (at least one year) to estimate annual conditions. However, sufficient data were not available for the seasonal period to consider high flow and low flow conditions. Since only two samples were taken during high flow conditions, a geometric mean cannot be established for that condition. Therefore an average geometric mean and average flow were used for the seasonal analysis.

The reductions of fecal bacteria required to meet water quality standards in each subwatershed of the Prettyboy Reservoir 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 %
GUN0476[1] Gunpowder Falls	Annual	Average	75.0	98.0	95.6	0.0
		Wet	13.8	95.0	25.8	0.0
		Dry	98.0	98.0	98.0	23.5
	Seasonal	Average	98.0	98.0	98.0	41.7
	Maximum Source Reduction		**98.0**	**98.0**	**98.0**	**41.7**
GRG0013 Grave Run	Annual	Average	0.0	0.0	0.0	0.0
		Wet	0.0	0.0	0.0	0.0
		Dry	0.0	0.0	0.0	0.0
	Seasonal	Average	0.0	54.4	0.0	0.0
	Maximum Source Reduction		**0.0**	**54.4**	**0.0**	**0.0**
GOB0042 Georges Run	Annual	Average	25.6	95.0	38.7	0.0
		Wet	0.0	70.1	0.0	0.0
		Dry	48.2	95.0	58.4	0.0
	Seasonal	Average	74.5	95.0	75.0	0.0
	Maximum Source Reduction		**74.5**	**95.0**	**75.0**	**0.0**
Downstream Subwatershed[1]	Annual	Average	47.2	95.0	61.4	0.0
		Wet	0.0	72.8	0.0	0.0
		Dry	80.1	98.0	79.2	0.0
	Seasonal	Average	84.5	98.0	96.8	0.0
	Maximum Source Reduction		**84.5**	**98.0**	**96.8**	**0.0**

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.

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)	
GUN0476[1]	21.1	62,256	26.3	77,633	30.1	88,783	22.6	66,677	295,349
GRG0013	26.8	8,659	17.6	5,669	27.1	8,740	28.6	9,225	32,293
GOB0042	23.8	40,088	14.9	25,164	36.1	60,726	25.2	42,459	168,437
Downstream Subwatershed[1]	23.9	59,590	19.6	48,856	31.1	77,450	25.5	63,463	249,359

[1] Subwatersheds partially located in Pennsylvania

First Scenario: Fecal Bacteria Practicable Reduction Targets

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

Table 4.6.2: Maximum Practicable Reduction Targets

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

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

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

[3] Agricultural BMP Descriptions as Defined for The Chesapeake Bay Program Watershed Model. Nutrient Subcommittee Agricultural Nutrient Reduction Workshop. EPA. 2004.

[4] Environmental Indicators and Shellfish Safety. 1994. Edited by Cameron, R., Mackeney and Merle D. Pierson, Chapman & Hall.

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

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

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

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:

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

In two of the subwatersheds, the constraints of this scenario could not be satisfied, indicating there was not a practicable solution. A summary of the first scenario analysis results is presented in Table 4.6.3.

Table 4.6.3: Practicable Reduction Scenario Results

Subwatershed	**Applied Reductions**				**Total Reduction %**	**Target Reduction %**
	Domestic %	**Human %**	**Livestock %**	**Wildlife %**		
GUN0476[1]	75.0	95.0	75.0	0.0	63.3	85.3
GRG0013	0.0	54.4	0.0	0.0	9.5	9.5
GOB0042	74.5	95.0	75.0	0.0	59.0	59.0
Downstream Subwatershed[1]	75.0	95.0	75.0	0.0	59.8	69.5

[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, two of the four subwatersheds could not 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:

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

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 %		
GUN0476[1]	98.0	98.0	98.0	41.7	85.3	85.3
GRG0013	0.0	54.4	0.0	0.0	9.5	9.5
GOB0042	74.5	95.0	75.0	0.0	59.0	59.0
Downstream Subwatershed[1]	84.5	98.0	96.8	0.0	69.5	69.5

[1] Subwatersheds partially located in Pennsylvania

4.7 TMDL Loading Caps

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

The TMDL loading caps are provided in billion MPN *E. coli*/day. These loading caps are for the three subwatersheds located upstream of their respective monitoring stations (GUN0476, GRG0013, and GOB0042) as well as the one downstream watershed. Loading caps for subwatersheds of Prettyboy Reservoir partially located in PA were included in the TMDL scenario. A TMDL summary for the entire Prettyboy Reservoir 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 Prettyboy Reservoir 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**
GUN0476[1]	295,349	43,464	85.3
GRG0013	32,293	29,210	9.5
GOB0042	168,437	69,103	59.0
Downstream Subwatershed[1]	249,359	76,154	69.5
Total	**745,438**	**217,931**	**70.8**

[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)	
GUN0476[1]	2.9	1,245	3.6	1,553	4.1	1,776	89.5	38,890	43,464
GRG0013	29.6	8,659	8.9	2,586	29.9	8,740	31.6	9,225	29,210
GOB0042	14.8	10,205	1.8	1,258	22.0	15,181	61.4	42,459	69,103
Downstream Subwatershed[1]	12.1	9,236	1.3	977	3.3	2,478	83.3	63,463	76,154

[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 Prettyboy Reservoir watershed 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 1991b); 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 Prettyboy Reservoir subwatersheds, including for computational purposes those partially located in PA, are shown in Table 4.7.3. The downstream subwatershed is assigned the average MDL of the three upstream subwatersheds.

Table 4.7.3: Prettyboy Reservoir Watershed Maximum Daily Loads Summary

Subwatershed	Flow Stratum	Maximum Daily Load (Billion *E. coli* MPN/day)	
		by Stratum	Weighted by Stratum
GUN0476[1]	High Low	2,749 697	1,425
GRG0013	High Low	2,032 363	955
GOB0042	High Low	7,272 168	2,690
Downstream Subwatershed[1]	High Low	4,018 409	1,690

[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 Prettyboy Reservoir watershed fecal bacteria TMDL is composed of the following components:

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

where,

LA_{PA} = Pennsylvania Load Allocation
LA_{PR} = MD Prettyboy Reservoir Watershed Load Allocation
WLA_{PR} = MD Prettyboy Reservoir Watershed Waste Load Allocation
MOS = Margin of Safety

The TMDL allocations for the MD 8-digit Prettyboy Reservoir basin include a load allocation (LA_{PR}) for certain nonpoint sources, and waste load allocations (WLA_{PR}) for point sources including WWTPs and NPDES-regulated stormwater discharges. The Stormwater (SW) WLA_{PR}

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_{PR} and to the $SW\text{-}WLA_{PR}$ and $WWTP\text{-}WLA_{PR}$ is provided in the subsections that follow.

In addition to these allocation categories for the MD 8-digit watershed, the Prettyboy Reservoir watershed 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 basin Prettyboy Reservoir, 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_{PR} (those nonpoint sources or portions thereof not transported and discharged by stormwater systems) and the WLA_{PR} (point sources including WWTPs, and NPDES regulated stormwater discharges). Only the final LA_{PR} or WLA_{PR} is reported in this TMDL.

Table 4.8.1: Potential Source Contributions for TMDL Allocation Categories in the MD 8-Digit Prettyboy Reservoir Watershed

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

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

$\underline{LA}_{PR}$

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. 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 typically assigned to the SW-WLA. For this TMDL, information provided by the two Counties identifies limited areas of the watershed that are subject to stormwater management controls. Therefore, in the Prettyboy Reservoir TMDL, the human nonpoint source load is distributed between the SW-WLA_{PR} and the LA on the basis of the delineation of these areas.

Livestock loads are all assigned to the LA_{PR}. Domestic animals (pets) loads are assigned to the LA in watersheds with no MS4s or other NPDES-regulated stormwater systems. Although the entire MD 8-digit Prettyboy Reservoir watershed lies within counties with Phase I NPDES MS4 permits, bacteria loads from domestic animal, human and wildlife sources are distributed between the SW-$WLA_{PR,}$ for areas delineated as subject to stormwater management, and the LA_{PR} for the remaining areas not served by stormwater systems.

$\underline{WLA}_{PR}$

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.

Information regarding the stormwater management status of the Prettyboy Reservoir watershed, provided to MDE by Baltimore and Carroll Counties, allowed for the determination of the SW-WLA_{PR} based on the spatial delineation of the extent of organized stormwater systems within each County's jurisdiction. In this case, bacteria loads from domestic animal sources and human nonpoint sources are distributed between the SW-WLA_{PR} and the LA_{PR} based on a ratio of the population in the areas under stormwater management to the population in remaining areas not served by organized stormwater systems. The bacteria load from wildlife sources is distributed between the SW-WLA_{PR} and the LA_{PR} based on a ratio of the per capita acreage in the areas under stormwater management to the per capita acreage in remaining areas not served by organized stormwater systems. This weighting allows for a greater domestic animal and human source allocation in areas more populated by humans, and a greater wildlife source allocation to areas less populated by humans. In watersheds with no existing NPDES-regulated stormwater permits, these loads will be included entirely in the LA. [Note: The human nonpoint source load in the SW-WLA is estimated by subtracting any loads allocated to WWTPs and CSOs, if present, from the total allowable (TMDL) human load. There is one municipal and no industrial wastewater treatment facilities with NPDES permits regulating the discharge of fecal bacteria in the Prettyboy Reservoir watershed. There are no NPDES CSO permits in the watershed.]

The MD portion of the Prettyboy Reservoir watershed lies within the jurisdictions of Baltimore County and Carroll County, which both have individual Phase I MS4 permits. The municipalities of Hampstead and Manchester in Carroll County are also covered by a general Phase II MS4 permit. Based on EPA's guidance and information made available to MDE by the two Counties, the SW-WLA_{PR} is presented as a combined load for each of the areas within the two Phase II jurisdictions that are subject to stormwater management, and includes any other NPDES regulated stormwater discharges within those areas that are permitted separately from the towns' MS4 permits. The remaining areas of the watershed are not within the reach of the Counties' organized stormwater systems and therefore not subject to WLA assignment. [See Section 2.4, Source Assessment, for the Counties' stormwater management assessments of the Prettyboy watershed (pp. 22-23).] The SW-WLA_{PR} 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_{PR}, provided the revisions are consistent with achieving water quality standards. Upon approval of the TMDL, "NPDES-regulated municipal stormwater and small construction stormwater discharges effluent limits should be expressed as BMPs or other similar requirements, rather than as numeric effluent limits" (US EPA 2002a). The SW-WLA_{PR} distribution in Baltimore County and Carroll County is presented in Table 4.8.2.

Table 4.8.2: Annual Average Stormwater Allocations in MD

Subwatershed	Baltimore County SW-WLA$_{PR}$	Carroll County Phase II SW-WLA$_{PR}$	
		Hampstead	Manchester
	(Billion MPN *E. coli*/year)		
GUN0476[1]	N/A	0	328
GRG0013	N/A	0	547
GOB0042	N/A	2,311	2,464
Downstream Subwatershed[1]	N/A	0	0

[1] MD portion of the subwatershed only.

Municipal and Industrial WWTPs

As explained in the source assessment section above, there is one NPDES permitted point source facility with a permit regulating the discharge of fecal bacteria in the Prettyboy Reservoir watershed. This facility discharges into the subwatershed of GOB0042 (Georges Run). The WLA for the 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 WWTP are allocated as the WWTP-WLA.

4.9 Summary

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

Table 4.9.1: MD 8-Digit Prettyboy Reservoir Watershed Annual Average TMDL

Subwatershed	Total Allocation	LA_{PR}	$SW\text{-}WLA_{PR}$	$WWTP\text{-}WLA_{PR}$
	(Billion MPN *E. coli* /year)			
GUN0476[1]	32,246	31,918	328	0
GRG0013	29,210	28,663	547	0
GOB0042	69,103	63,458	4,775	870
Downstream Subwatershed[1]	75,878	75,878	0	0
MD Total	206,437	199,917	5,650	870
PA Upstream Load	11,494			
TMDL[2]	**217,931**			

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

Table 4.9.2: MD 8-Digit Prettyboy Reservoir Watershed Maximum Daily Loads

Subwatershed	Total Allocation	LA_{PR}	$SW\text{-}WLA_{PR}$	$WWTP\text{-}WLA_{PR}$
	(Billion MPN *E. coli* /day)			
GUN0476[1]	1,057	1,046	11	0
GRG0013	955	937	18	0
GOB0042	2,690	2,497	186	7
Downstream Subwatershed[1]	1,684	1,684	0	0
MD Total	6,386	6,164	215	7
PA Upstream Load	374			
TMDL[2]	**6,760**			

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

The long-term annual average fecal bacteria TMDL summary for the MD 8-digit Prettyboy Reservoir 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 8-digit Prettyboy Reservoir watershed. Although reported here as a single value, it may include both point and nonpoint sources.

Table 4.9.3: MD 8-Digit Prettyboy Reservoir Watershed Annual Average TMDL Summary

(Billion MPN *E. coli*/year)										
TMDL	=	**LA**			+	**WLA**			+	**MOS**
		LA$_{PA}$[1]	+	**LA$_{PR}$**		**SW WLA$_{PR}$**	+	**WWTP WLA$_{PR}$**		
217,931	=	11,494	+	199,917	+	5,650	+	870	+	Incorporated

Upstream Load Allocation

MD 8-digit Prettyboy Reservoir TMDL Contribution (206,437)

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

Table 4.9.4: MD 8-Digit Prettyboy Reservoir Watershed MDL Summary

(Billion MPN *E. coli*/day)										
MDL	=	**LA**			+	**WLA**			+	**MOS**
		LA$_{PA}$[1]	+	**LA$_{PR}$**		**SW WLA$_{PR}$**	+	**WWTP WLA$_{PR}$**		
6,760	=	374	+	6,164	+	215	+	7	+	Incorporated

Upstream MDL

MD 8-digit Prettyboy Reservoir MDL Contribution (6,386)

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 Prettyboy Reservoir subwatersheds, water quality standards cannot be achieved with the maximum practicable reduction rates specified in Table 4.6.3. The TMDLs shown in Tables 4.9.1 and 4.9.2 represent reductions from current bacteria loadings that are beyond practical reductions. In cases where such high reductions are required to meet standards, it is expected that the first stage of implementation will be to carry out the MPR scenario.

5.0 ASSURANCE OF IMPLEMENTATION

Section 303(d) of the Clean Water Act and current EPA regulations require reasonable assurance that the TMDL load and wasteload allocations can and will be implemented. In the Prettyboy Reservoir watershed, the TMDL analysis indicates that, for two of the four 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. The tributaries of Prettyboy Reservoir may not be able to attain water quality standards. The fecal bacteria load reductions required to meet water quality criteria in two of the four Prettyboy Reservoir subwatersheds 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 fecal bacteria loads that contribute to the MD 8-digit Prettyboy Reservoir watershed 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 EPA to ensure that the Upstream Load Allocations presented in this document are achieved to meet Maryland's downstream water quality standards.

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 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 an April 3, 2008 MDE mailing of a notice of intent to develop a fecal bacteria TMDL for the Prettyboy Reservoir basin. The notice letters provided MDE contact information and offered upon request an informational briefing on the proposed TMDL. MDE received requests for a briefing from Carroll County's Health Department and Department of Planning, as well as from Mr. Gould Charshee of the Baltimore Metropolitan Council's Reservoir Technical Group (RTG). An informational briefing was provided to the RTG on July 10, 2008 and notification letters announcing availability of the draft TMDL for public review provided information on the briefing, noting that it was open to all interested parties. Another briefing was provided to officials of the Carroll County government on July 17, 2008.

A public notice of intent to establish the Prettyboy Reservoir fecal bacteria TMDL, announcing the opening and closing dates of the formal 30-day Public Comment Period, was published in The Carroll County Times and the Baltimore County newspaper, The Jeffersonian. The notice was also sent to MDE's stakeholder distribution list for the Liberty Reservoir 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 documents, which were placed in identified public libraries located in each of the two counties that share the watershed. The 30-day 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.

REFERENCES

Baltimore County, MD. 2006. NPDES - Municipal Stormwater Discharge Permit, 2006 Annual Report. Department of Environmental Protection and Resource Management. June 15, 2006. Towson, MD.

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

Carroll County, MD. 2008. NPDES - Municipal Stormwater Discharge Permit. 2008 Annual Report (Draft). Office of Environmental Compliance, Department of Planning. June 16, 2008. Westminster, MD.

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

Code of Maryland Regulations, 26.08.02.03-3, and 26.08.02.08. Website http://www.dsd.state.md.us/comar, last visited 03/10/08.

Code of Maryland Regulations, 26.08.10. Website http://www.dsd.state.md.us/comar, last visited 07/29/06.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

————. 1986. Ambient Water Quality Criteria for Bacteria-1986. EPA-440/5-84-002.

————. 1991a. Guidance for Water Quality-Based Decisions: The TMDL Process. EPA 440/4-91-001.

————. 1991b. Technical Support Document for Water Quality-Based Toxics Control (1991 TSD). Washington, D.C.

————. 1999. Preliminary Data Summary of Urban Storm Water Best Management Practices. EPA-821-R-99-012.

————. 2002a. Establishing Total Maximum Daily Load (TMDL) Wasteload Allocations (WLAs) for Storm Water Sources and NPDES Permit Requirements Based on Those WLAs. November 22, 2002 U.S. EPA Memorandum.

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

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

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

————. 2006a. Establishing TMDL “Daily” Loads in Light of the Decision by the U.S. Court of Appeals for the D.C. Circuit in *Friends of the Earth, Inc. v. EPA, et al.*, No. 05-5015, (April 25, 2006) and Implications for NPDES Permits. Memorandum from Benjamin Grumbles, Assistant Administrator. Office of Water, Washington, D.C. November 15, 2006.

————. 2006b. Approaches For Developing a Daily Load Expression for TMDLs Computed for Longer Term Averages. Draft Guidance Document. Office of Water. Washington, D.C. October 2006.

————. 2007. An Approach for Using Load Duration Curves in the Development of TMDLs. EPA 841-B-07-006.

U.S. Geological Survey. 1996. HYSEP: A Computer Program for Streamflow Hydrograph Separation and Analysis. USGS Water-Resource Investigations Report 96-4040. Website http://pa.water.usgs.gov/reports/wrir96-4040.pdf, last visited 08/16/07.

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

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

Appendix A – Bacteria Data

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

Station	Date	Daily flow frequency	*E. coli* Concentration (MPN/100ml)
GOB0042	11/05/2003	13.8119	130
	11/19/2003	1.8472	70
	12/03/2003	18.3459	100
	12/17/2003	1.5113	15530
	01/05/2004	8.5642	20
	01/20/2004	18.3459	110
	02/02/2004	12.5525	90
	02/17/2004	14.8615	200
	03/01/2004	18.3459	150
	03/15/2004	35.1385	20
	04/05/2004	16.4148	70
	04/19/2004	24.7271	20
	05/10/2004	39.1688	130
	05/24/2004	44.5424	110
	06/07/2004	18.3459	480
	06/21/2004	39.1688	310
	07/06/2004	52.7708	930
	07/19/2004	44.5424	260
	08/09/2004	44.5424	140
	08/23/2004	52.7708	210
	09/07/2004	60.8312	300
	09/20/2004	35.1385	850
	10/04/2004	49.0764	190
	10/18/2004	52.7708	100

Station	**Date**	**Daily flow frequency**	***E. coli* Concentration (MPN/100ml)**
GRG0013	11/05/2003	15.7549	40
	11/19/2003	1.5682	60
	12/03/2003	18.8913	120
	12/17/2003	1.1306	4880
	01/05/2004	9.7374	40
	01/20/2004	23.4136	180
	02/02/2004	29.1758	40
	02/17/2004	29.1758	50
	03/01/2004	29.1758	60
	03/15/2004	29.1758	20
	04/05/2004	13.2020	70
	04/19/2004	18.8913	40
	05/10/2004	36.3968	10
	05/24/2004	43.5449	160
	06/07/2004	11.3056	310
	06/21/2004	29.1758	290
	07/06/2004	45.5872	250
	07/19/2004	41.0649	200
	08/09/2004	40.2626	120
	08/23/2004	48.5777	160
	09/07/2004	60.6492	30
	09/20/2004	42.5602	460
	10/04/2004	44.8578	50
	10/18/2004	53.3187	140

Station	**Date**	**Daily flow frequency**	***E. coli* Concentration (MPN/100ml)**
GUN0476	11/05/2003	13.1770	260
	11/19/2003	1.7484	300
	12/03/2003	16.9723	160
	12/17/2003	1.1940	9210
	01/05/2004	9.9360	160
	01/20/2004	21.4925	160
	02/02/2004	17.9531	60
	02/17/2004	25.1599	90
	03/01/2004	23.5821	20
	03/15/2004	27.4627	70
	04/05/2004	15.6930	150
	04/19/2004	16.9723	50
	05/10/2004	35.6077	560
	05/24/2004	43.7953	1370
	06/07/2004	11.8977	860
	06/21/2004	21.4925	390
	07/06/2004	37.7825	5200
	07/19/2004	41.7484	590
	08/09/2004	61.4072	360
	08/23/2004	55.1812	470
	09/07/2004	71.0874	340
	09/20/2004	41.7484	1250
	10/04/2004	48.3582	210
	10/18/2004	55.1812	230

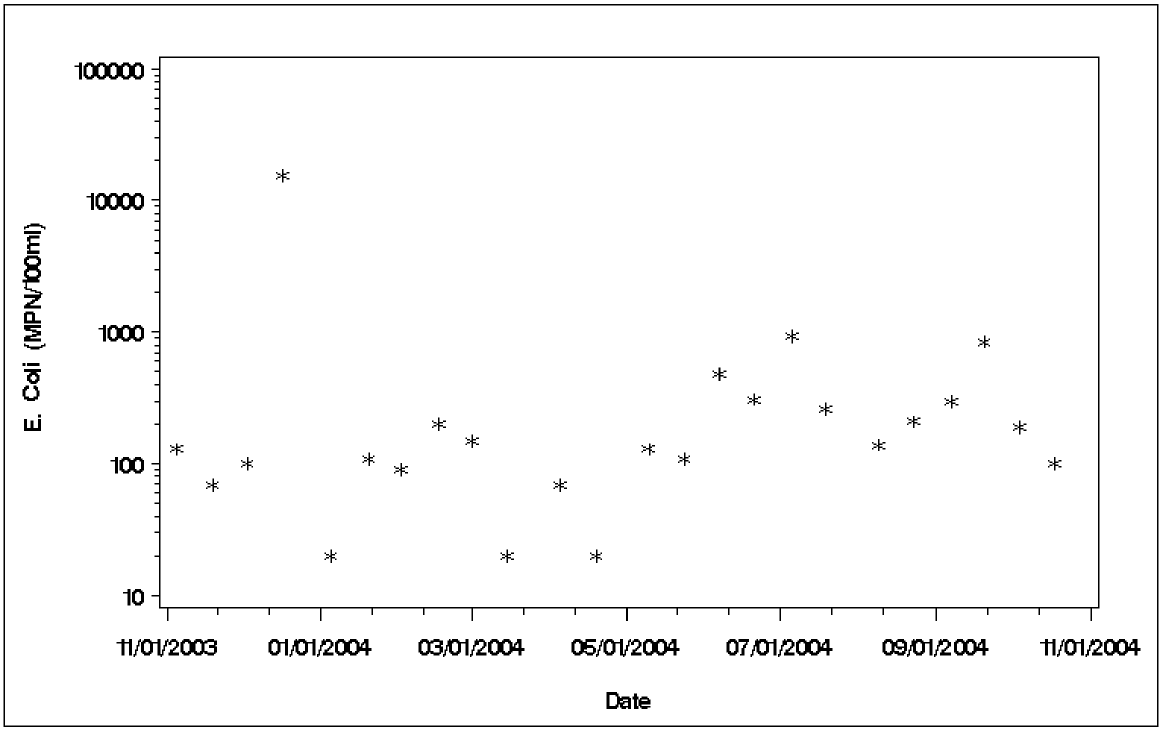

Figure A-1: *E. coli* Concentration vs. Time for MDE Monitoring Station GOB0042

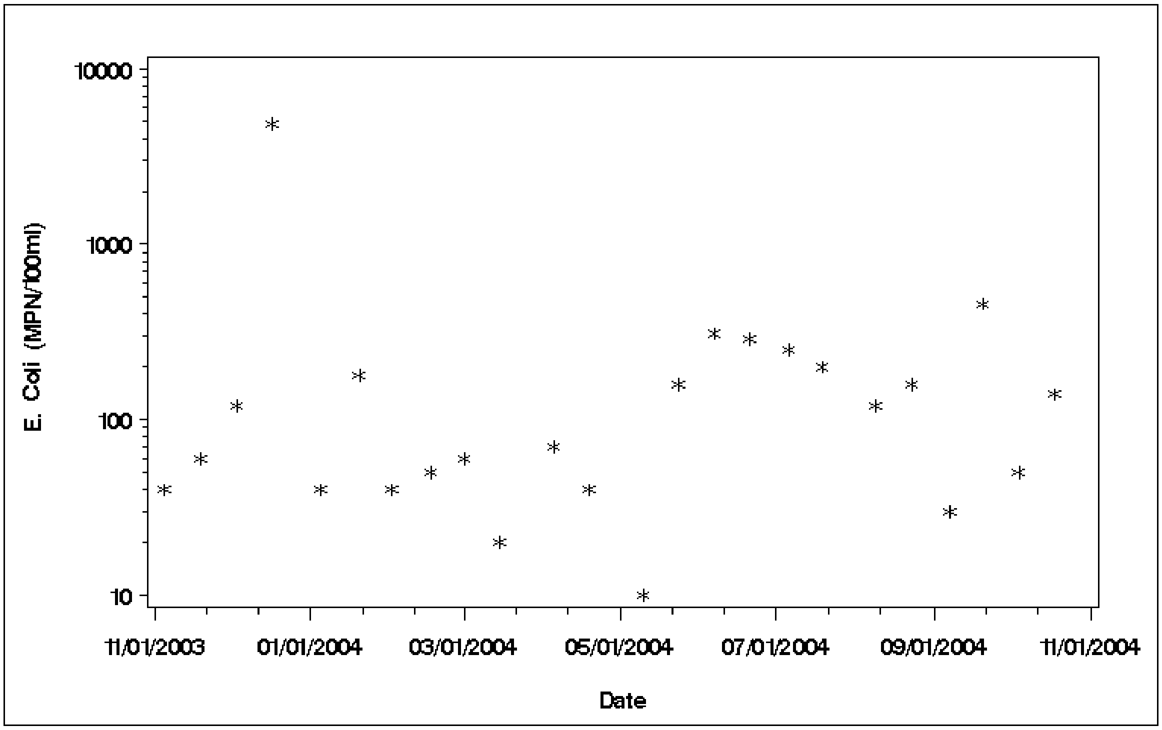

Figure A-2: *E. coli* Concentration vs. Time for MDE Monitoring Station GRG0013

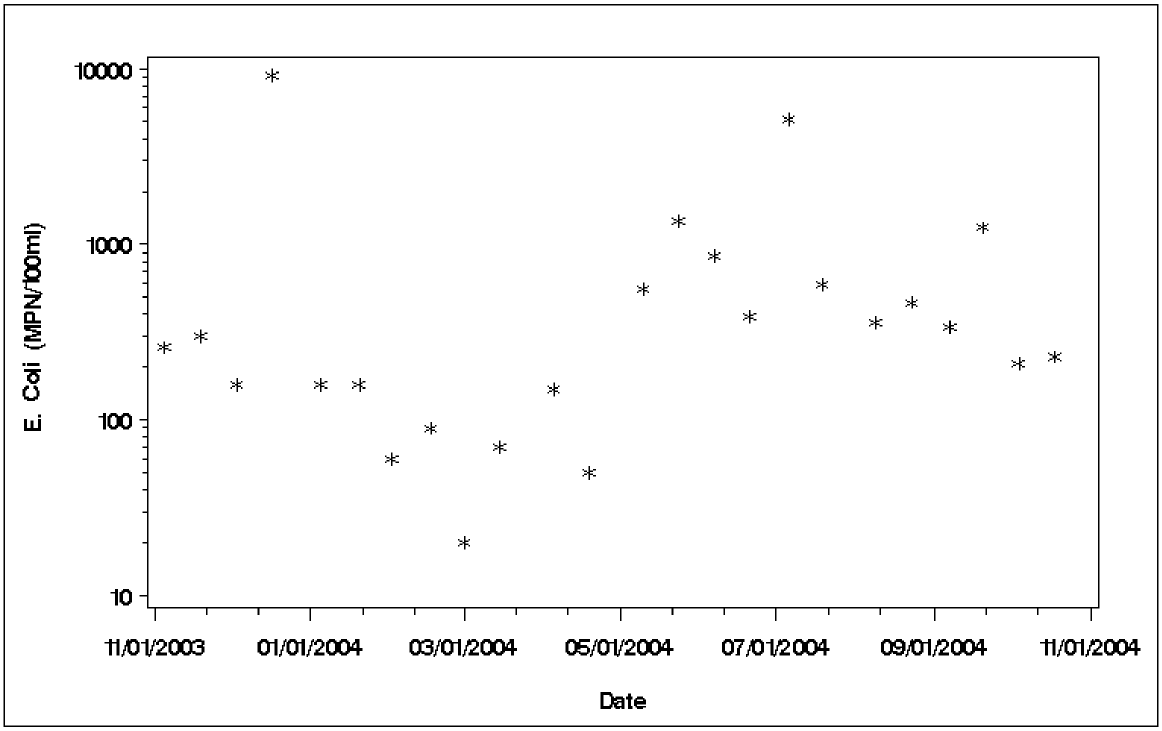

Figure A-3: ***E. coli*** **Concentration vs. Time for MDE Monitoring Station GUN0476**

Appendix B - Flow Duration Curve Analysis to Define Strata

The Prettyboy Reservoir 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

Of the three USGS gage stations in the Prettyboy Reservoir watershed, none of have sufficient historical data. The nearby station, station #01582000 located on Little Falls at Blue Mount, 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.

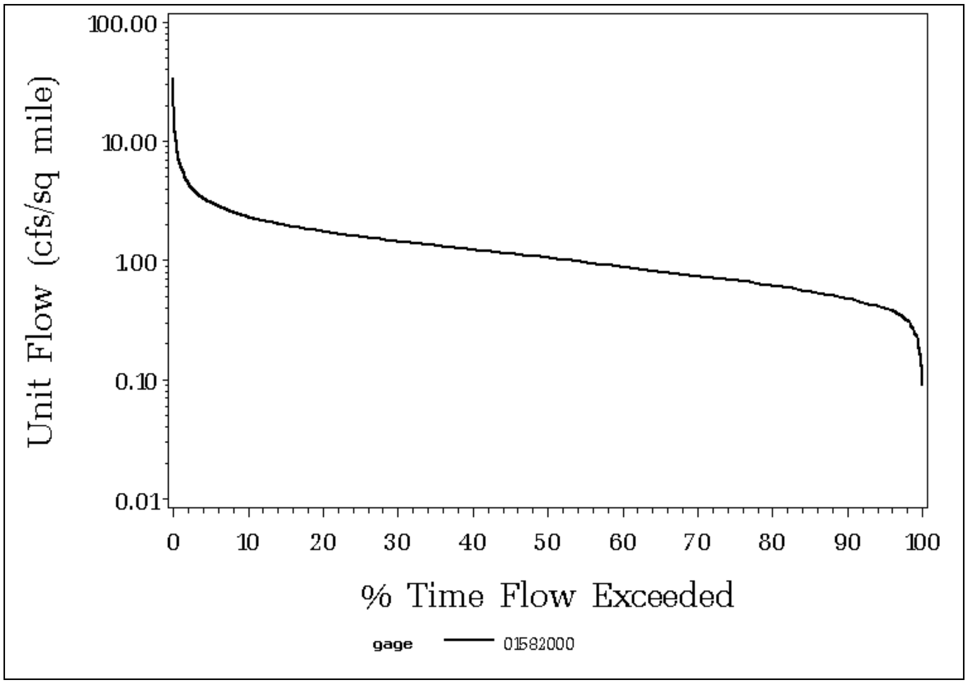

Figure B-1: Flow Duration Curve for USGS Gage 01582000

Based on the flow data from the Little Falls gage station the long-term average daily unit flow is 1.33 cfs/sq. mile, which corresponds to a flow frequency of 35.5%. 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 35.5 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 35.5% and a low flow condition will be defined as occurring when the daily flow duration percentile is greater than 35.5%. 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-7 show the Prettyboy Reservoir 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 Prettyboy Reservoir watershed, for the annual average flow condition, there are sufficient samples in both the high flow and low flow strata to estimate the geometric means. However, in the seasonal (May 1st – September 30th) flow condition, there are only two samples within the high flow strata; therefore, for this condition an average seasonal geometric mean will be calculated.

Weighting factors for estimating a weighted geometric mean are based on the frequency of each flow stratum during the averaging period. The weighting factors for the averaging periods and hydrological conditions are presented in Table B-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-7.

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	0.355	0.645	Long-Term Average
	Wet (High Flow)	365 days	All	0.951	0.049	Aug. 2003 – Aug. 2004
	Dry (Low Flow)	365 days	All	0.016	0.984	Aug. 2001 – Aug. 2002
Seasonal	Average	May 1st – Sept. 30th	May 1st – Sept. 30th	1.000		N/A

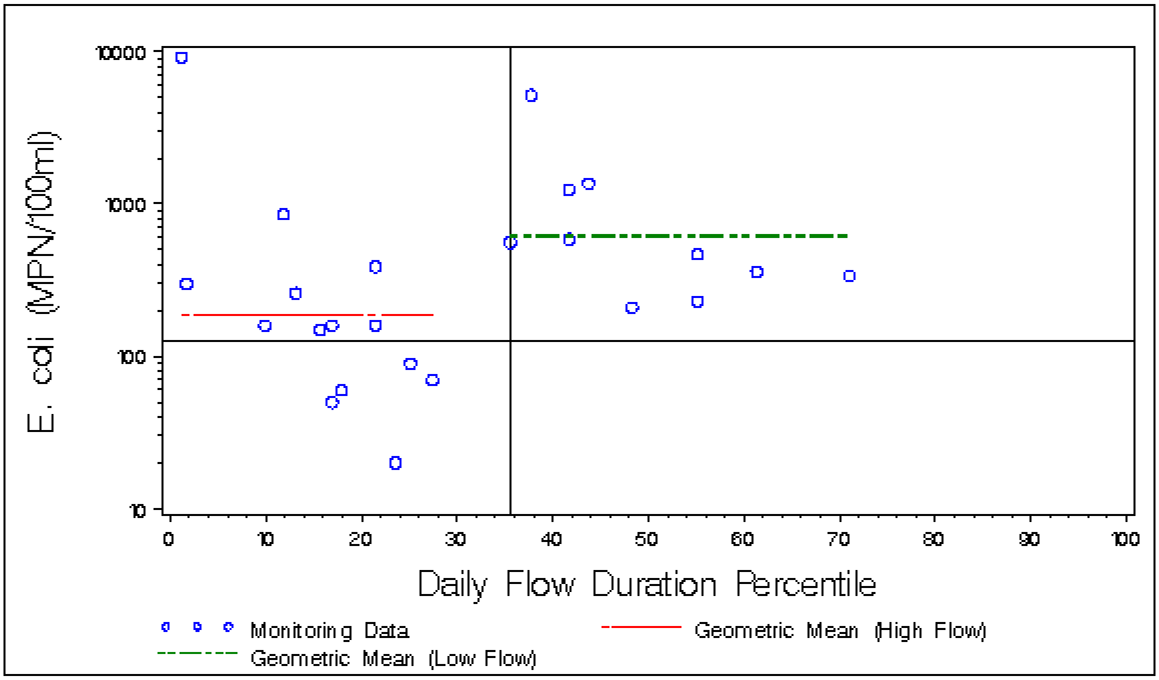

Figure B-2: ***E. coli*** **Concentration vs. Flow Duration for Monitoring Station GUN0476 (Annual Condition)**

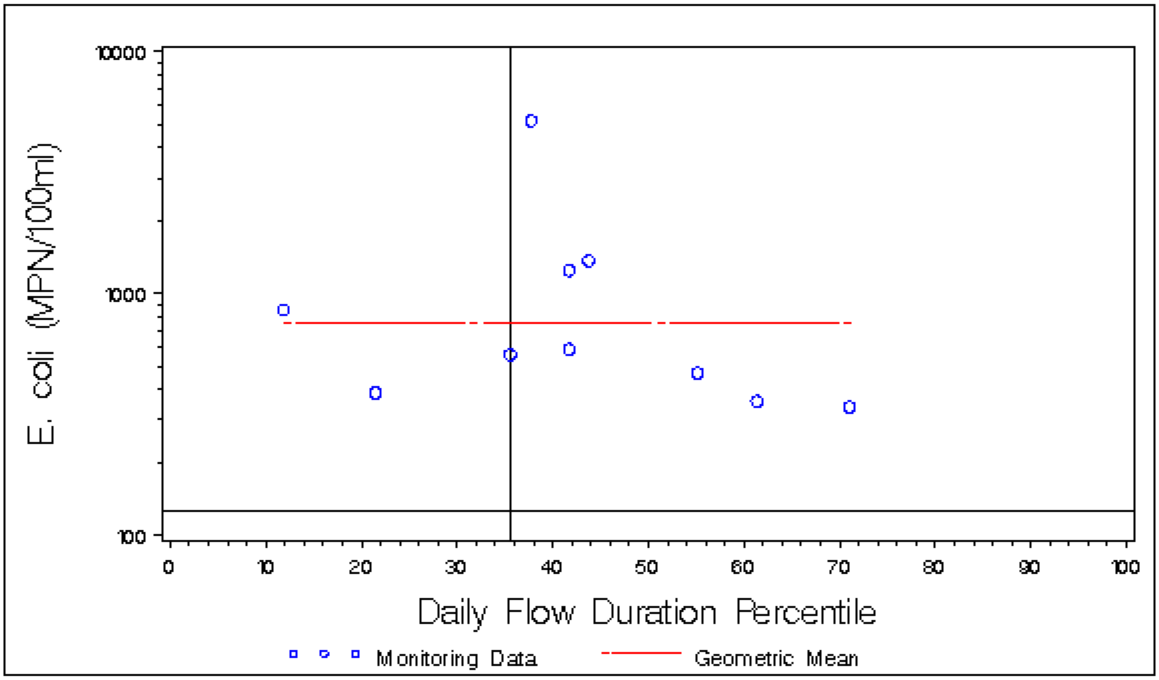

Figure B-3: ***E. coli*** **Concentration vs. Flow Duration for Monitoring Station GUN0476 (Seasonal Condition)**

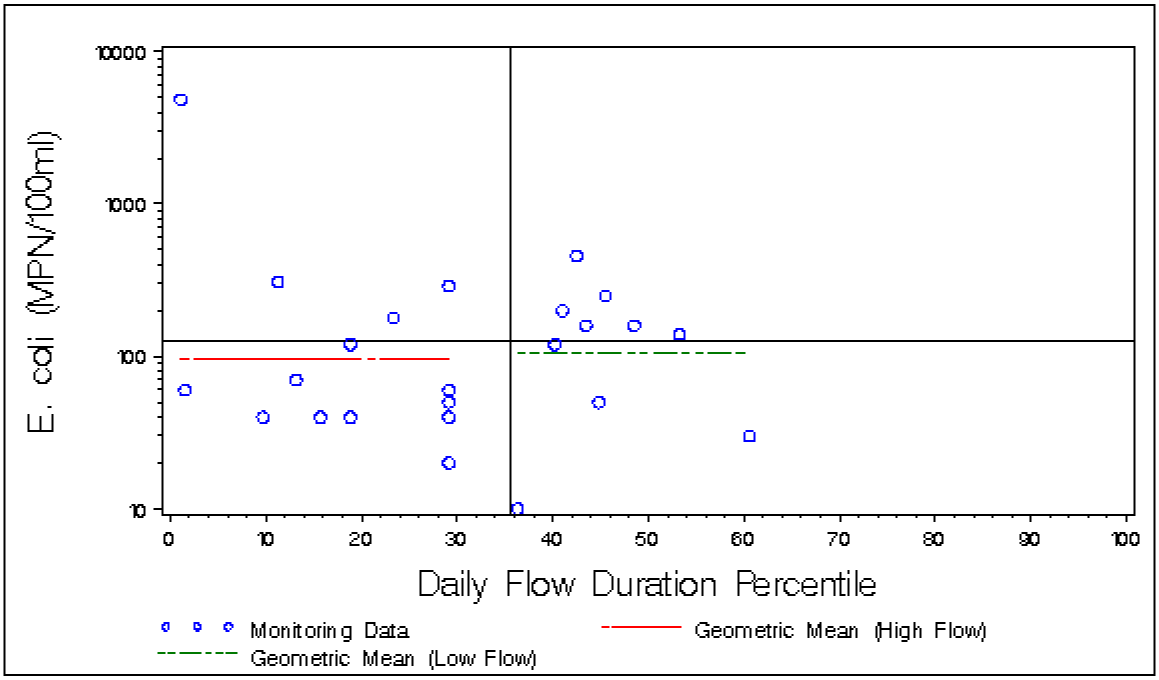

Figure B-4: ***E. coli*** **Concentration vs. Flow Duration for Monitoring Station GRG0013 (Annual Condition)**

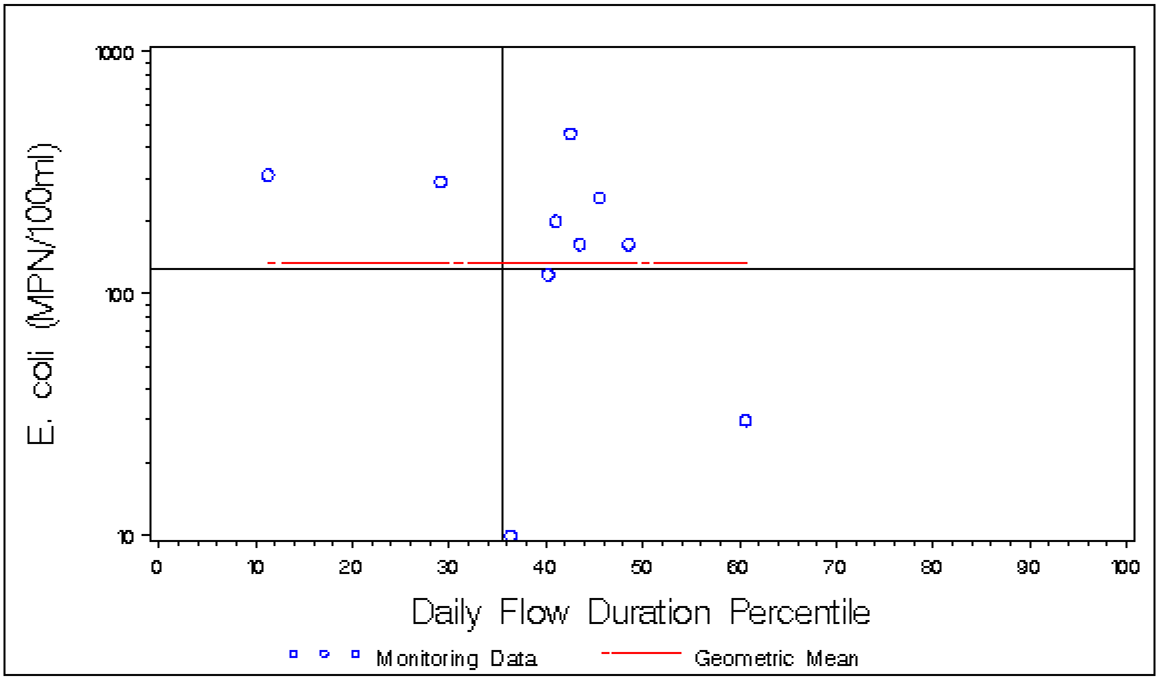

Figure B-5: ***E. coli*** **Concentration vs. Flow Duration for Monitoring Station GRG0013 (Seasonal Condition)**

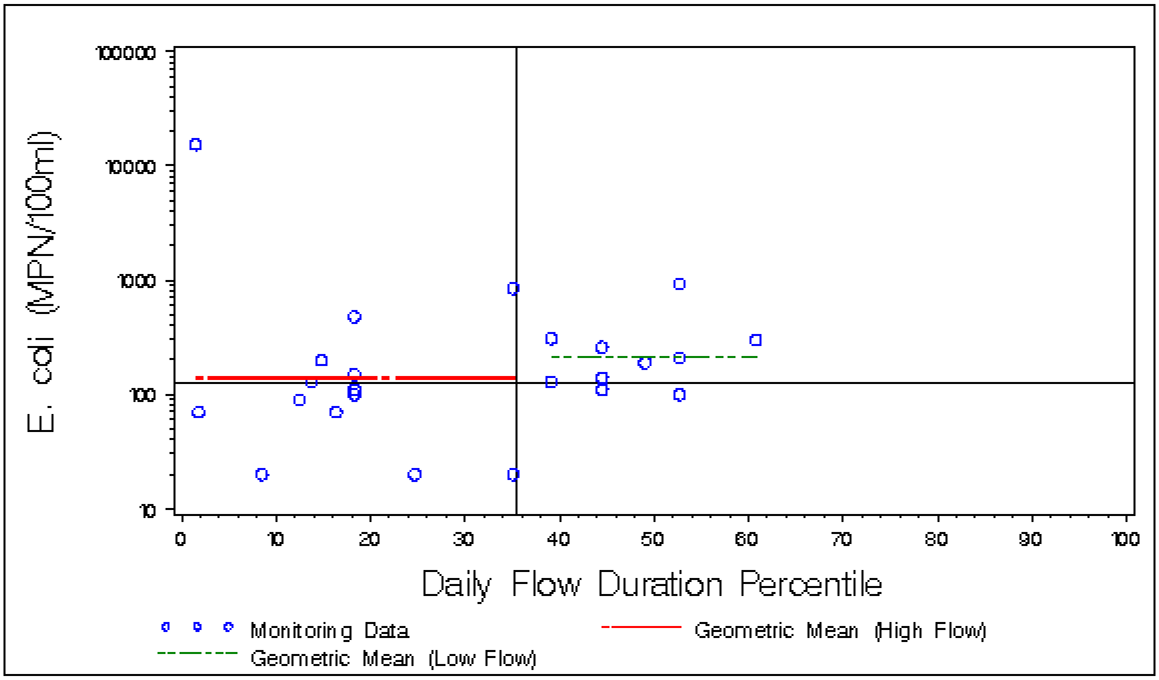

Figure B-6: *E. coli* Concentration vs. Flow Duration for Monitoring Station GOB0042 (Annual Condition)

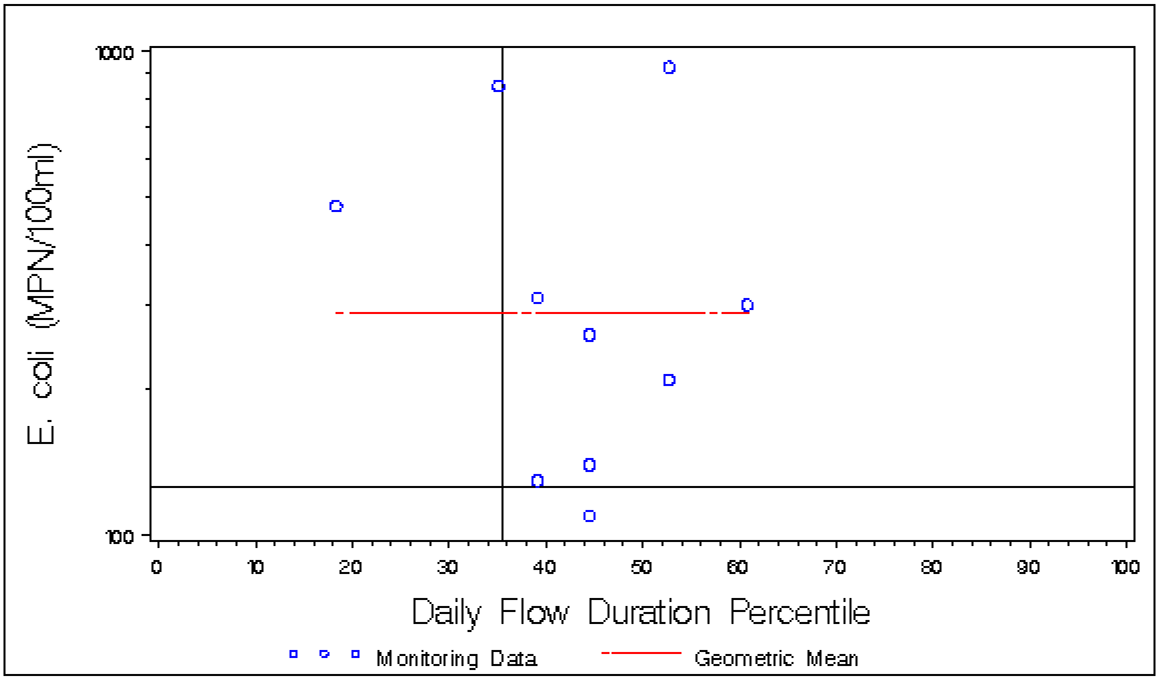

Figure B-7: *E. coli* Concentration vs. Flow Duration for Monitoring Station GOB0042 (Seasonal Condition)

Appendix C – BST Report

Maryland Department of the Environment

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

November 2005 – June 2007

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

Final Report
June 30, 2007

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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: Deep Creek, Dividing Creek, Little Youghiogheny River, Patapsco River, Prettyboy Reservoir, and the Youghiogheny River. Also included in the study were the following tidal shellfish harvesting areas: the Chester River, Corsica River, Herring and Turnville Creeks, Laws and Upper Thorofare, Manokin River, and the Pocomoke River watersheds. 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 Pocomoke 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° 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° 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, cow, goat, horse, dog, bear, beaver, deer, duck, fox, goose, heron, opossum, rabbit, raccoon, and squirrel). 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 the nontidal Little Youghiogheny River and the Youghiogheny River 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 the nontidal Patapsco River and Pretty Boy Reservoir Watersheds, with water isolate patterns of each compared to this combined library. For the tidal watersheds, no combined known-source libraries were used for any shellfish harvesting area; a known-source isolate library collected from each area was used for the particular watershed.

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.

Pretty Boy Reservoir Watershed ARA Results

Known-Source Library. A 615 known-source isolate library was constructed from sources in the Pretty Boy Reservoir Watershed (Table C-2a) and combined with the 501 known-source isolate library for the Patapsco River (Table C-2b), for a total of 1,116 known-source isolates in the PRE-PAT library (Table C-2c). The number of unique antibiotic resistance patterns was calculated, and the known sources in the combined library were grouped into four categories: human, livestock (cow, goat, horse), pet (dog), and wildlife (deer, fox, goose, heron, rabbit, squirrel) (Table C-2a, Table C-2b, Table C-2c). 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-2a: Category, total number, and number of unique patterns in the Prettyboy Reservoir known-source library.

Category	Potential Sources	Total Isolates	Unique Patterns
human	human	163	105
livestock	cow, goat, horse	221	66
pet	dog	64	31
wildlife	deer, fox, goose	167	56
Total		615	258

Table C-2b: Category, total number, and number of unique patterns in the Patapsco River known-source library.

Category	Potential Sources	Total Isolates	Unique Patterns
human	human	93	53
livestock	horse	58	16
pet	dog	86	47
wildlife	deer, fox, goose, heron, rabbit, squirrel	264	48
Total		501	164

Table C-2c: Category and total number in the combined Prettyboy Reservoir and Patapsco River known-source library.

Category	Potential Sources	Total Isolates
human	human	256
livestock	horse	279
Pet	dog	150
wildlife	deer, fox, goose, heron, rabbit, squirrel	431
Total		1,116

For Pretty Boy Reservoir Watershed, a cutoff probability of 0.50 (50%) was shown to yield an overall rate of correct classification of 82% (Table C-3). The resulting rates of correction classification (RCCs) for the four categories of sources in the Pretty Boy Reservoir portion of the library are shown in Table C-4.

Table C-3: Number of isolates not classified, percent unknown, and percent correct for eight (8) cutoff probabilities for Pretty Boy Reservoir known-source isolates using the combined Pretty Boy Reservoir – Patapsco know-source library.

Threshold	0	0.25	0.375	**0.5**	0.6	0.7	0.8	0.9
% correct	68.8%	68.8%	70.3%	**82.0%**	89.3%	90.7%	92.5%	96.7%
% unknown	0.0%	0.0%	2.4%	**32.4%**	49.9%	56.1%	61.1%	75.3%
# not classified	0	0	15	**199**	307	345	376	463

Figure C-1: Pretty Boy Reservoir Classification Model: Percent Correct versus Percent Unknown using the combined Pretty Boy Reservoir – Patapsco River library.

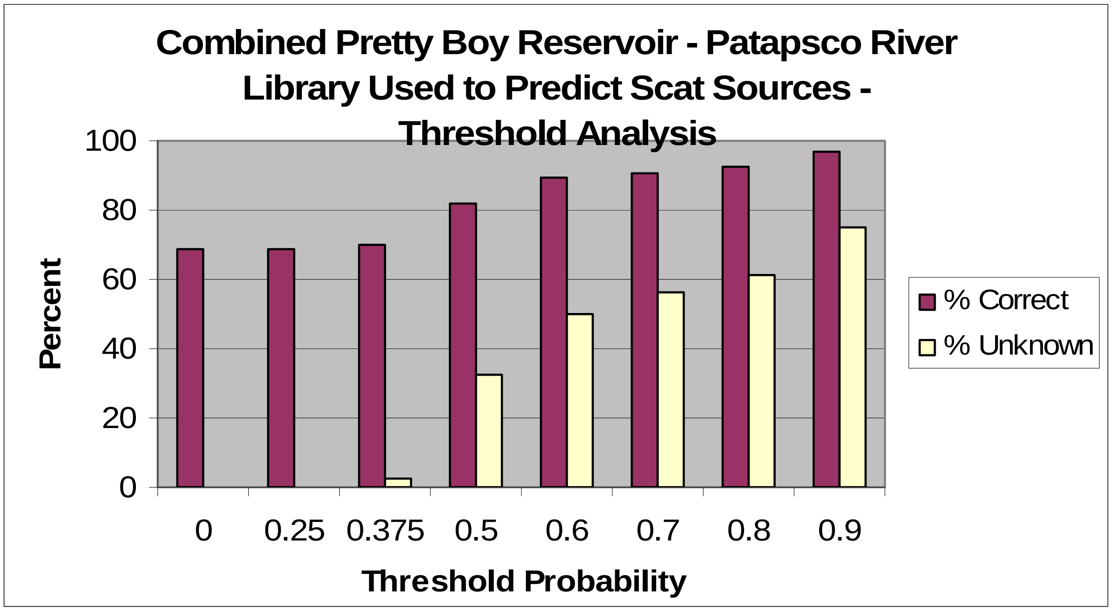


Table C-4: Actual species categories versus predicted categories, at 50% probability cutoff, with rates of correct classification (RCC) for each category.

	Predicted						
Actual	Human	Livestock	Pet	Wildlife	Unknown	Total	RCC*
human	122	11	6	3	21	163	85.9%
livestock	12	115	3	0	91	221	88.5%
pet	0	5	53	2	4	64	88.3%
wildlife	2	13	18	51	83	167	60.7%
Total	136	144	80	56	199	615	

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

Pretty Boy Reservoir Water Samples. Monthly monitoring from three (3) monitoring stations on Pretty Boy Reservoir was the source of water samples. The maximum number of *Enterococcus* isolates per water sample was 24, although the number of isolates that actually grew was sometimes less than 24. A total of 730 *Enterococcus* isolates were analyzed by statistical analysis. The BST results by species category, shown in Table C-5, indicate that 73% of the water isolates were able to be classified to a probable host source when using a 0.50 (50%) probability threshold.

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%.

Source	Count	Percent	Percent Without Unknowns
human	122	16.7%	23.1%
livestock	167	22.9%	31.6%
pet	210	28.8%	39.7%
wildlife	30	4.1%	5.7%
unknown	201	27.5%	
Total	730	100.0%	100.0%
% classified	72.5%		

*Percentages may not add up to 100% due to rounding.

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 at the Pretty Boy Reservoir's three (3) monitoring stations.

Station	Spring	Summer	Fall	Winter	Total
GOB0042	55	68	63	56	242
GRG0013	57	64	65	38	224
GUN0476	72	71	69	51	263
GRG0014	0	1	0	0	1
Total	184	204	197	145	730

Tables C-7 and C-8 on the following pages show the number and percent of the probable sources for each monitoring station by month.

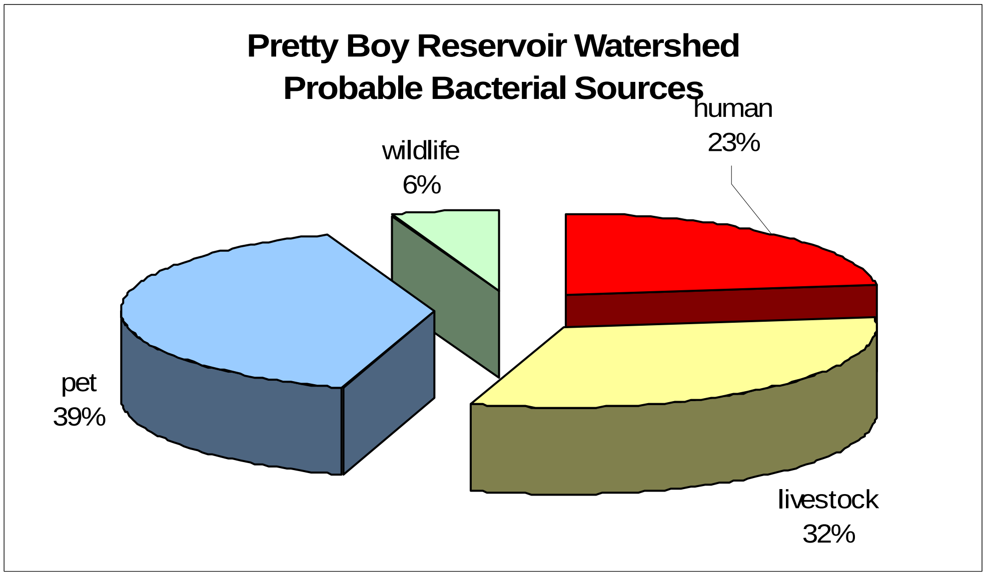
Table C-7: BST Analysis: Number of Isolates per Station per Date.

		Predicted Source					
Station	Date	Human	Livestock	Pet	Wildlife	Unknown	Total
GOB0042	11/19/03	2	11	6	0	4	23
GRG0013	11/19/03	0	2	8	3	10	23
GUN0476	11/19/03	6	5	5	1	5	22
GOB0042	12/03/03	1	11	5	2	4	23
GRG0013	12/03/03	1	2	5	2	8	18
GUN0476	12/03/03	5	5	4	1	8	23
GOB0042	01/05/04	3	1	2	2	7	15
GRG0013	01/05/04	0	2	3	0	2	7
GUN0476	01/05/04	9	4	7	0	4	24
GOB0042	02/17/04	1	14	1	0	2	18
GRG0013	02/17/04	5	14	0	0	5	24
GUN0476	02/17/04	5	11	5	0	3	24
GOB0042	03/01/04	8	8	5	1	1	23
GRG0013	03/01/04	2	2	0	0	3	7
GUN0476	03/01/04	0	0	2	0	1	3
GOB0042	04/05/04	6	8	4	0	3	21
GRG0013	04/05/04	8	6	3	3	4	24
GUN0476	04/05/04	9	7	4	1	3	24
GOB0042	05/10/04	1	2	0	0	7	10
GRG0013	05/10/04	5	0	4	1	0	10
GUN0476	05/10/04	7	4	12	0	1	24
GOB0042	06/07/04	5	4	6	0	9	24
GRG0013	06/07/04	6	2	7	1	8	24
GUN0476	06/07/04	7	5	3	1	8	24
GOB0042	07/06/04	0	4	16	0	0	20
GRG0013	07/06/04	0	0	20	0	4	24
GUN0476	07/06/04	2	3	5	2	11	23
GOB0042	08/09/04	1	2	9	0	12	24
GRG0013	08/09/04	2	2	10	0	6	20
GUN0476	08/09/04	10	2	4	1	7	24
GOB0042	09/07/04	0	6	7	0	11	24
GRG0013	09/07/04	0	6	1	0	13	20
GUN0476	09/07/04	2	4	9	1	8	24
GOB0042	10/04/04	0	0	8	1	8	17
GRG0013	10/04/04	0	0	9	6	9	24
GUN0476	10/04/04	3	8	11	0	2	24
Total		122	167	210	30	201	730

Table C-8: BST Analysis: Percent of Isolates per Station per Date.

		Predicted Source					
Station	Date	Human	Livestock	Pet	Wildlife	Unknown	Total
GOB0042	11/19/03	8.7%	47.8%	26.1%	0.0%	17.4%	100.0%
GRG0013	11/19/03	0.0%	8.7%	34.8%	13.0%	43.5%	100.0%
GUN0476	11/19/03	27.3%	22.7%	22.7%	4.5%	22.7%	100.0%
GOB0042	12/03/03	4.3%	47.8%	21.7%	8.7%	17.4%	100.0%
GRG0013	12/03/03	5.6%	11.1%	27.8%	11.1%	44.4%	100.0%
GUN0476	12/03/03	21.7%	21.7%	17.4%	4.3%	34.8%	100.0%
GOB0042	01/05/04	20.0%	6.7%	13.3%	13.3%	46.7%	100.0%
GRG0013	01/05/04	0.0%	28.6%	42.9%	0.0%	28.6%	100.0%
GUN0476	01/05/04	37.5%	16.7%	29.2%	0.0%	16.7%	100.0%
GOB0042	02/17/04	5.6%	77.8%	5.6%	0.0%	11.1%	100.0%
GRG0013	02/17/04	20.8%	58.3%	0.0%	0.0%	20.8%	100.0%
GUN0476	02/17/04	20.8%	45.8%	20.8%	0.0%	12.5%	100.0%
GOB0042	03/01/04	34.8%	34.8%	21.7%	4.3%	4.3%	100.0%
GRG0013	03/01/04	28.6%	28.6%	0.0%	0.0%	42.9%	100.0%
GUN0476	03/01/04	0.0%	0.0%	66.7%	0.0%	33.3%	100.0%
GOB0042	04/05/04	28.6%	38.1%	19.0%	0.0%	14.3%	100.0%
GRG0013	04/05/04	33.3%	25.0%	12.5%	12.5%	16.7%	100.0%
GUN0476	04/05/04	37.5%	29.2%	16.7%	4.2%	12.5%	100.0%
GOB0042	05/10/04	10.0%	20.0%	0.0%	0.0%	70.0%	100.0%
GRG0013	05/10/04	50.0%	0.0%	40.0%	10.0%	0.0%	100.0%
GUN0476	05/10/04	29.2%	16.7%	50.0%	0.0%	4.2%	100.0%
GOB0042	06/07/04	20.8%	16.7%	25.0%	0.0%	37.5%	100.0%
GRG0013	06/07/04	25.0%	8.3%	29.2%	4.2%	33.3%	100.0%
GUN0476	06/07/04	29.2%	20.8%	12.5%	4.2%	33.3%	100.0%
GOB0042	07/06/04	0.0%	20.0%	80.0%	0.0%	0.0%	100.0%
GRG0013	07/06/04	0.0%	0.0%	83.3%	0.0%	16.7%	100.0%
GUN0476	07/06/04	8.7%	13.0%	21.7%	8.7%	47.8%	100.0%
GOB0042	08/09/04	4.2%	8.3%	37.5%	0.0%	50.0%	100.0%
GRG0013	08/09/04	10.0%	10.0%	50.0%	0.0%	30.0%	100.0%
GUN0476	08/09/04	41.7%	8.3%	16.7%	4.2%	29.2%	100.0%
GOB0042	09/07/04	0.0%	25.0%	29.2%	0.0%	45.8%	100.0%
GRG0013	09/07/04	0.0%	30.0%	5.0%	0.0%	65.0%	100.0%
GUN0476	09/07/04	8.3%	16.7%	37.5%	4.2%	33.3%	100.0%
GOB0042	10/04/04	0.0%	0.0%	47.1%	5.9%	47.1%	100.0%
GRG0013	10/04/04	0.0%	0.0%	37.5%	25.0%	37.5%	100.0%
GUN0476	10/04/04	12.5%	33.3%	45.8%	0.0%	8.3%	100.0%
Total		16.7%	22.9%	28.8%	4.1%	27.5%	100.0%

Figure C-2. Pretty Boy Reservoir Watershed relative contributions by probable sources of *Enterococcus* contamination.



Pretty Boy Reservoir Summary

When water isolates were compared to the library and potential sources predicted, 73% of the isolates were classified as to category by statistical analysis. The highest RCC for the library was 89% (for livestock), followed by 88% for pet). The RCCs for human and wildlife sources were 86% and 61%, respectively.

The largest category of potential sources in the watershed as a whole was pet (39% of classified water isolates), followed by livestock (32%), human (23%), and wildlife (6%) (Figure C-2).

REFERENCES

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

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

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

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

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

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

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

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

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Adjustment of BST Results

As explained in the BST Summary for the Prettyboy Reservoir, the percent of correct classification (RCC) for bacteria sources can introduce a potential misclassification of the more probable sources in the watershed. This is seen in Table C-4, which shows results of the analysis of samples from known sources. For example, out of 615, 221 isolates were known to be of livestock source but only 115 were classified by the analysis as being of livestock source. Of those 221, 12 were classified as human, 3 as pet and 91 as unknown. Similarly, of the other three categories, 11 isolates known to be human, 5 isolates known to be pet, and 13 known wildlife isolates were classified as livestock, resulting in a total of 144 of all 567 isolates classified as livestock of which only 115 were known to be of livestock source.

The results provided by the BST methodology can be adjusted based on the known source percent of correct classification results provided in Table C-4.

Example:

The current BST methodology provides the following source percentages for station GUN0476 during high flow conditions:

Source Category	**Original Percentage**
Pets	23.56 %
Human	26.62 %
Livestock	23.28 %
Wildlife	2.76 %
Unknown	23.77 %

To get the correct human source percentage we redistributed the above percentages based on the % of correct classification as follows.

From Table C-4:

Source Category	**Isolates known to be from Human Source**	**Total Isolates Predicted for Each category**	**Percentage**
Pets	6	80	7.5 %
Human	122	136	89.7 %
Livestock	11	144	7.6 %
Wildlife	3	56	5.4 %
Unknown	21	199	10.6 %
Total	163	615	26.5 %

Applying those percentages to the original estimated source distribution presented above will result in the adjusted percentage for human sources:

= (7.5 x 23.56) + (89.7 x 26.62) + (7.6 x 23.28) + (5.4 x 2.76) + (10.6 x 23.77) = 30.08 %

Thus the correct human source percentage, the value used in the TMDL analysis, is 30.08% and not 26.62%. Corrected percentages are also calculated as above for domestic animal (pet), livestock and wildlife sources. The classification of unknown is eliminated in the process as all known isolates are of known source. For station GUN0476 during high flow condition the corrected source percentages are as follows:

Source Category	**Adjusted Percentage**
Pets	17.0 %
Human	30.1 %
Livestock	32.7 %
Wildlife	20.2 %

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 Prettyboy Reservoir 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 Prettyboy Reservoir 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,

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

where,

MDLC = maximum daily load concentration (MPN/100ml)
LTAC = long-term average TMDL concentration (MPN/100ml)
MDL = Maximum Daily Load (MPN/day)
Z = z-score associated with upper bound percentile (unitless)

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 three monitoring stations of the Prettyboy Reservoir 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 Prettyboy Reservoir watershed, a value measured during high-flow conditions at the GRG0013 station resulted in the highest percentile of both strata of the three stations. This value translates to the 99.8th 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 (%)
GUN0476[1]	High	9,210	99.6
	Low	5,200	98.6
GRG0013	High	4,880	99.8
	Low	460	90.6
GOB0042	High	15,530	99.7
	Low	930	98.8

[1] Subwatersheds partially located in Pennsylvania

The 99.8th percentile value results in a maximum daily load that would not be exceeded 99.8% 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):

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

And from equation (10):

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

Therefore,

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

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:

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

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

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)
GUN0476[1]	High	27	80
	Low	91	146
GRG0013	High	87	228
	Low	94	178
GOB0042	High	57	262
	Low	87	108

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

The next step is to calculate the 99.8th 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 99.8th 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)
GUN0476[1]	High	2.76	1,741
	Low	1.26	1,435
GRG0013	High	2.41	4,414
	Low	1.60	2,293
GOB0042	High	4.51	8,031
	Low	0.74	561

[1] Subwatersheds partially located in Pennsylvania

With the 99.8th 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:

$$\text{Daily TMDL (MPN/day)} = Q_H*(99.8^{th}C_{LTA\text{-}H})*F_{1H}*W_H + Q_L*(99.8^{th}C_{LTA\text{-}L})*F_{1L}*W_L \qquad \text{(D7)}$$

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

$$\text{WWTP-WLA MDL}_{\text{(billion MPN/day)}} = [\text{WWTP-WLA}_{\text{(billion MPN/year)}}]*(3.11/365) \qquad \text{(D8)}$$

The Maximum Daily Loads for the Prettyboy Reservoir subwatersheds, including those partially located in PA, are presented in Table D-4 below. For the unmonitored downstream subwatershed an average of the three upstream station loads is used.

Table D-4: Maximum Daily Loads Summary

Subwatershed	Flow Stratum	Maximum Daily Load (Billion *E. coli* MPN/day) by Stratum	Maximum Daily Load (Billion *E. coli* MPN/day) Weighted by Stratum
GUN0476[1]	High Low	2,749 697	1,425
GRG0013	High Low	2,032 363	955
GOB0042	High Low	7,272 168	2,690
Downstream Subwatershed[1]	High Low	4,018 409	1,690

[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 Prettyboy Reservoir watershed are presented in Table D-5.

Table D-5: Prettyboy Reservoir Watershed Maximum Daily Loads in MD

Subwatershed	Total Allocation	LA	SW-WLA	WWTP-WLA
	(Billion MPN *E. coli* /day)			
GUN0476[1]	1,057	1,042	15	0
GRG0013	955	932	23	0
GOB0042	2,690	2,536	147	7
Downstream Subwatershed[1]	1,684	1,684	0	0
Total	**6,386**	**6,194**	**185**	**7**

[1] MD portion of the subwatershed only.

REFERENCES

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

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

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

Ott, Wayne R. Environmental Statistics and Data Analysis. 1995. CRC Press. Pages 276 – 283.