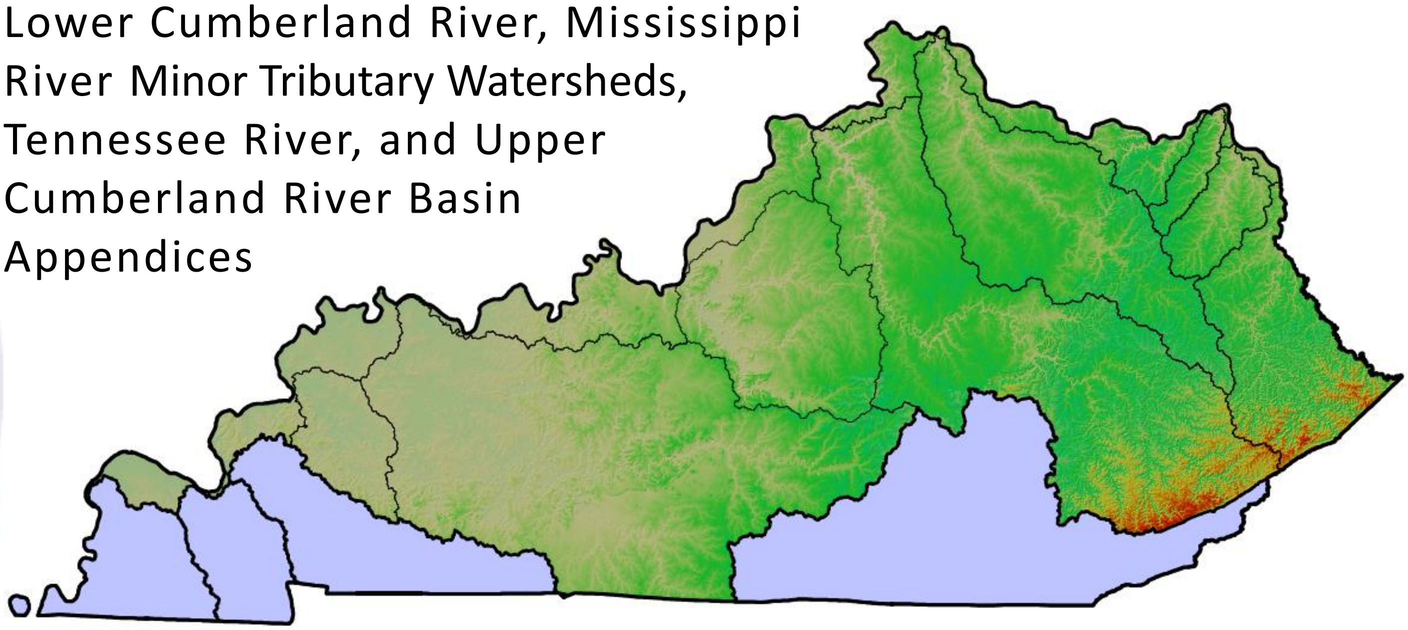
Addendum to
Kentucky Statewide Total Maximum Daily Load
for *Bacteria Impaired Waters*:

Lower Cumberland River, Mississippi River Minor Tributary Watersheds, Tennessee River, and Upper Cumberland River Basin Appendices



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Kentucky Department for Environmental Protection
Division of Water
Frankfort, Kentucky

This report is approved for release

Carey Johnson, Director
Division of Water

August 9, 2022
Date

TEAM KENTUCKY
ENERGY AND ENVIRONMENT CABINET

DOCUMENT REVISION HISTORY

Date of Revision	Section(s) Revised	Revision Explanation

TABLE OF CONTENTS

LIST OF TABLES .... ***vi***

GLOSSARY OF ACRONYMS AND ABBREVIATIONS .... ***vi***

1.0 INTRODUCTION ***1***

1.1 Overview of Section 303(d) of the Clean Water Act 1

1.2 Purpose of this Addendum 1

1.3 Where to Find TMDL Information for this Addendum 3

2.0 PUBLIC PARTICIPATION ***6***

REFERENCES ***7***

Appendix H – Lower Cumberland River Basin ***H-1***

Appendix I – Mississippi River Minor Tributary Watersheds ***I-1***

Appendix L – Tennessee River Basin ***L-1***

Appendix O – Upper Cumberland River Basin ***O-1***

LIST OF TABLES

Table 1.3-1 Bacteria TMDL Water Quality Criteria for All Surface Waters 3
Table 1.3-2 Expired Fecal Coliform Water Quality Criteria 4
Table 1.3-3 Where to Find Information in this Addendum and the Core TMDL Document 4

GLOSSARY OF ACRONYMS AND ABBREVIATIONS

Co.	County
CSO	Combined Sewer Overflow
CWA	Clean Water Act
DOW	Kentucky Division of Water
EEC	Kentucky Energy and Environment Cabinet
EPA	United States Environmental Protection Agency
HUC	Hydrologic Unit Code
KAR	Kentucky Administrative Regulations
KPDES	Kentucky Pollutant Discharge Elimination System
LA	Load Allocation
ml	Milliliter
MOS	Margin of Safety
MS4	Municipal Separate Storm Sewer System
NHD	National Hydrography Dataset
PCR	Primary Contact Recreation
RM	River Mile
SCR	Secondary Contact Recreation
SWS	Sanitary Wastewater System
TMDL	Total Maximum Daily Load
WLA	Wasteload Allocation
WQC	Water Quality Criteria
SWQMP	Storm Water Quality Management Plan

1.0 INTRODUCTION

The *Kentucky Statewide Total Maximum Daily Load* (TMDL) *for Bacteria Impaired Waters* is a new type of TMDL report that will address bacteria-impaired waters on Kentucky's 303(d) list in one streamlined report (DOW 2019). This new type of TMDL report will consist of a core document and a set of addendums. Initially, there will be a corresponding appendix for each of the 13 major river basins in Kentucky. Each appendix will contain TMDLs for the bacteria-impaired segments within that basin as of the 2016 303(d) list (i.e. the most recent approved 303(d) list used to prioritize waters for TMDL development under EPA's 303(d) Program Long-Term Vision). The core background and methodology document and first river basin appendices (Green River and Tradewater River) were approved in 2019 by the U.S. Environmental Protection Agency (EPA). Six river basin appendices (Big Sandy River, Little Sandy River, Tygarts Creek, Kentucky River, Licking River, and Salt River) were approved in 2021 by EPA. Subsequent river basin appendices will be added to the Kentucky Statewide Bacteria TMDL as they are completed. This addendum adds four new river basin appendices and provides references or updates where appropriate to the core background and methodology document.

1.1 Overview of Section 303(d) of the Clean Water Act

The Clean Water Act (CWA) requires states to designate uses for surface waters within their jurisdiction and to establish water quality standards to protect those designated uses. The designated uses assigned to waterbodies in Kentucky can be found in Kentucky Administrative Regulations (KAR) at 401 KAR 10:026. The water quality standards can be found at 401 KAR 10:031.

Section 303(d) of the CWA requires states to develop a list of impaired waters called the 303(d) list. Waterbodies placed on the 303(d) list have been assessed, have one or more designated uses impaired by one or more pollutants, and require the development of a TMDL for each pollutant causing an impairment. The TMDL establishes the allowable amount (i.e., load) of the pollutant the waterbody can naturally assimilate while continuing to meet the water quality standards for each designated use. Additional information on TMDLs can be found on the EPA website.

The Kentucky Division of Water (DOW) submits the 303(d) list to the EPA during even-numbered years. Each submittal replaces the previous list. Listings of bacteria-impaired segments can be found in DOW's most recent *Integrated Report to Congress on the Condition of Water Resources in Kentucky* and associated supplementary workbook.

1.2 Purpose of this Addendum

The purpose of this addendum is to:

- Add an appendix to the *Kentucky Statewide TMDL for Bacteria Impaired Waters* for each of the following major river basins: 1) Lower Cumberland River basin, 2) Mississippi

River Minor Tributary Watersheds, 3) Tennessee River basin and 4) Upper Cumberland River basin
- Add TMDLs for 35 stream segments listed as impaired for bacteria on Kentucky's 2016 303(d) list
- Provide the waterbody-specific information for all bacteria-impaired stream segments addressed by a TMDL in this addendum

This addendum is not a stand-alone document. The method for developing a TMDL for each of the bacteria-impaired segments within this addendum (including general information and the TMDL loadings) can be found in the core TMDL document that was approved in 2019.

If an approved TMDL report existed for a bacteria-impaired segment within the Lower Cumberland, Mississippi Minor Tributary Watersheds, Tennessee, or Upper Cumberland River basins prior to the development of this addendum that TMDL report is still in effect and can be found on the Watershed-Scale TMDL Reports list.

DOW will provide public notice and seek comment when subsequent appendices are added to the Statewide Bacteria TMDL.

For more information, please review the Statewide Bacteria Fact Sheet [PDF, 1.1 MB] or contact the TMDL Program at TMDL@ky.gov or call (502) 564-3410.

In accordance with EPA's 303(d) Program Long-Term Vision, DOW recognizes that in some cases activities to address water quality impairments are already in the planning stages or underway. Where these activities are on track to fully restore water quality, the development of a TMDL may temporarily be given a lower priority while an alternative restoration plan is being pursued. Some Kentucky stream segments have been identified as good candidates for such alternative approaches. There are no alternative restoration plans under development or already in place for any stream segments addressed in this TMDL.

1.3 Where to Find TMDL Information for this Addendum

The appendices within this addendum rely upon the core TMDL document for TMDL development. The bacteria TMDL water quality criteria (WQC) for all surface waters in Kentucky are promulgated in 401 KAR 10:031, which in Section 7(1)(a) states that for the Primary Contact Recreation (PCR) use and season (May 1-October 31),

Escherichia coli content shall not exceed 130 colonies per 100 ml as a geometric mean based on not less than five (5) samples taken during a thirty (30) day period. Content also shall not exceed 240 colonies per 100 ml in twenty (20) percent or more of all samples taken during a thirty (30) day period for Escherichia coli.

For the year-round Secondary Contact Recreation (SCR) use, Section 7(2)(a) states,

Fecal coliform content shall not exceed 1,000 colonies per 100 ml as a thirty (30) day geometric mean based on not less than five (5) samples; nor exceed 2,000 colonies per 100 ml in twenty (20) percent or more of all samples taken during a thirty (30) day period.

The bacteria WQC are summarized below in Table 1.3-1.

Table 1.3-1. Bacteria TMDL Water Quality Criteria for All Surface Waters[1]

Designated Use	Numeric Criterion
PCR	240 *E. coli* colonies/100 ml which must be met in at least 80% of all samples taken within a 30-day period during the Primary Contact Recreational season of May through October
PCR	130 *E. coli* colonies/100 ml as a geometric mean based on not less than 5 samples taken within a 30-day period during the Primary Contact Recreational season of May through October
SCR	2000 fecal coliform colonies/100 ml which must be met in at least 80% of all samples taken within a 30-day period
SCR	1000 fecal coliform colonies/100 ml as a geometric mean based on not less than 5 samples taken within a 30-day period

[1] The Primary Contact Recreation (PCR) designated use WQC are in effect from May 1 through October 31. The Secondary Contact Recreation (SCR) designated use WQC are in effect for the entire year.

Prior to November 1, 2019, PCR criteria also existed for fecal coliform. Those WQC are summarized in Table 1.3-2 for informational purposes. Prior to the expiration of the fecal coliform PCR criteria, several waterbodies within these river basins had been assessed as failing to meet those WQC and were listed as impaired due to fecal coliform. On the 2018/2020 303(d) list, these fecal coliform listings were replaced with the cause “pathogens” to reflect the impaired use. The TMDLs for waterbodies with pathogen impairments are calculated in this document using the *E. coli* criteria, since the *E. coli* WQC must be met for a waterbody to support the PCR designated use.

Table 1.3-2 Expired Fecal Coliform Water Quality Criteria

Designated Use	Numeric Criterion
PCR	400 fecal coliform colonies/100 ml which must be met in at least 80% of all samples taken within a 30-day period during the Primary Contact Recreational season of May through October
PCR	200 fecal coliform colonies/100 ml as a geometric mean based on not less than 5 samples taken within a 30-day period during the Primary Contact Recreational season of May through October

A list of TMDL elements and their location within this addendum or the core TMDL document is provided in Table 1.3-3.

Table 1.3-3 Where to Find Information in this Addendum and the Core TMDL Document

TMDL Element	Description	Location
Water Quality Standards	Describes recreational uses, water quality standards, and waterbody assessment	Sections 1.0 and 2.0 of Core TMDL
Water Quality Criteria	Provides the indicator bacteria used to assess pathogen levels in waterbodies and the bacteria standards for Kentucky's surface waters	Section 1.3 of this addendum
Physical Setting	Provides an overview of Kentucky's physical setting including soils, geology, and hydrology	Section 3.0 of Core TMDL
Source Assessment	Defines point and non-point sources of bacteria pollution and provides examples of bacteria sources that affect Kentucky's waterbodies	Section 4.0 of Core TMDL
Monitoring and Data Validation	Describes the types of data used for assessment and TMDL development	Section 5.0 of Core TMDL
TMDL Development	Provides a description of the TMDL calculation process and of required components such as the margin of safety factor, seasonality, and critical conditions	Section 6.0 of Core TMDL
Implementation	Provides a description of the implementation process (e.g. permit translation, development of watershed plans, coordination with local stakeholders, types of funding assistance and other resources)	Section 7.0 of Core TMDL
Public Participation	Provides a summary of the process used to solicit public comment on this addendum and DOW response to those comments	Section 2.0 of this addendum

TMDL Element	Description	Location
MS4 Communities in Kentucky	Provides a list organized by county of Municipal Separate Storm Sewer System (MS4) communities in Kentucky (as of September 2018)	Appendix A of Core TMDL
Percent of Households Serviceable by Sewer	Provides the percent of households serviceable by sewer in Kentucky (2010). The list is organized by county and includes county population totals, and total number of households and serviceable households	Appendix B of Core TMDL
National Land Cover Database Classification Descriptions (NLCD 2011)	Defines the nationwide land cover classifications. The descriptions provide information on land cover and land use	Appendix P of Core TMDL

2.0 PUBLIC PARTICIPATION

The public was invited to provide written comments on this Proposed Draft Addendum to the Kentucky Statewide TMDL for Bacteria Impaired Waters during the period of March 9, 2022 through April 11, 2022.

Notice of the public comment period was posted on the Division of Water Public Notices website and distributed to the TMDL email distribution list (TMDL@ky.gov), which is a list of persons who have expressed interest in receiving information and announcements related to the 303(d) and TMDL program. The announcement was also distributed to the Nonpoint Source Pollution Control email list of persons interested in water quality issues (ollietheotter@ky.gov), posted to the Kentucky Energy and Environment Cabinet's weblog Naturally Connected, the Kentucky Energy and Environment Cabinet Facebook page and the KY Wild Waters Facebook page.

Legal advertisements were purchased in the following local newspapers throughout the state: Bowling Green Daily News (Bowling Green, Warren Co.), Kentucky New Era (Hopkinsville, Christian Co.), The Middlesboro News (Middlesboro, Bell Co.), The Paducah Sun (Paducah, McCracken Co.) and Commonwealth Journal (Somerset, Pulaski Co.).

No comments were received during the public comment period.

REFERENCES

33 U.S.C. § 1251. Section 303(d). Clean Water Act. 1972.

401 KAR 10:026. Designation of uses of surface waters. Kentucky Energy and Environment Cabinet, Department for Environmental Protection, Division of Water. 2009.

401 KAR 10:031. Surface water standards. Kentucky Energy and Environment Cabinet, Department for Environmental Protection, Division of Water. 2009. Frankfort, KY.

DOW (Kentucky Division of Water). 2019. *Kentucky Statewide Total Maximum Daily Load for Bacteria Impaired Waters*. February 2019. Kentucky Department of Environmental Protection.

NLCD 2011. National Land Cover Database 2011 Legend and Land Cover Classification Description. Available at URL: https://www.mrlc.gov/data/legends/national-land-cover-database-2011-nlcd2011-legend.

APPENDIX H

Appendix H
Lower Cumberland River Basin

HUC 8s: 05130205, 05130206

Level IV Ecoregions: Crawford-Mammoth Cave Uplands, Western Pennyroyal Karst Plain, Western Highland Rim, Wabash-Ohio Bottomlands

Drainage Area Within Kentucky: 2,037.72 square miles

Counties: Caldwell, Christian, Crittenden, Livingston, Logan, Lyon, Simpson, Todd, Trigg

Major Cities: Hopkinsville, Elkton, Princeton, Adairville, Cadiz, Eddyville, Fredonia, Grand Rivers, Guthrie, Kuttawa, Oak Grove

The Lower Cumberland River basin is located in western Kentucky and lies entirely within the Western Pennyroyal physiographic region.

The Cumberland River originates in southeastern Kentucky in Harlan Co. and is formed by the convergence of Martins Fork, Clover Fork, and Poor Fork in Baxter, Ky. The Cumberland River flows west and meanders south through Monroe Co., Ky. before entering Tennessee. The Cumberland River flows through middle Tennessee and reenters in Trigg County, Kentucky in the southwest portion of the state. Much of the Lower Cumberland River in Kentucky is impounded as Lake Barkley, which was formed by Barkley Lock and Dam and completed by the U.S. Army Corps of Engineers in 1966. Downstream of the Barkley Dam, the Cumberland River flows approximately thirty miles northwest until it meets the Ohio River, having drained an area of approximately 2,038 square miles within Kentucky.

Table H.1 provides a summary of all stream segments in the Lower Cumberland River basin that are on the Kentucky 2018/2020 303(d) list for impairment due to fecal coliform, *E. coli* and/or pathogens. Segments addressed by a TMDL in this report are listed in the table with the TMDL pollutant. Segments not addressed by a TMDL in this report have a footnote explaining why they are not included. Note that stream segments listed for the first time for a bacteria-related cause on the 2018/2020 303(d) list have not yet been prioritized for TMDL development. Table H.1 also provides a crosswalk between the waterbody IDs on the 2016 303(d) list and the corresponding waterbody IDs on the 2018/2020 303(d) list. This information is provided to assist with cross-referencing waterbodies to prior lists following the implementation of a new system of waterbody IDs with the 2018/2020 list. Figure H.1 shows the location of all segments in the Lower Cumberland River basin addressed by a TMDL in this report.

The river miles for each TMDL segment in this appendix match those reported in the 2018/2020 303(d) list. Since the National Hydrography Dataset (NHD) is continually updated to maintain accurate waterbody information, the river mile information in this appendix may not reflect the current 1:24,000 NHD for Kentucky. River mile information for stream segments is updated in each new 303(d) list submitted to EPA.

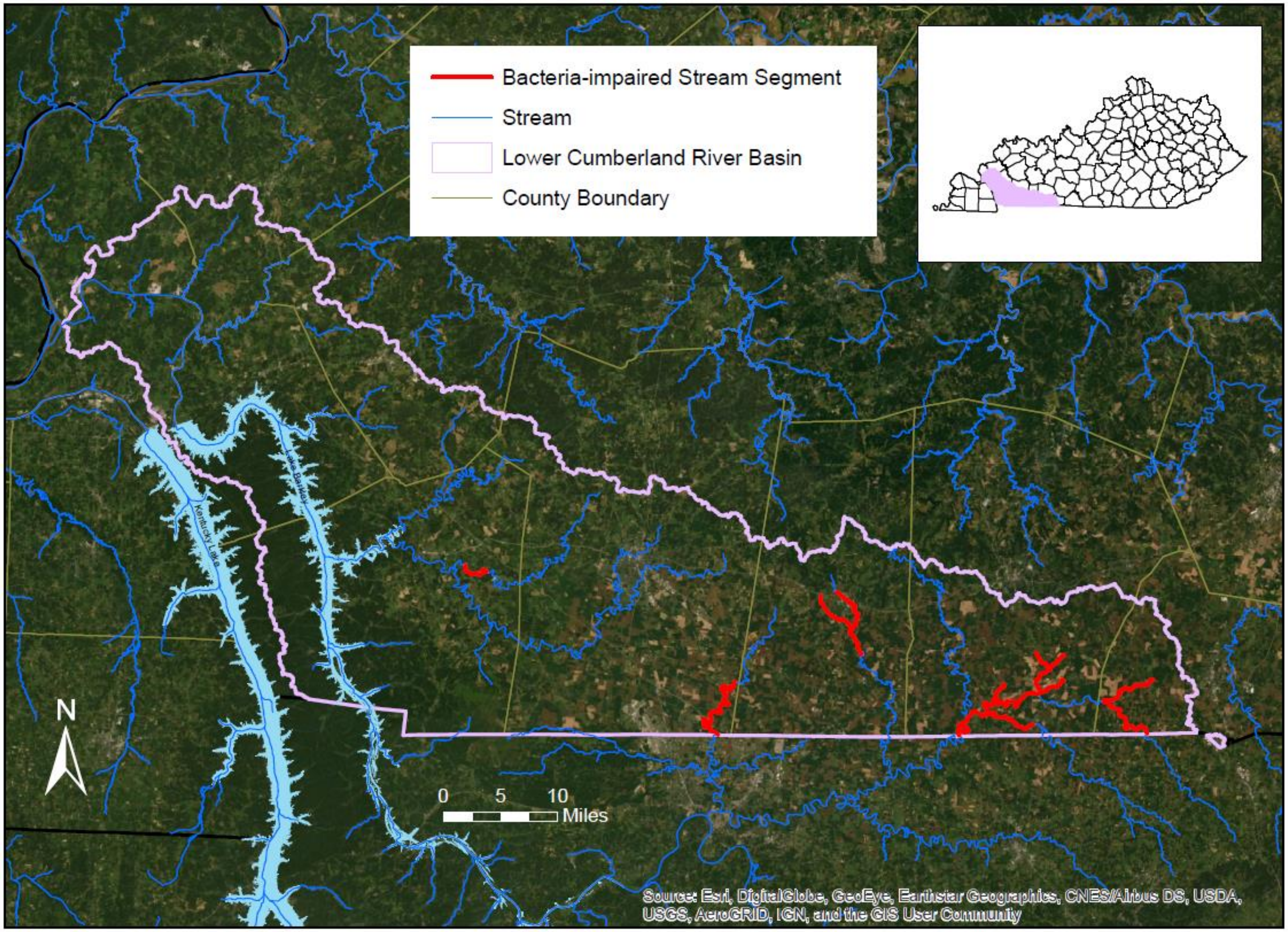
Table H.1 2018/2020 303(d) List Bacteria-impaired Stream Segments in the Lower Cumberland River Basin

Waterbody Name	Waterbody ID	2016 Waterbody ID	Impaired Use (Support Status)	Listed Pollutant	TMDL Pollutant	Suspected Source(s)	County
Axel Creek 2.7 to 4.7[1]	KY-3268	n/a	PCR (nonsupport)	*E. coli*	TMDL not included in this document	Agriculture, Non-Point Source	Crittenden
Claylick Creek 2.05 to 4.85[1]	KY-510	KY489591_01	PCR (nonsupport)	*E. coli*	TMDL not included in this document	Agriculture, Non-Point Source, On-site Treatment Systems (Septic Systems and Similar Decentralized Systems)	Crittenden, Livingston
Claylick Creek 4.85 to 10.8[1]	KY-511	KY489591_02	PCR (nonsupport)	*E. coli*	TMDL not included in this document	Agriculture, Non-Point Source	Crittenden
Claylick Creek 10.8 to 14.0[1]	KY-512	KY489591_03	PCR (partial support)	*E. coli*	TMDL not included in this document	Agriculture, Non-Point Source, On-site Treatment Systems (Septic Systems and Similar Decentralized Systems)	Crittenden
Clement Creek 0.0 to 4.75[1]	KY-3283	n/a	PCR (nonsupport)	*E. coli*	TMDL not included in this document	Agriculture, Non-Point Source	Crittenden
Cox Spring Branch 0.0 to 2.75[1]	KY-3284	n/a	PCR (nonsupport)	*E. coli*	TMDL not included in this document	Agriculture, Non-Point Source, On-site Treatment Systems (Septic Systems and Similar Decentralized Systems)	Livingston
Dry Creek 0.0 to 2.25[1]	KY-3286	n/a	PCR (nonsupport)	*E. coli*	TMDL not included in this document	Agriculture, Non-Point Source, On-site Treatment Systems (Septic Systems and Similar Decentralized Systems)	Livingston, Crittenden
Dry Creek 2.25 to 6.5[1]	KY-3287	n/a	PCR (nonsupport)	*E. coli*	TMDL not included in this document	Agriculture, Non-Point Source, On-site Treatment Systems (Septic Systems and Similar Decentralized Systems)	Crittenden
Dry Fork Creek 0.0 to 1.9[1]	KY-3289	n/a	PCR (partial support)	*E. coli*	TMDL not included in this document	Agriculture, Non-Point Source	Crittenden
Elk Fork 22.4 to 30.3	KY-720	KY491660_02	PCR (nonsupport)	*E. coli*	*E. coli*	Source Unknown	Todd
Elk Fork 30.3 to 32.45	KY-721	KY491660_03	PCR (nonsupport)	*E. coli*	*E. coli*	Source Unknown, Unspecified Urban Stormwater	Todd

Little River 20.7 to 30.1[1]	KY-1146	KY496838_02	PCR (nonsupport)	*E. coli*	TMDL not included in this document	Non-Point Source	Trigg
Little Whippoorwill Creek 0.0 to 4.1	KY-1165	KY496894_01	PCR (nonsupport)	*E. coli*	*E. coli*	Non-Point Source	Logan
Little Whippoorwill Creek 4.1 to 7.0	KY-1166	KY496894_02	PCR (nonsupport)	*E. coli*	*E. coli*	Non-Point Source	Logan
McHaley Creek 1.7 to 2.2[1]	KY-3291	n/a	PCR (partial support)	*E. coli*	TMDL not included in this document	Agriculture, Non-Point Source	Crittenden
Muddy Fork Little River 2.4 to 6.6[1]	KY-1353	KY499043_01	PCR (nonsupport)	*E. coli*	TMDL not included in this document	Non-Point Source	Trigg
Pleasant Grove Creek 0.0 to 2.3	KY-1481	KY500832_01	PCR (nonsupport)	*E. coli*	*E. coli*	Grazing in Riparian or Shoreline Zones, Managed Pasture Grazing, On-site Treatment Systems (Septic Systems and Similar Decentralized Systems)	Logan
Pleasant Run 0.0 to 2.15	KY-1482	KY500905_01	PCR (nonsupport)	*E. coli*	*E. coli*	Agriculture, Non-Point Source	Logan
Red River 50.9 to 54.5	KY-1559	KY501672_01	PCR (partial support)	*E. coli*	*E. coli*	Agriculture, Grazing in Riparian or Shoreline Zones	Logan
Red River 54.5 to 56.90	KY-1560	KY501672_02	PCR (partial support)	*E. coli*	*E. coli*	Agriculture, Rural (Residential Areas)	Logan
Red River 56.9 to 65.75	KY-1561	KY501672_03	PCR (nonsupport)	*E. coli*	*E. coli*	Agriculture	Logan
Red River 74.3 to 81.3	KY-1563	KY501672_05	PCR (nonsupport)	*E. coli*	*E. coli*	Agriculture	Simpson
Sinking Creek 0.0 to 3.3	KY-1716	KY503559_01	PCR (nonsupport)	*E. coli*	*E. coli*	Non-Point Source	Logan
Sinking Fork 2.1 to 5.65	KY-1718	KY503569_01	PCR (nonsupport)	*E. coli*	*E. coli*	Non-Point Source, On-site Treatment Systems (Septic Systems and Similar Decentralized Systems)	Trigg
South Fork Red River 0.0 to 5.3	KY-1783	KY503943_01	PCR (nonsupport)	*E. coli*	*E. coli*	Agriculture, Non-Point Source	Logan
Sulphur Spring Creek 0.0 to 6.6	KY-1868	KY504760_01	PCR (partial support)	*E. coli*	*E. coli*	Agriculture, Non-Point Source	Simpson

UT of Cox Spring Branch 0.0 to 1.55[1]	KY-3285	n/a	PCR (nonsupport)	*E. coli*	TMDL not included in this document	Agriculture, Non-Point Source, On-site Treatment Systems (Septic Systems and Similar Decentralized Systems)	Livingston
UT of Doan Spring Creek 0.0 to 2.3[1]	KY-3270	n/a	PCR (nonsupport)	*E. coli*	TMDL not included in this document	Agriculture, Non-Point Source	Crittenden
UT of Dry Creek 0.0 to 2.0[1]	KY-3288	n/a	PCR (nonsupport)	*E. coli*	TMDL not included in this document	Agriculture, Non-Point Source	Crittenden, Livingston
UT of Elk Fork Creek 0.0 to 4.8	KY-723	KY491660-26.4_01	PCR (partial support)	*E. coli*	*E. coli*	Source Unknown	Todd
West Fork Red River 14.65 to 26.8	KY-4	KY1269347_01	PCR (partial support)	*E. coli*	*E. coli*	Non-Point Source, Source Unknown	Christian

[1] TMDLs for these segments will be developed in a future TMDL report. These are new 2018/2020 bacteria listings. These segments may have a 2016 waterbody ID listed in the table if they had any assessed use prior to the 2018/2020 IR reporting cycle.



Source: Esri, DigitalGlobe, GeoEye, Earthstar Geographics, CNES/Airbus DS, USDA, USGS, AeroGRID, IGN, and the GIS User Community

Figure H.1 Location of the Lower Cumberland River Basin and Bacteria-impaired Streams Addressed by a TMDL in This Report

Land cover data is summarized in Table H.2, and its geographic distribution is shown in Figure H.2. Cultivated crops is the predominant class of land cover in the Lower Cumberland River basin, accounting for approximately 38 percent. The next three classes by magnitude are deciduous forest, pasture/hay, and open developed. Land cover classes are described in Appendix P of the core TMDL document.

Table H.2 Land Cover Classes in the Lower Cumberland River basin (NLCD 2011)

Land Cover	Percent of Total Area	Square Miles	Acres
Open Water	3.40	69.18	44,278.13
Developed, Open	4.66	94.94	60,758.88
Developed, Low Intensity	0.76	15.58	9,972.75
Developed, Medium Intensity	0.34	6.98	4,465.83
Developed, High Intensity	0.16	3.34	2,137.54
Barren Land (Rock, Sand, Clay)	0.14	2.84	1,819.41
Deciduous Forest	32.60	664.37	425,195.70
Evergreen Forest	2.09	42.67	27,306.74
Mixed Forest	0.04	0.75	478.42
Shrub/Scrub	0.35	7.21	4,617.45
Grassland/Herbaceous	1.72	35.14	22,491.21
Pasture/Hay	15.23	310.40	198,655.59
Cultivated Crops	37.62	766.60	490,624.50
Woody Wetlands	0.74	15.04	9,625.50
Emergent Herbaceous Wetlands	0.13	2.68	1,713.15

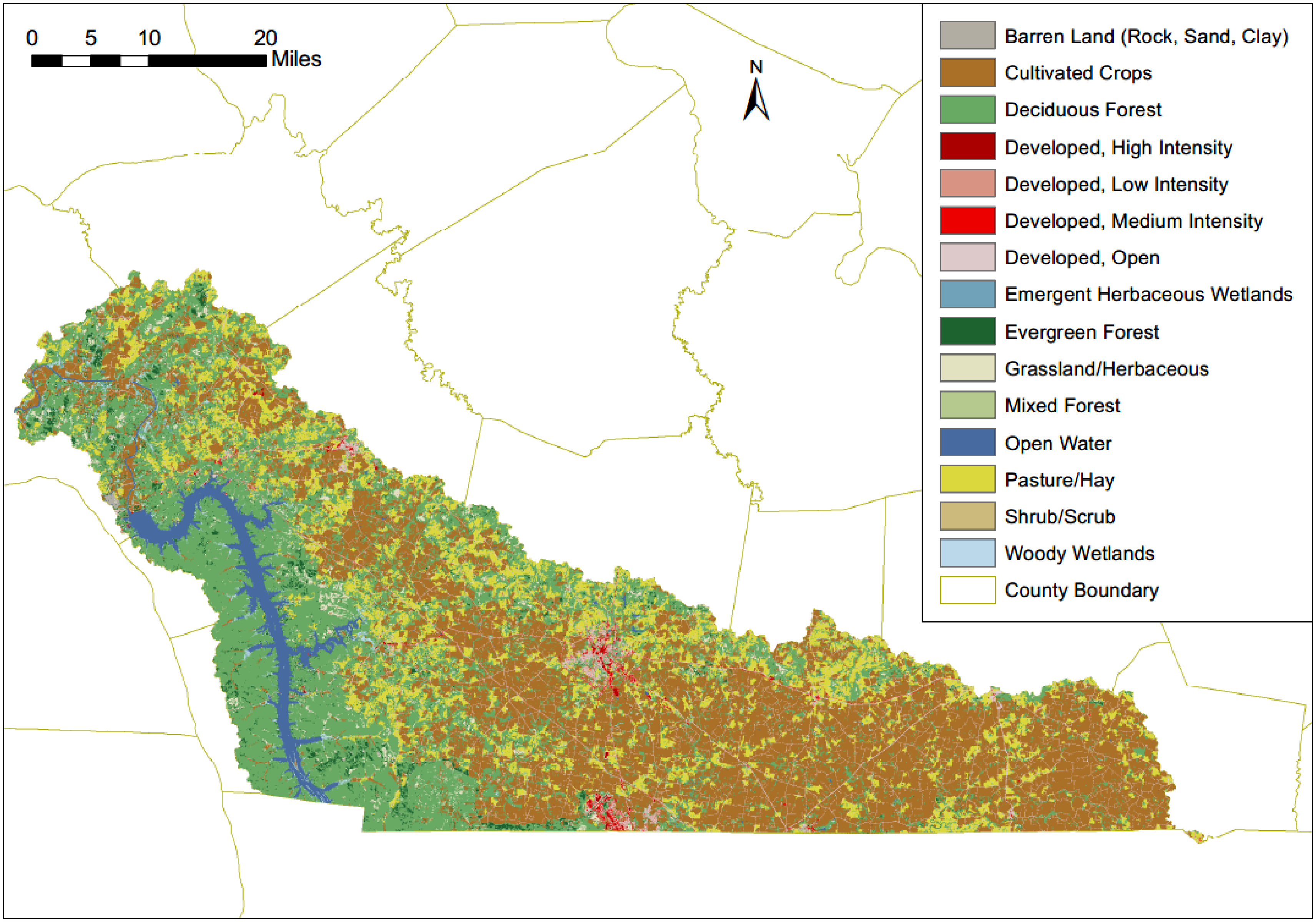


Figure H.2 Land Cover Types in the Lower Cumberland River Basin

Section H.1 Elk Fork 22.4 to 30.3

Waterbody ID: KY-720

Receiving Water: Red River

Impaired Use: PCR

Support Status: nonsupport

Listed Pollutant/TMDL Pollutant: *E. coli*

HUC 12: 051302060703

County: Todd

The Division of Water (DOW) collected samples during the PCR season from three stations on this segment. In 2008, nine samples were collected from station DOW20019005, DOW20019006, and DOW20019008. Table H.1-1 summarizes information about these sampling stations; Table H.1-2 summarizes the data collected from these stations.

Table H.1-1 DOW Sample Site Locations

Station Name	Latitude	Longitude	Stream Segment	River Mile
DOW20019005	36.75643	-87.13746	Elk Fork 22.4 to 30.3	24.05
DOW20019006	36.7793	-87.14628	Elk Fork 22.4 to 30.3	26.65
DOW20019008	36.79225	-87.13873	Elk Fork 22.4 to 30.3	28.1

Table H.1-2 DOW Sample Data Summary(1)

Station Name	Indicator Bacteria(2)	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
DOW20019005	*E. coli*	9	63	324	176
DOW20019006	*E. coli*	9	132	306	204
DOW20019008	*E. coli*	9	33	>1,500	368

(1)The full data set for samples collected from DOW20019005, DOW20019006, and DOW20019008 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.

(2)The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for Elk Fork 22.4 to 30.3 are presented in Table H.1-3.

Table H.1-3 Elk Fork 22.4 to 30.3 *E. coli* TMDL Allocations(1)

TMDL(2)	Allocations for Direct Loads to the Segment		Allocations for Upstream Loads to the Segment(5)	Allocations for Tributary Loads to the Segment(6)	MOS(7)
	SWS-WLA(3)	LA(4)			
$Q_S \times WQC \times CF$	$\sum(Q_{SWS} \times WQC \times CF)$	$\sum(Q_{LA} \times WQC \times CF)$	$\sum(Q_{Upstream} \times WQC \times CF)$	$\sum(Q_{Tributary} \times WQC \times CF)$	Implicit

(1)All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2)Q_S is the flow (ft^3/s) in the segment.

(3)Q_{SWS} is the flow (ft^3/s) in the segment due to a SWS entity. New or expanded SWS sources will be allowed to discharge to the segment contingent upon them meeting the PCR bacterial WQCs found in 401 KAR 10:031. SWS-WLAs will be translated into KPDES permit limits as an *E. coli* effluent gross limit of 130 colonies/100 ml as a monthly average (geometric mean) and 240 colonies/100 ml as a maximum weekly average (geometric mean).

(4)Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(5)$Q_{Upstream}$ is the flow contribution (ft^3/s) from upstream of the segment. This load includes both WLA and LA sources upstream of the impaired segment.

(6)$Q_{Tributary}$ is the flow contribution (ft^3/s) from a tributary to the segment. This load includes both WLA and LA sources on tributaries to the impaired segment.

(7)The following assumptions provide an implicit MOS:

(a)Upstream and tributary bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b)Although all sources are provided an allocation at the Water Quality Standard, not all sources discharge at this maximum allocation at the same time.

(c)There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

One facility permitted under the Kentucky Pollutant Discharge Elimination System (KPDES) discharges treated effluent directly into this segment of Elk Fork. The directly discharging facility is a sanitary wastewater system. There are no MS4 communities or CSOs discharging directly to this segment of Elk Fork. The definitions for MS4 and CSO are found in 401 KAR 5:002. The facility is identified in Table H.1-4 and the location of the segment within the Upper Elk Fork watershed is shown in Figure H.1-1.

Table H.1-4 Summary of Active KPDES-permitted Sources as of September 2021

KPDES Permit Number	Facility Name	Design Flow (MGD)	Outfall Latitude	Outfall Longitude	Permit Expiration Date(1)	WLA(2) (colonies *E. coli* /day)
KY0023442	Elkton STP	0.46	36.804444	-87.144722	10/31/2022	Q_{SWS}×WQC×CF

(1)Permit expiration dates identify the permits in effect when the draft TMDL was written, including any permits that may be expired (but not terminated) or in administrative continuance. Permits issued after the approval of this TMDL will address the TMDL.

(2)Q_{SWS} is the flow in the segment due to a SWS entity. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day).

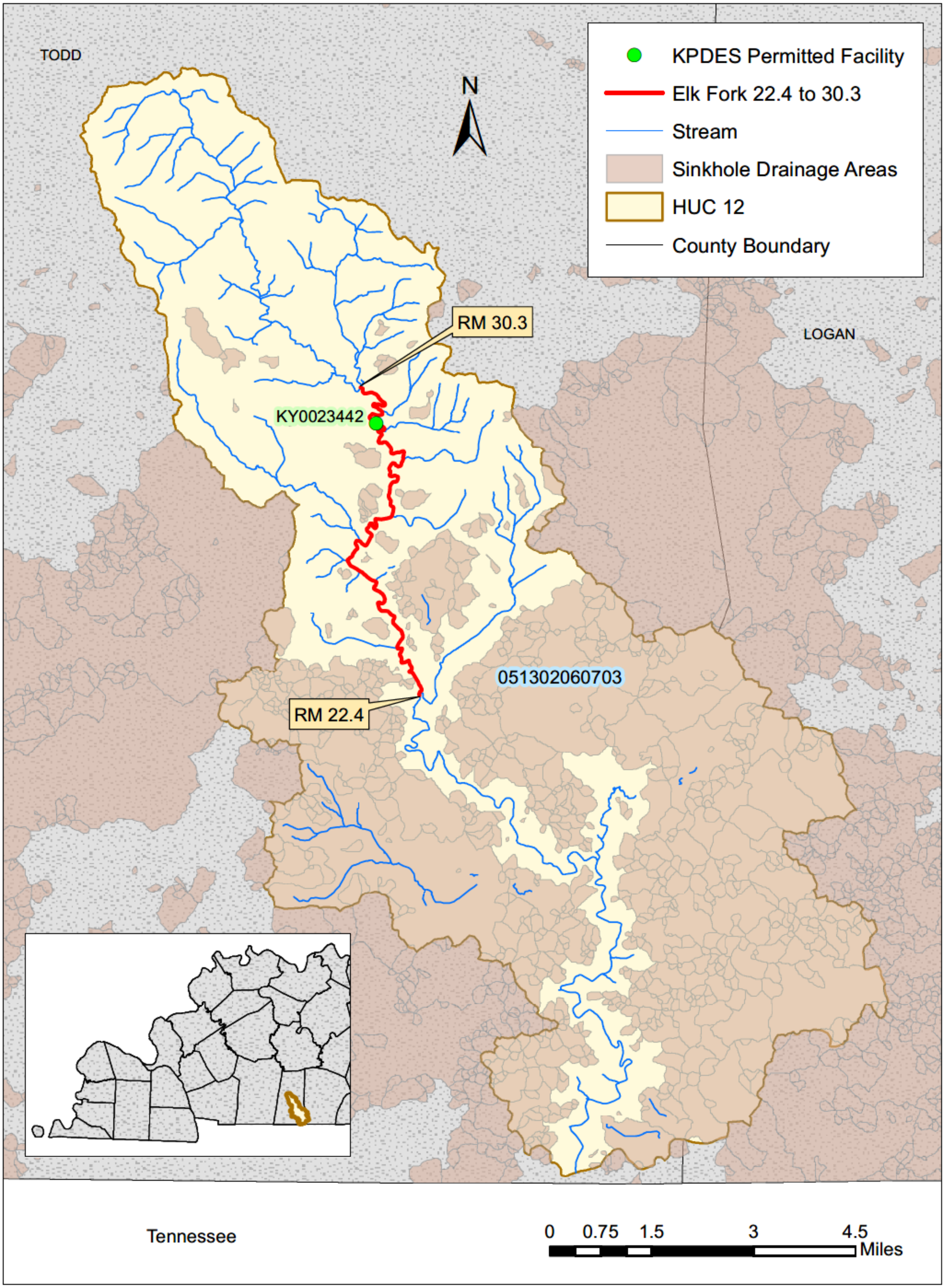


Figure H.1-1 Location of the KPDES-permitted Facility on Elk Fork 22.4 to 30.3

Section H.2 Elk Fork 30.3 to 32.45

Waterbody ID: KY-721

Receiving Water: Red River

Impaired Use: PCR

Support Status: nonsupport

Listed Pollutant/TMDL Pollutant: *E. coli*

HUC 12: 051302060703

County: Todd

The Division of Water (DOW) collected samples from station DOW20019009, located near river mile 31.55, in 2008. The station was sampled nine times during the PCR season. Table H.2-1 summarizes information about this sampling station; Table H.2-2 provides a summary of the data collected from this station.

Table H.2-1 DOW Sample Site Location

Station Name	Latitude	Longitude	Stream Segment	River Mile
DOW20019009	36.81388	-87.15315	Elk Fork 30.3 to 32.45	31.55

Table H.2-2 DOW Sample Data Summary(1)

Station Name	Indicator Bacteria(2)	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
DOW20019009	*E. coli*	9	75	>1,500	431

(1)The full data set for samples collected from DOW20019009 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.

(2)The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for Elk Fork 30.3 to 32.45 are presented in Table H.2-3. As of September 2021, there are no KPDES-permitted discharges of bacteria into this segment of Elk Fork. The location of the segment within the Upper Elk Fork watershed is shown in Figure H.2-1.

Table H.2-3 Elk Fork 30.3 to 32.45 *E. coli* TMDL Allocations(1)

TMDL(2)	Allocations for Direct Loads to the Segment	Allocations for Upstream Loads to the Segment(4)	Allocations for Tributary Loads to the Segment(5)	MOS(6)
	LA(3)			
$Q_S \times WQC \times CF$	$\sum(Q_{LA} \times WQC \times CF)$	$\sum(Q_{Upstream} \times WQC \times CF)$	$\sum(Q_{Tributary} \times WQC \times CF)$	Implicit

(1)All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2)Q_S is the flow (ft^3/s) in the segment.

(3)Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(4)$Q_{Upstream}$ is the flow contribution (ft^3/s) from upstream of the segment. This load includes both WLA and LA sources upstream of the impaired segment.

(5)$Q_{Tributary}$ is the flow contribution (ft^3/s) from a tributary to the segment. This load includes both WLA and LA sources on tributaries to the impaired segment.

(6)The following assumptions provide an implicit MOS:

(a)Upstream and tributary bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b)There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

Figure H.2-1 shows some karst features such as sinkholes exist in this watershed. The sink features may capture surface drainage and channel it underground to resurface later at one or more springs. These discharging springs may occur outside the watershed where the drainage originated. However, unless karst dye trace studies indicate otherwise, groundwater catchment is presumed to correspond to the topographic watershed boundaries of surface drainage. No dye tracing information is available from the area of the Upper Elk Fork watershed. For more detailed information about karst geology, see Section 3.2, Karst, of the Core TMDL.

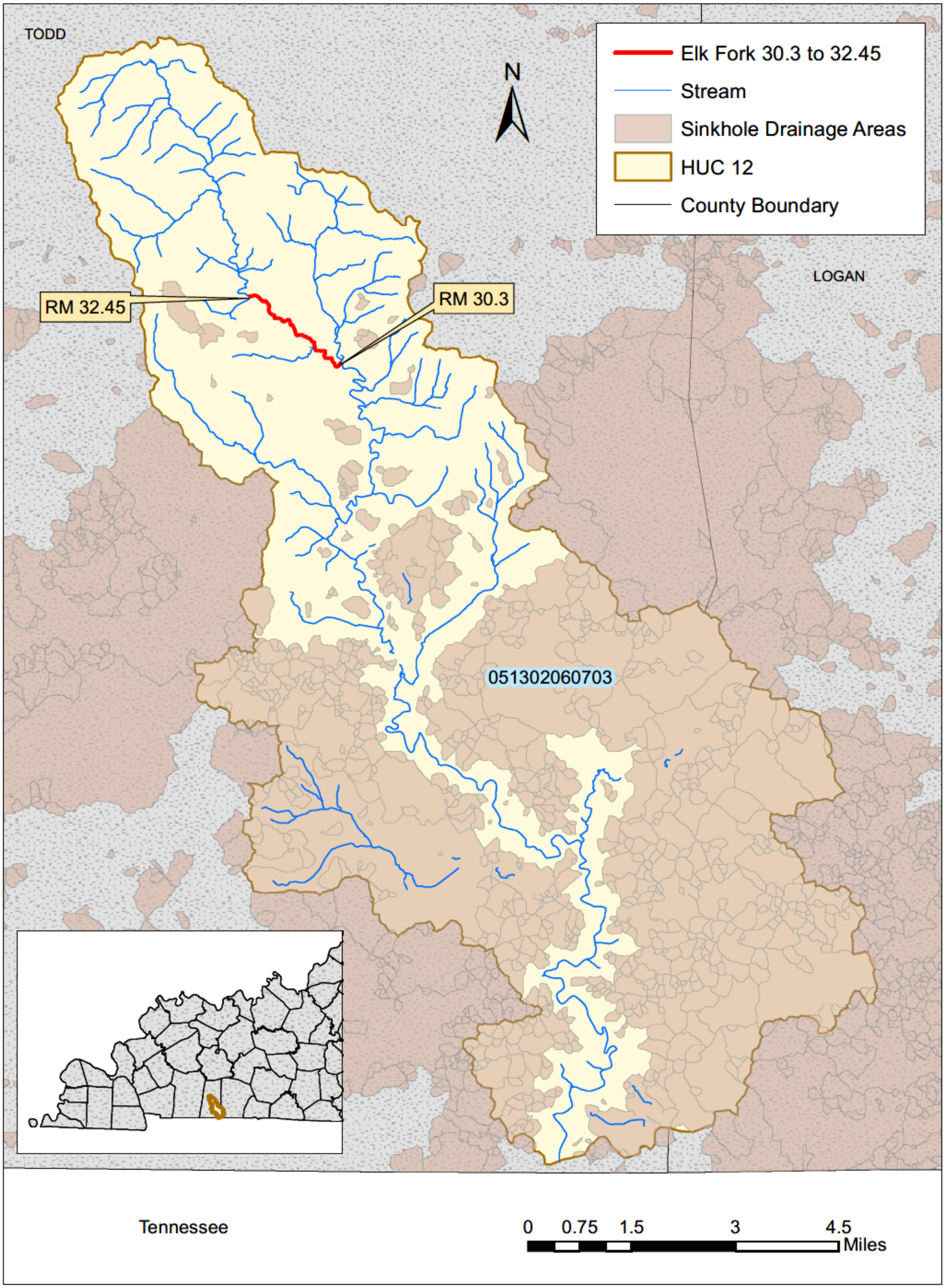


Figure H.2-1 Location of Elk Fork 30.3 to 32.45

Section H.3 Little Whippoorwill Creek 0.0 to 4.1

Waterbody ID: KY-1165

Receiving Water: Red River

Impaired Use: PCR

Support Status: nonsupport

Listed Pollutant/TMDL Pollutant: *E. coli*

HUC 12: 051302060204

County: Logan

The Division of Water (DOW) collected samples from station DOW20020015, located near river mile 2.4, in 2010. The station was sampled twelve times during the PCR season. Table H.3-1 summarizes information about this sampling station; Table H.3-2 provides a summary of the data collected from this station.

Table H.3-1 DOW Sample Site Location

Station Name	Latitude	Longitude	Stream Segment	River Mile
DOW20020015	36.7209	-86.8499	Little Whippoorwill Creek 0.0 to 4.1	2.4

Table H.3-2 DOW Sample Data Summary(1)

Station Name	Indicator Bacteria(2)	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
DOW20020015	*E. coli*	12	52	>2,420	589

(1)The full data set for samples collected from DOW20020015 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.

(2)The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for Little Whippoorwill Creek 0.0 to 4.1 are presented in Table H.3-3. As of September 2021, there are no KPDES-permitted discharges of bacteria into this segment of Little Whippoorwill Creek. The location of the segment within the Little Whippoorwill Creek watershed is shown in Figure H.3-1.

Table H.3-3 Little Whippoorwill Creek 0.0 to 4.1 *E. coli* TMDL Allocations[1]

TMDL[2]	Allocations for Direct Loads to the Segment	Allocations for Upstream Loads to the Segment[4]	Allocations for Tributary Loads to the Segment[5]	MOS[6]
	LA[3]			
$Q_S \times WQC \times CF$	$\sum(Q_{LA} \times WQC \times CF)$	$\sum(Q_{Upstream} \times WQC \times CF)$	$\sum(Q_{Tributary} \times WQC \times CF)$	Implicit

[1] All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

[2] Q_S is the flow (ft^3/s) in the segment.

[3] Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

[4] $Q_{Upstream}$ is the flow contribution (ft^3/s) from upstream of the segment. This load includes both WLA and LA sources upstream of the impaired segment.

[5] $Q_{Tributary}$ is the flow contribution (ft^3/s) from a tributary to the segment. This load includes both WLA and LA sources on tributaries to the impaired segment.

[6] The following assumptions provide an implicit MOS:

(a) Upstream and tributary bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b) There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

Figure H.3-2 shows the segment is located in an area where karst features such as sinkholes, sinking streams, and springs exist. The sink features may capture surface drainage and channel it underground to resurface later at one or more springs. These discharging springs may occur outside the watershed where the drainage originated. However, unless karst dye trace studies indicate otherwise, groundwater catchment is presumed to correspond to the topographic watershed boundaries of surface drainage. Dye tracing in the region identified an area outside the western boundary of the Little Whippoorwill Creek watershed that contributes drainage to the segment.

Figure H.3-1 Location of Little Whippoorwill Creek 0.0 to 4.1

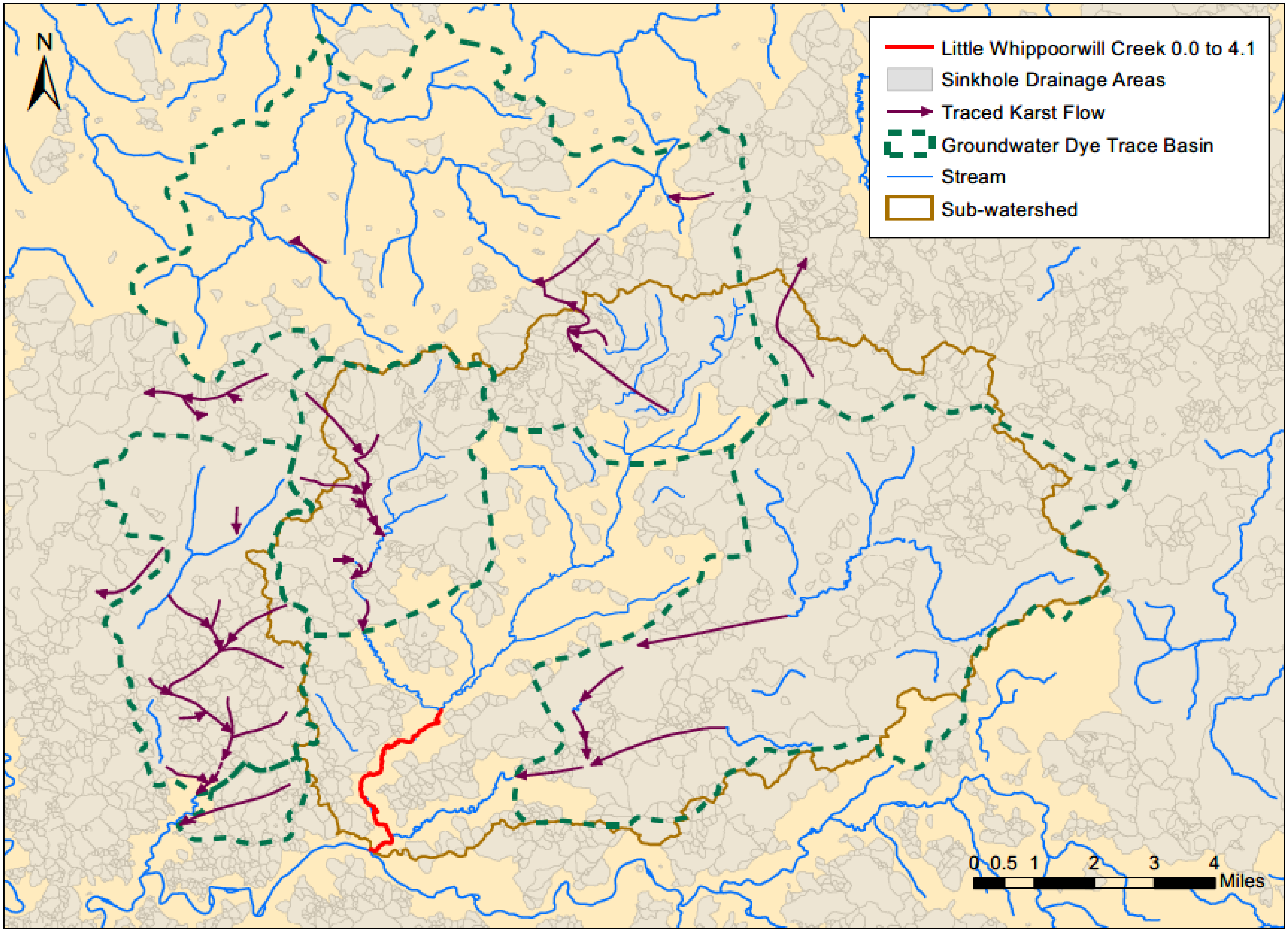


Figure H.3-2 Karst Influence in the Region of Little Whippoorwill Creek 0.0 to 4.1

Section H.4 Little Whippoorwill Creek 4.1 to 7.0

Waterbody ID: KY-1166

Receiving Water: Red River

Impaired Use: PCR

Support Status: nonsupport

Listed Pollutant/TMDL Pollutant: *E. coli*

HUC 12: 051302060204

County: Logan

The Division of Water (DOW) collected samples from station DOW20020030, located near river mile 5.85, in 2010. The station was sampled eleven times during the PCR season. Table H.4-1 summarizes information about this sampling station; Table H.4-2 provides a summary of the data collected from this station.

Table H.4-1 DOW Sample Site Location

Station Name	Latitude	Longitude	Stream Segment	River Mile
DOW20020030	36.74358	-86.84978	Little Whippoorwill Creek 4.1 to 7.0	5.85

Table H.4-2 DOW Sample Data Summary(1)

Station Name	Indicator Bacteria(2)	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
DOW20020030	*E. coli*	11	51	980	340

(1)The full data set for samples collected from station DOW20020030 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.

(2)The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for Little Whippoorwill Creek 4.1 to 7.0 are presented in Table H.4-3. As of September 2021, there are no KPDES-permitted discharges of bacteria into this segment of Little Whippoorwill Creek. The location of the segment within the Little Whippoorwill Creek watershed is shown in Figure H.4-1.

Table H.4-3 Little Whippoorwill Creek 4.1 to 7.0 *E. coli* TMDL Allocations(1)

TMDL(2)	Allocations for Direct Loads to the Segment	Allocations for Upstream Loads to the Segment(4)	MOS(5)
	LA(3)		
Q_S×WQC×CF	∑(Q_{LA}×WQC×CF)	∑($Q_{Upstream}$×WQC×CF)	Implicit

(1)All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2)Q_S is the flow (ft^3/s) in the segment.

(3)Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(4)$Q_{Upstream}$ is the flow contribution (ft^3/s) from upstream of the segment. This load includes both WLA and LA sources upstream of the impaired segment.

(5)The following assumptions provide an implicit MOS:

(a)Upstream bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b)There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

Figure H.4-2 shows the segment is located in an area where karst features such as sinkholes, sinking streams, and springs exist. The sink features may capture surface drainage and channel it underground to resurface later at one or more springs. These discharging springs may occur outside the watershed where the drainage originated. However, unless karst dye trace studies indicate otherwise, groundwater catchment is presumed to correspond to the topographic watershed boundaries of surface drainage. Dye tracing in the region identified an area outside the western boundary of the Little Whippoorwill Creek watershed that contributes drainage to the segment.

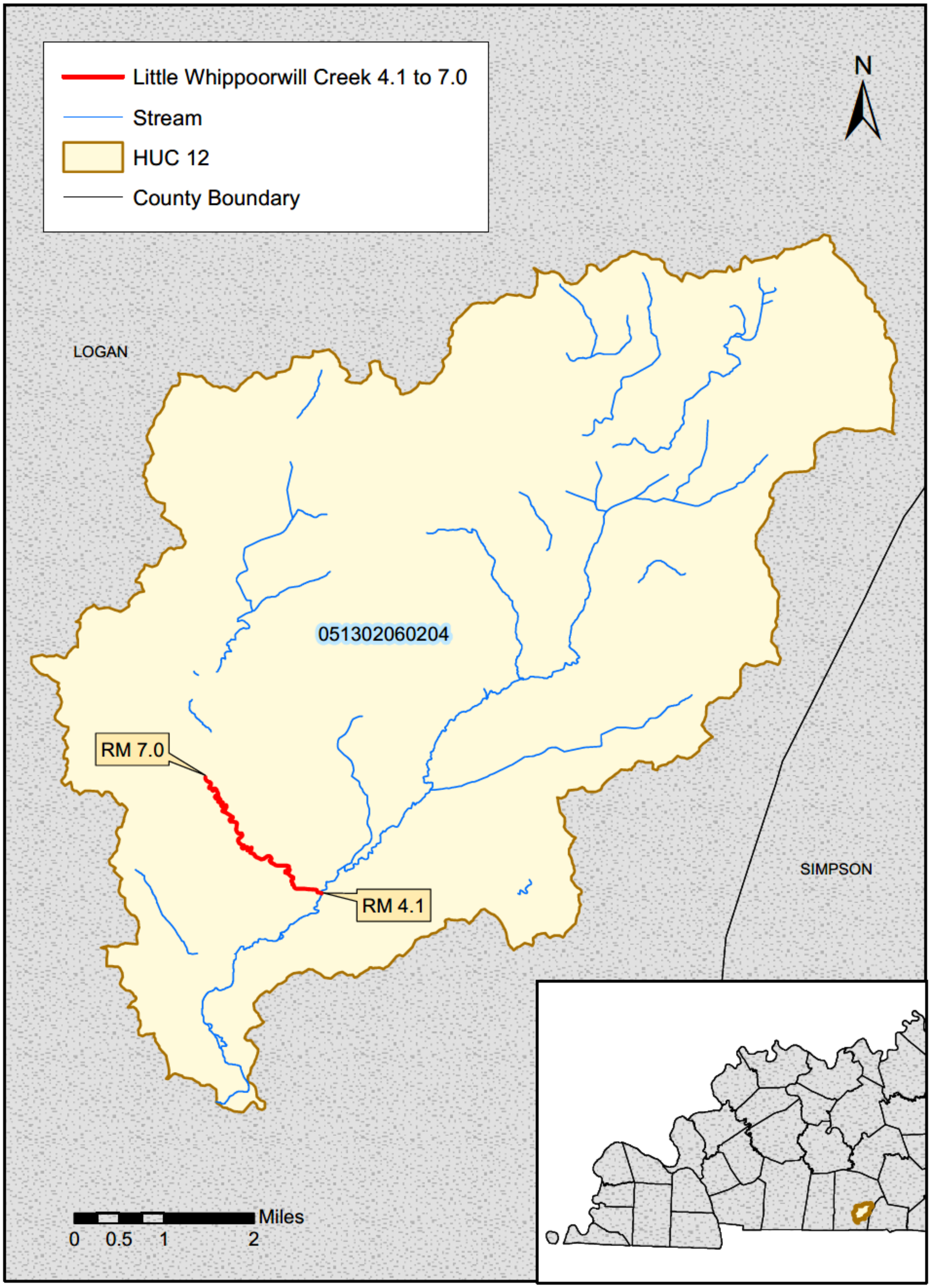


Figure H.4-1 Location of Little Whippoorwill Creek 4.1 to 7.0

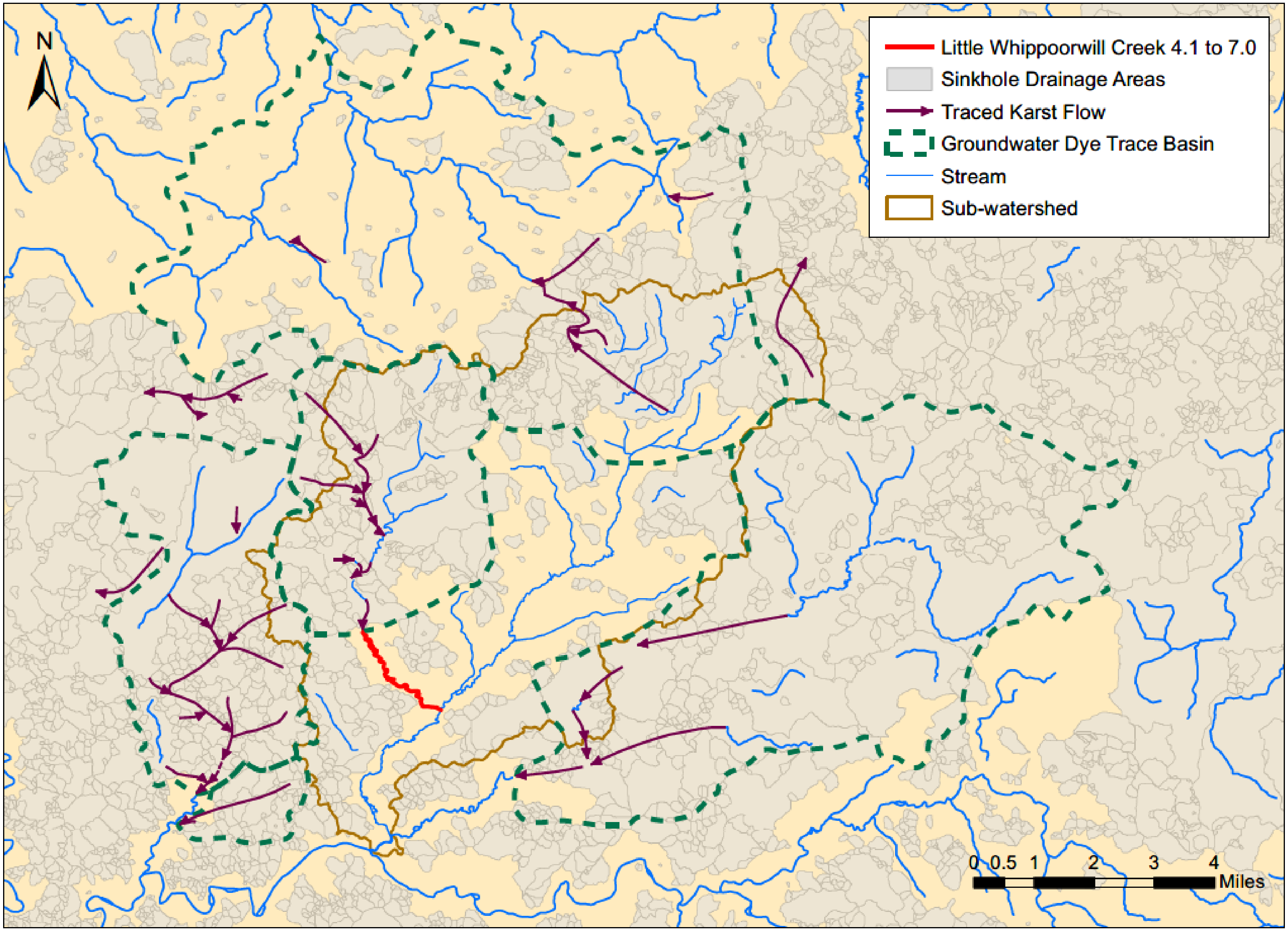


Figure H.4-2 Karst Influence in the Region of Little Whippoorwill Creek 4.1 to 7.0

Section H.5 Pleasant Grove Creek 0.0 to 2.3

Waterbody ID: KY-1481

Receiving Water: Red River

Impaired Use: PCR

Support Status: nonsupport

Listed Pollutant/TMDL Pollutant: *E. coli*

HUC 12: 051302060205

County: Logan

The Division of Water (DOW) collected samples from station DOW20020013, located near river mile 0.4, in 2010. The station was sampled twelve times during the PCR season. Table H.5-1 summarizes information about this sampling station; Table H.5-2 provides a summary of the data collected from this station.

Table H.5-1 DOW Sample Site Location

Station Name	Latitude	Longitude	Stream Segment	River Mile
DOW20020013	36.69669	-86.91889	Pleasant Grove Creek 0.0 to 2.3	0.4

Table H.5-2 DOW Sample Data Summary[1]

Station Name	Indicator Bacteria[2]	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
DOW20020013	*E. coli*	12	435	>2,420	1,176

[1] The full data set for samples collected from station DOW20020013 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.

[2] The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for Pleasant Grove Creek 0.0 to 2.3 are presented in Table H.5-3. As of September 2021, there are no KPDES-permitted discharges of bacteria into this segment of Pleasant Grove Creek. The location of the segment within the Pleasant Grove Creek-Red River watershed is shown in Figure H.5-1.

Table H.5-3 Pleasant Grove Creek 0.0 to 2.3 *E. coli* TMDL Allocations(1)

TMDL(2)	Allocations for Direct Loads to the Segment	Allocations for Upstream Loads to the Segment(4)	Allocations for Tributary Loads to the Segment(5)	MOS(6)
	LA(3)			
Q_S×WQC×CF	∑(Q_{LA}×WQC×CF)	∑($Q_{Upstream}$×WQC×CF)	∑($Q_{Tributary}$×WQC×CF)	Implicit

(1)All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2)Q_S is the flow (ft^3/s) in the segment.

(3)Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(4)$Q_{Upstream}$ is the flow contribution (ft^3/s) from upstream of the segment. This load includes both WLA and LA sources upstream of the impaired segment.

(5)$Q_{Tributary}$ is the flow contribution (ft^3/s) from a tributary to the segment. This load includes both WLA and LA sources on tributaries to the impaired segment.

(6)The following assumptions provide an implicit MOS:

(a)Upstream and tributary bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b)There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

Figure H.5-2 shows the segment is located in an area where karst features such as sinkholes, sinking streams, and springs exist. The sink features may capture surface drainage and channel it underground to resurface later at one or more springs. These discharging springs may occur outside the watershed where the drainage originated. However, unless karst dye trace studies indicate otherwise, groundwater catchment is presumed to correspond to the topographic watershed boundaries of surface drainage. Dye tracing in the region did not identify any areas outside the boundary of the Pleasant Grove Creek watershed that contribute drainage to the segment.

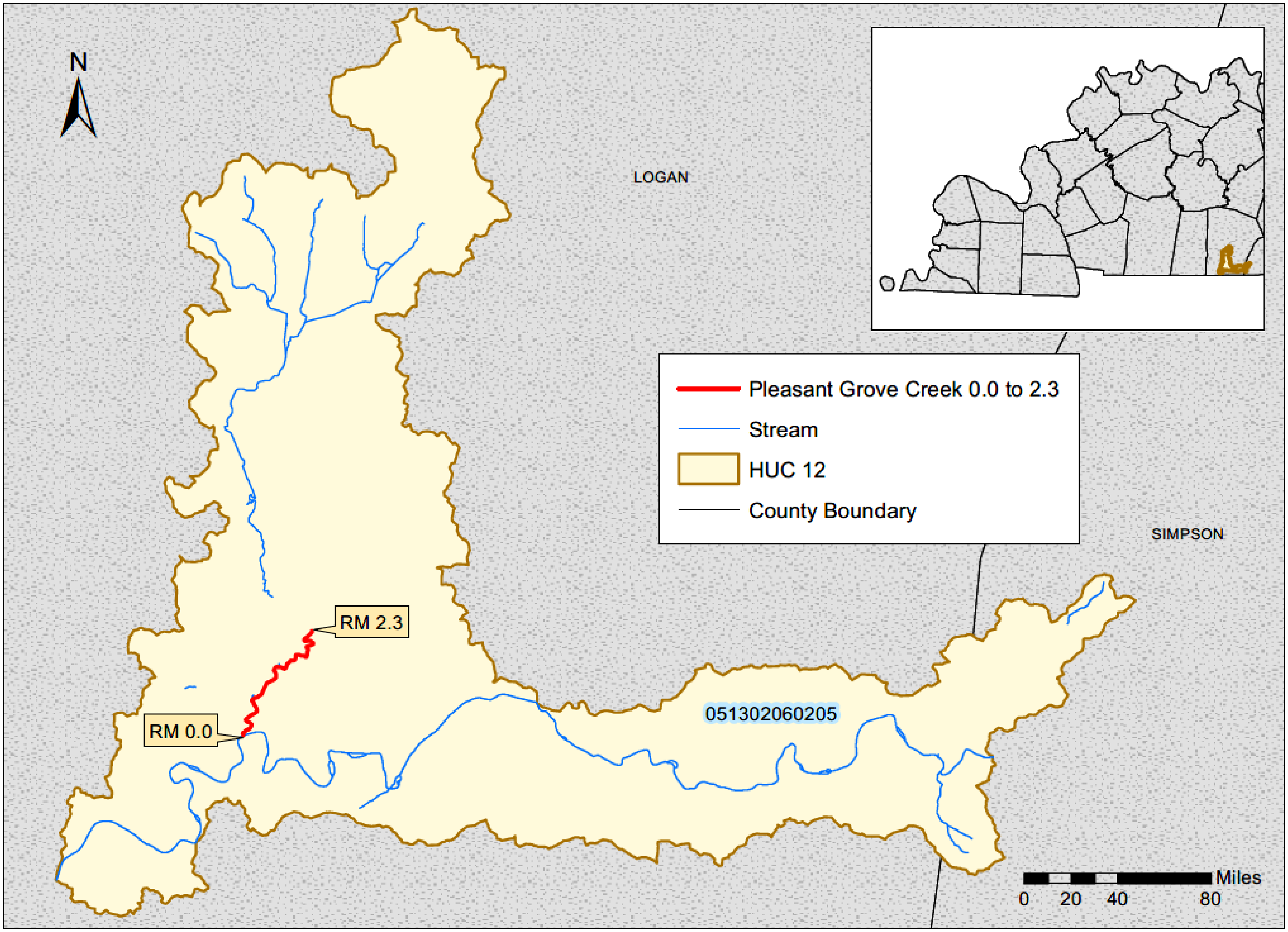


Figure H.5-1 Location of Pleasant Grove Creek 0.0 to 2.3

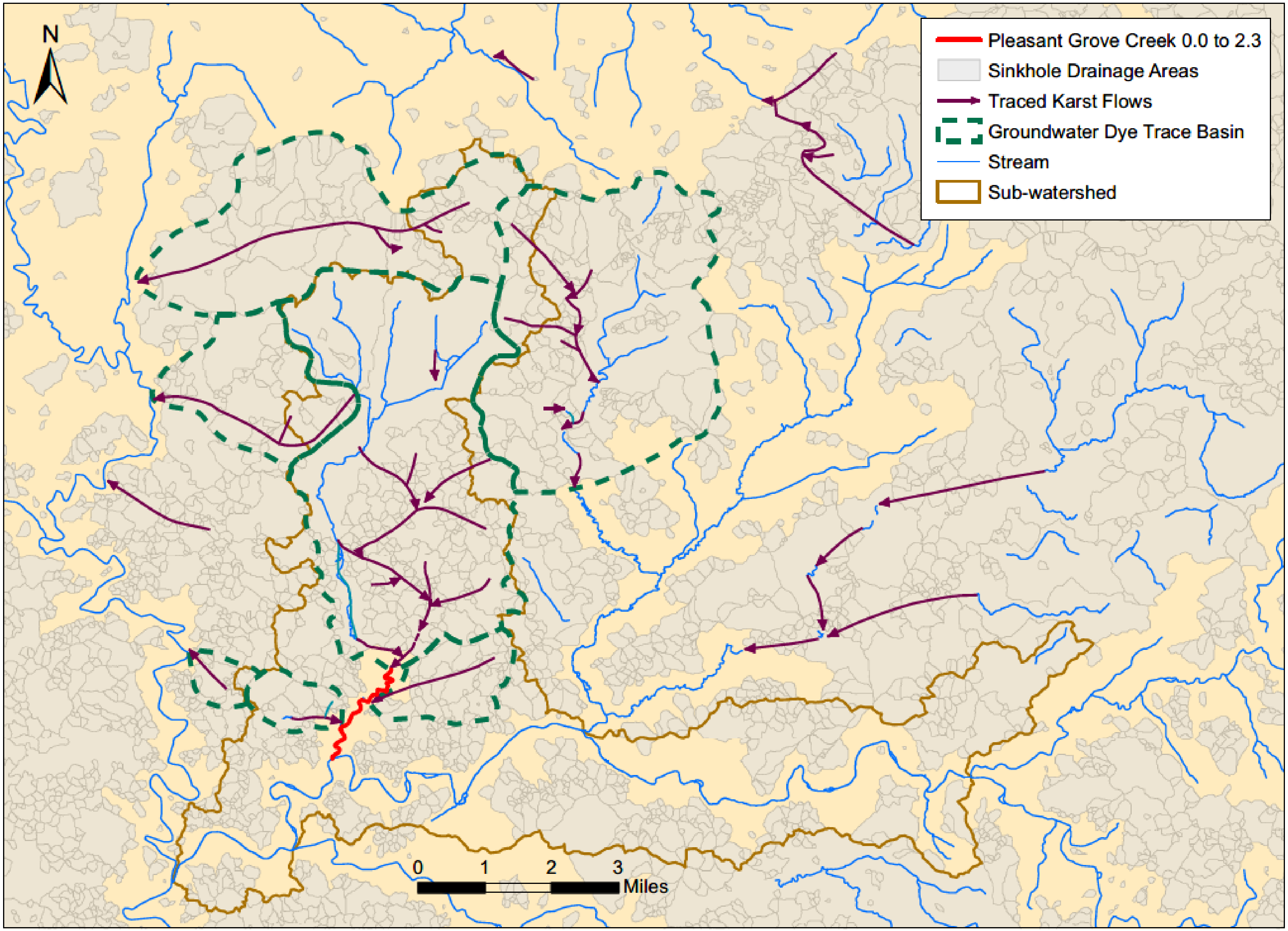


Figure H.5-2 Karst Influence in the Region of Pleasant Grove Creek 0.0 to 2.3

Section H.6 Pleasant Run 0.0 to 2.15

Waterbody ID: KY-1482

Receiving Water: Little Whippoorwill Creek

Impaired Use: PCR

Support Status: nonsupport

Listed Pollutant/TMDL Pollutant: *E. coli*

HUC 12: 051302060204

County: Logan

The Division of Water (DOW) collected samples from station DOW20020014, located near river mile 1.6, in 2010. The station was sampled six times during the PCR season. Table H.6-1 summarizes information about this sampling station; Table H.6-2 provides a summary of the data collected from this station.

Table H.6-1 DOW Sample Site Location

Station Name	Latitude	Longitude	Stream Segment	River Mile
DOW20020014	36.74549	-86.81672	Pleasant Run 0.0 to 2.15	1.6

Table H.6-2 DOW Sample Data Summary(1)

Station Name	Indicator Bacteria(2)	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
DOW20020014	*E. coli*	6	172	>2,420	1,084

(1)The full data set for samples collected from station DOW20020014 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.
(2)The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for Pleasant Run 0.0 to 2.15 are presented in Table H.6-3. As of September 2021, there are no KPDES-permitted discharges of bacteria into this segment of Pleasant Run. The location of the segment within the Little Whippoorwill Creek watershed is shown in Figure H.6-1.

Table H.6-3 Pleasant Run 0.0 to 2.15 *E. coli* TMDL Allocations[1]

TMDL[2]	Allocations for Direct Loads to the Segment LA[3]	Allocations for Upstream Loads to the Segment[4]	Allocations for Tributary Loads to the Segment[5]	MOS[6]
Q_S×WQC×CF	∑(Q_{LA}×WQC×CF)	∑($Q_{Upstream}$×WQC×CF)	∑($Q_{Tributary}$×WQC×CF)	Implicit

(1)All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2)Q_S is the flow (ft^3/s) in the segment.

(3)Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(4)$Q_{Upstream}$ is the flow contribution (ft^3/s) from upstream of the segment. This load includes both WLA and LA sources upstream of the impaired segment.

(5)$Q_{Tributary}$ is the flow contribution (ft^3/s) from a tributary to the segment. This load includes both WLA and LA sources on tributaries to the impaired segment.

(6)The following assumptions provide an implicit MOS:

(a)Upstream and tributary bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b)There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

Figure H.6-2 shows the segment is located in an area where karst features such as sinkholes, sinking streams, and springs exist. The sink features may capture surface drainage and channel it underground to resurface later at one or more springs. These discharging springs may occur outside the watershed where the drainage originated. However, unless karst dye trace studies indicate otherwise, groundwater catchment is presumed to correspond to the topographic watershed boundaries of surface drainage. Dye tracing in the region did not identify any areas outside the boundary of the Little Whippoorwill Creek watershed that contribute drainage to the segment.

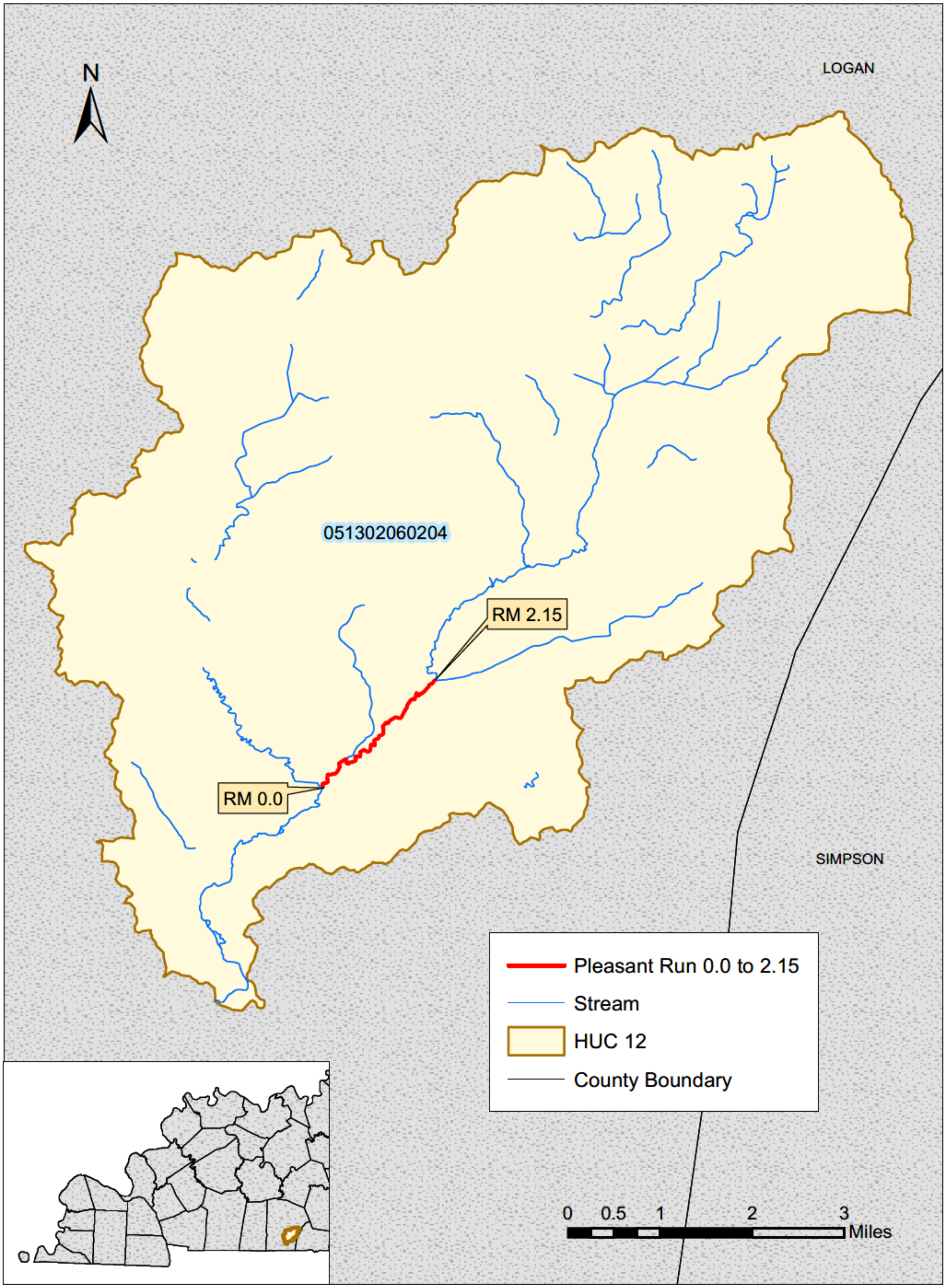


Figure H.6-1 Location of Pleasant Run 0.0 to 2.15

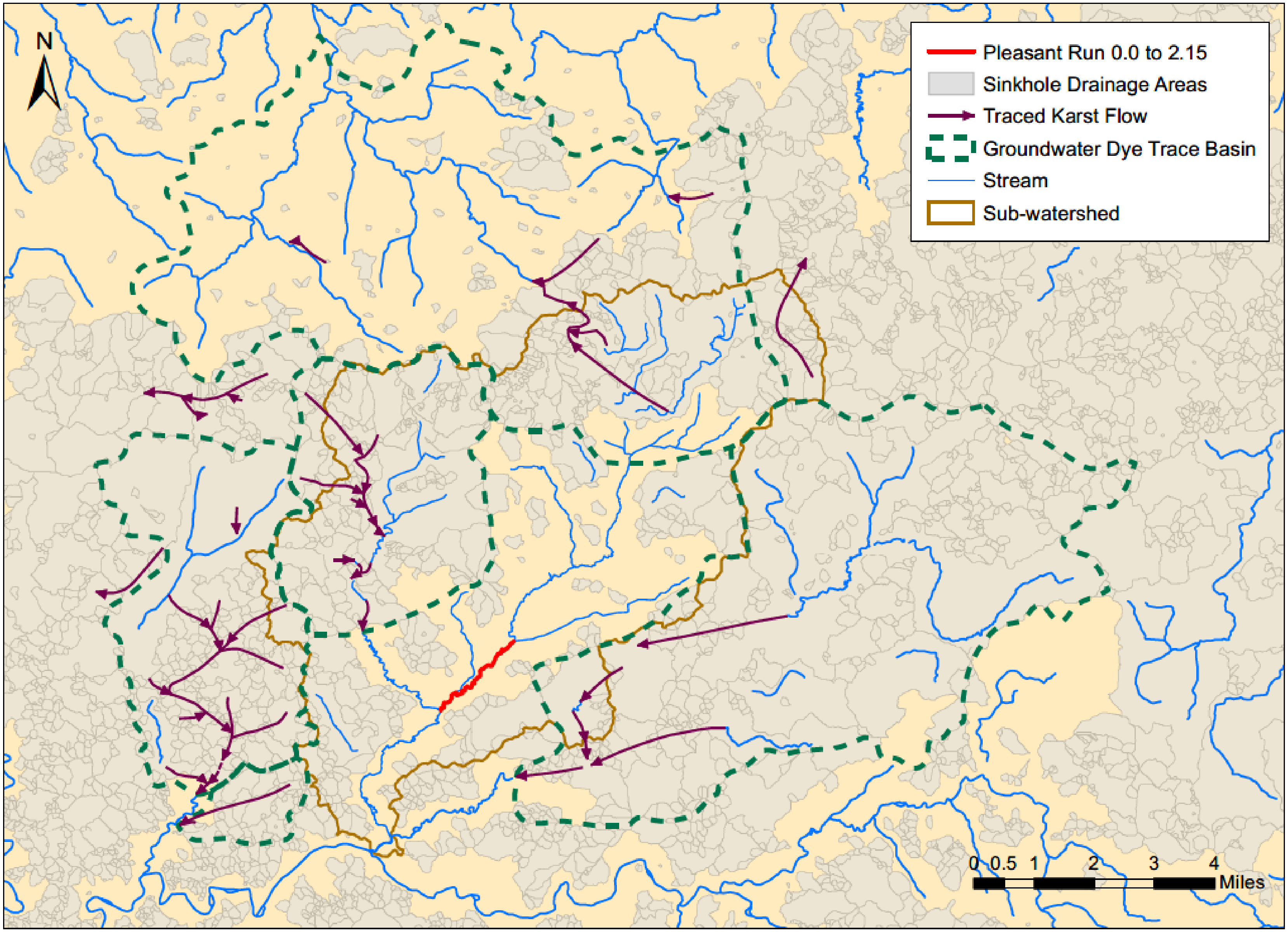


Figure H.6-2 Karst Influence in the Region of Pleasant Run 0.0 to 2.15

Section H.7 Red River 50.9 to 54.5

Waterbody ID: KY-1559

Receiving Water: Cumberland River

Impaired Use: PCR

Support Status: partial support

Listed Pollutant/TMDL Pollutant: *E. coli*

HUC 12: 051302060702

County: Logan

The Division of Water (DOW) collected one to six samples at station PRI069, located near river mile 47.6, every year between 1999 and 2020 except for 2004. DOW collected samples from station DOW20020023, located near river mile 49.6. The station was sampled nine times during the PCR season in 2010. Table H.7-1 summarizes information about these sampling stations; Table H.7-2 provides a summary of the data collected from these stations.

Table H.7-1 DOW Sample Site Locations

Station Name	Latitude	Longitude	Stream Segment	River Mile
PRI069	36.640657	-97.9693	Red River 50.9 to 54.5	47.6
DOW20020023	36.64071	-86.9798	Red River 50.9 to 54.5	49.6

Table H.7-2 DOW Sample Data Summary(1)

Station Name	Indicator Bacteria(2)	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
PRI069	*E. coli*	49	45	>2,420	557
PRI069	fecal coliform	27	1	1,700	327
DOW20020023	*E. coli*	9	46	>2,420	492

(1)The full data set for samples collected from stations PRI069 and DOW20020023 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.

(2)The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for Red River 50.9 to 54.5 are presented in Table H.7-3. As of September 2021, there are no KPDES-permitted discharges of bacteria into this segment of Red River. The location of the segment within the Buzzard Creek-Red River watershed is shown in Figure H.7-1.

Table H.7-3 Red River 50.9 to 54.5 *E. coli* TMDL Allocations(1)

TMDL(2)	Allocations for Direct Loads to the Segment	Allocations for Upstream Loads to the Segment(4)	Allocations for Tributary Loads to the Segment(5)	MOS(6)
	LA(3)			
Q_S×WQC×CF	∑(Q_{LA}×WQC×CF)	∑($Q_{Upstream}$×WQC×CF)	∑($Q_{Tributary}$×WQC×CF)	Implicit

(1)All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2)Q_S is the flow (ft^3/s) in the segment.

(3)Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(4)$Q_{Upstream}$ is the flow contribution (ft^3/s) from upstream of the segment. This load includes both WLA and LA sources upstream of the impaired segment.

(5)$Q_{Tributary}$ is the flow contribution (ft^3/s) from a tributary to the segment. This load includes both WLA and LA sources on tributaries to the impaired segment.

(6)The following assumptions provide an implicit MOS:

(a)Upstream and tributary bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b)There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

Figure H.7-2 shows the segment is located in an area where karst features such as sinkholes, sinking streams, and springs exist. The sink features may capture surface drainage and channel it underground to resurface later at one or more springs. These discharging springs may occur outside the watershed where the drainage originated. However, unless karst dye trace studies indicate otherwise, groundwater catchment is presumed to correspond to the topographic watershed boundaries of surface drainage. Dye tracing in Kentucky identified a small area from the Brush Creek watershed of the Green River basin, northeast of the Red River sub-watershed boundary, that may contribute drainage to tributaries of Red River.

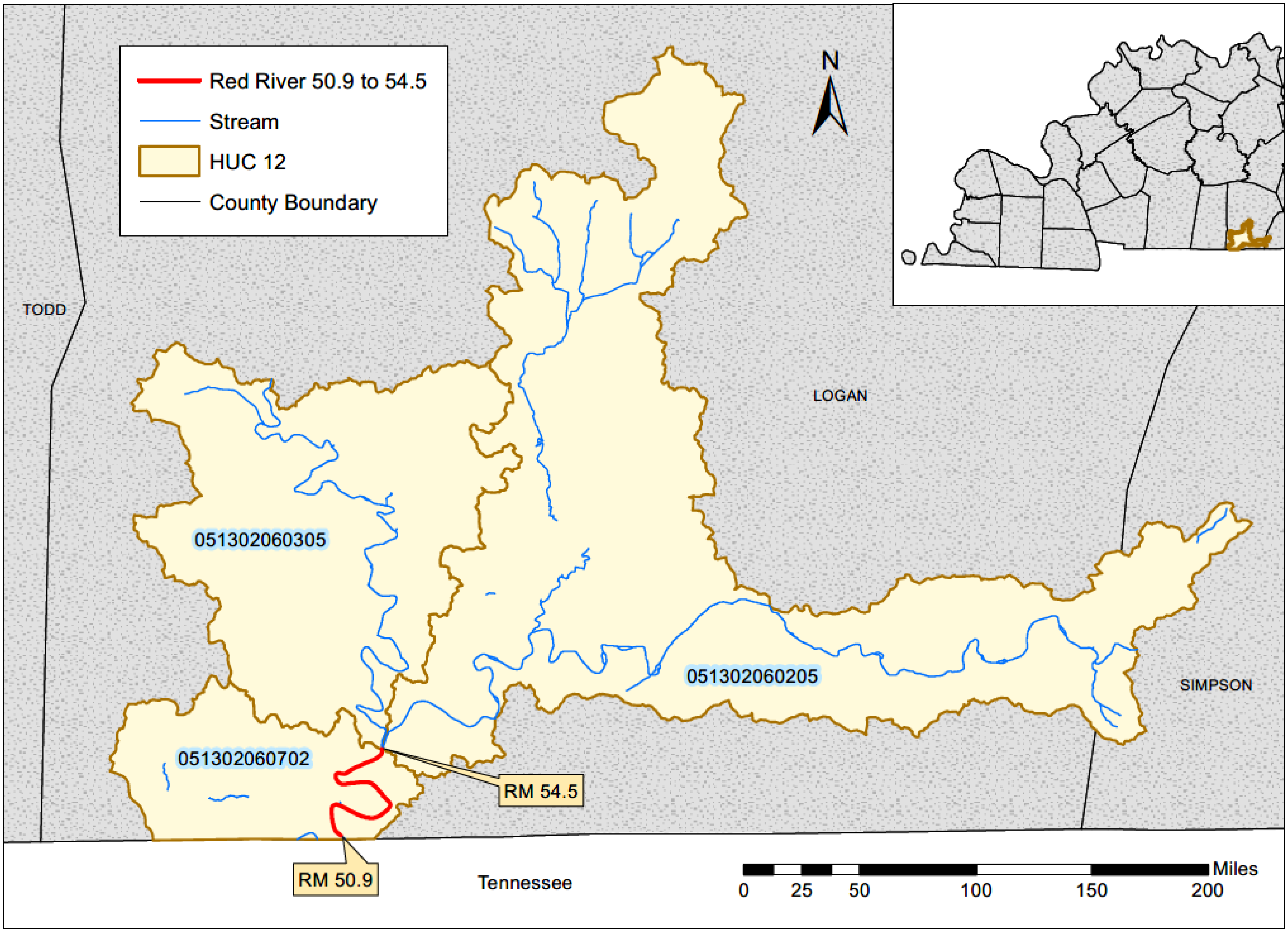


Figure H.7-1 Location of Red River 50.9 to 54.5

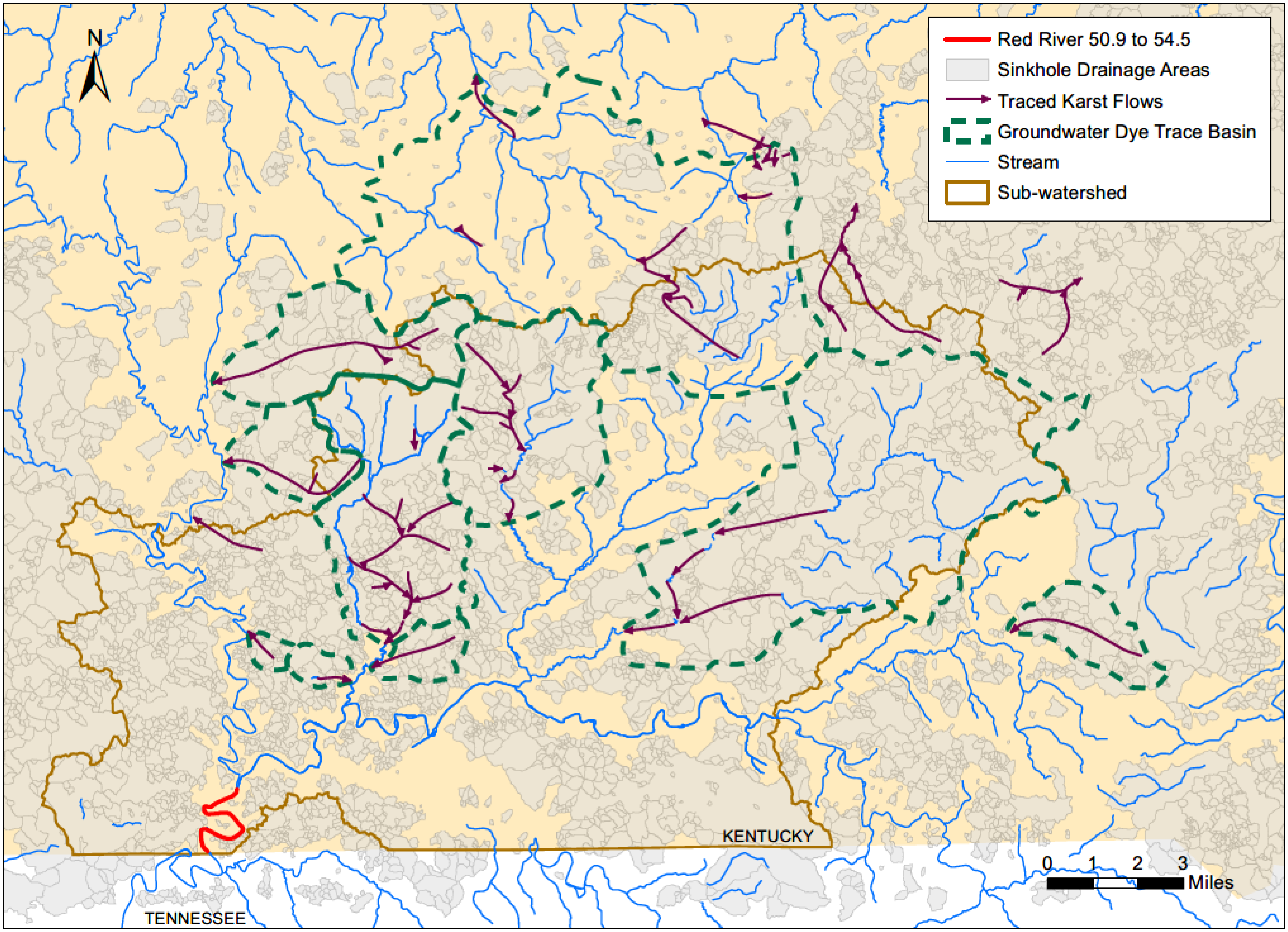


Figure H.7-2 Karst Influence in the Region of Red River 50.9 to 54.5

Section H.8 Red River 54.5 to 56.90

Waterbody ID: KY-1560

Receiving Water: Cumberland River

Impaired Use: PCR

Support Status: partial support

Listed Pollutant/TMDL Pollutant: *E. coli*

HUC 12: 051302060205

County: Logan

The Division of Water (DOW) collected samples from station SWD02120502, located near river mile 55.6, in 2010. The station was sampled twelve times during the PCR season. Table H.8-1 summarizes information about this sampling station; Table H.8-2 provides a summary of the data collected from this station.

Table H.8-1 DOW Sample Site Location

Station Name	Latitude	Longitude	Stream Segment	River Mile
SWD02120502	36.67694	-86.95167	Red River 54.5 to 56.90	55.6

Table H.8-2 DOW Sample Data Summary(1)

Station Name	Indicator Bacteria(2)	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
SWD02120502	*E. coli*	12	66	>2,420	395

(1)The full data set for samples collected from SWD02120502 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.

(2)The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for Red River 54.5 to 56.90 are presented in Table H.8-3. As of September 2021, there are no KPDES-permitted discharges of bacteria into this segment of Red River. The location of the segment within the Pleasant Grove Creek-Red River watershed is shown in Figure H.8-1.

Table H.8-3 Red River 54.5 to 56.90 *E. coli* TMDL Allocations(1)

TMDL(2)	Allocations for Direct Loads to the Segment	Allocations for Upstream Loads to the Segment(4)	MOS(5)
	LA(3)		
Q_S×WQC×CF	∑(Q_{LA}×WQC×CF)	∑($Q_{Upstream}$×WQC×CF)	Implicit

(1)All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2)Q_S is the flow (ft^3/s) in the segment.

(3)Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(4)$Q_{Upstream}$ is the flow contribution (ft^3/s) from upstream of the segment. This load includes both WLA and LA sources upstream of the impaired segment.

(5)The following assumptions provide an implicit MOS:

(a)Upstream bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b)There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

Figure H.8-2 shows the segment is located in an area where karst features such as sinkholes, sinking streams, and springs exist. The sink features may capture surface drainage and channel it underground to resurface later at one or more springs. These discharging springs may occur outside the watershed where the drainage originated. However, unless karst dye trace studies indicate otherwise, groundwater catchment is presumed to correspond to the topographic watershed boundaries of surface drainage. Dye tracing in Kentucky identified a small area from the Brush Creek watershed of the Green River basin, northeast of the Red River sub-watershed boundary, that may contribute drainage to tributaries of Red River.

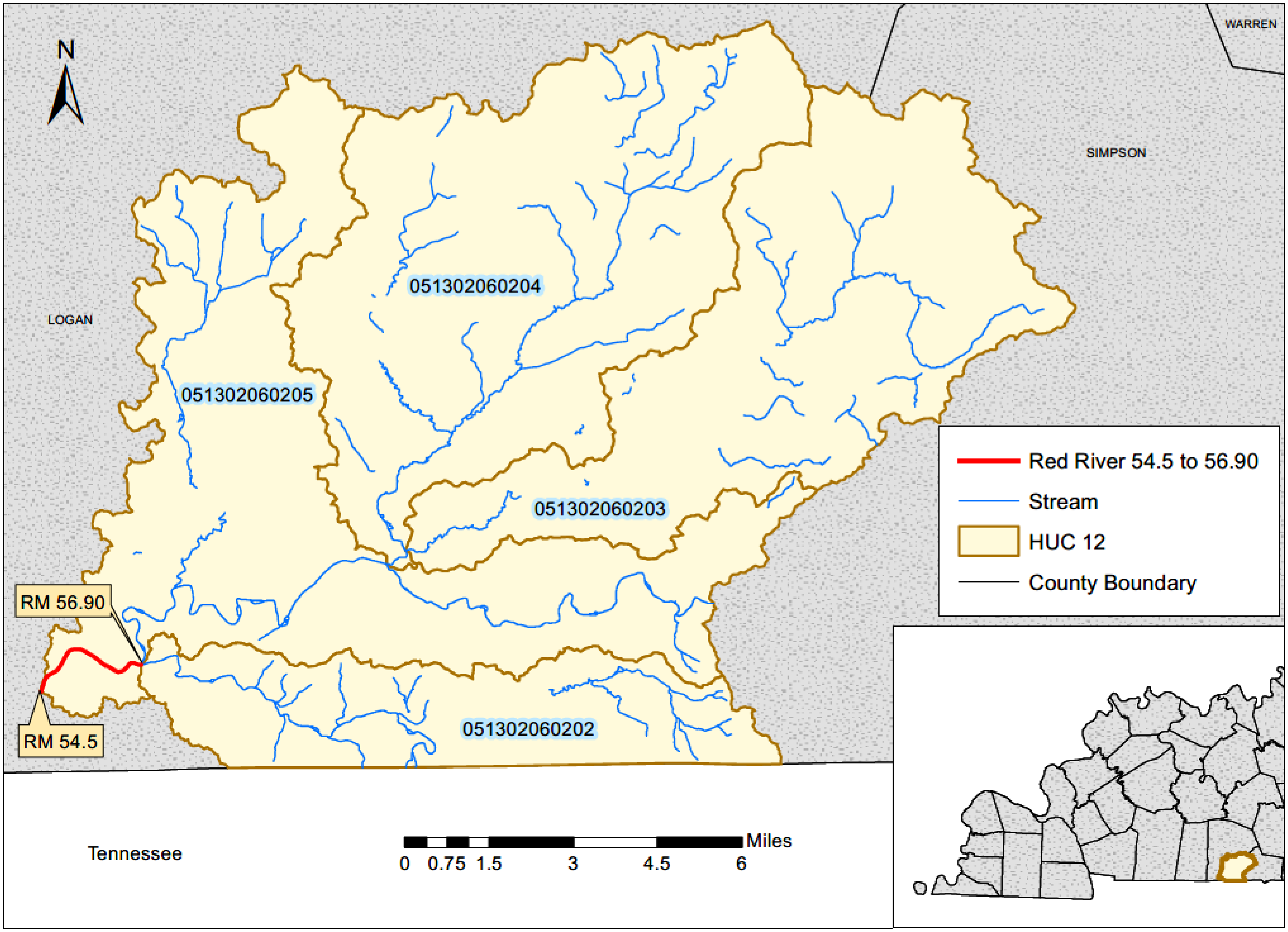
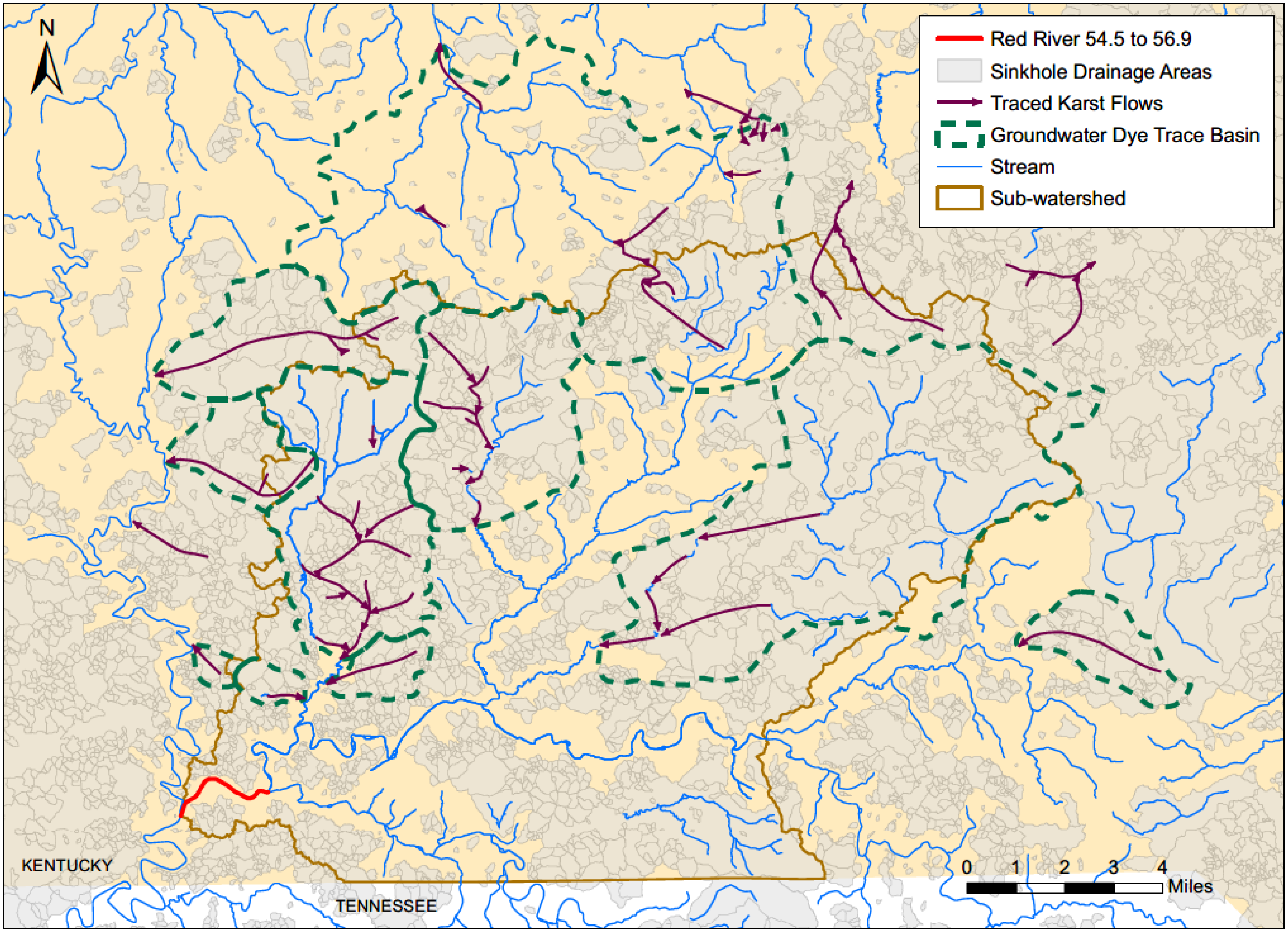


Figure H.8-1 Location of Red River 54.5 to 56.90



H.8-2 Karst Influence in the Region of Red River 54.5 to 56.90

Section H.9 Red River 56.9 to 65.75

Waterbody ID: KY-1561

Receiving Water: Cumberland River

Impaired Use: PCR

Support Status: nonsupport

Listed Pollutant/TMDL Pollutant: *E. coli*

HUC 12: 051302060205

County: Logan

The Division of Water (DOW) collected samples during the PCR season from three stations on this segment. In 2010, twelve samples were collected during the PCR season from stations DOW20020021 and DOW20020016. The station, RED001, was sampled six times during the PCR season in 2005 and was discontinued as an Ambient Monitoring Network Station. Table H.9-1 summarizes information about these sampling stations; Table H.9-2 provides a summary of the data collected from these stations.

Table H.9-1 DOW Sample Site Locations

Station Name	Latitude	Longitude	Stream Segment	River Mile
DOW20020021	36.67304	-86.9314	Red River 56.9 to 65.75	56.95
DOW20020016	36.7011	-86.8616	Red River 56.9 to 65.75	65.25
RED001	36.67819	-86.93212	Red River 56.9 to 65.75	57.3

Table H.9-2 DOW Sample Data Summary(1)

Station Name	Indicator Bacteria(2)	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
DOW20020021	*E. coli*	12	118	>2,420	425
DOW20020016	*E. coli*	12	250	>2,420	943
RED001	fecal coliform	6	139	431	287

(1)The full data set for samples collected from DOW20020021, DOW20020016 and RED001 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.

(2)The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for Red River 56.9 to 65.75 are presented in Table H.9-3. As of September 2021, there are no KPDES-permitted discharges of bacteria into this segment of Red River. The location of the segment within the Pleasant Grove Creek-Red River watershed is shown in Figure H.9-1.

Table H.9-3 Red River 56.9 to 65.75 *E. coli* TMDL Allocations(1)

TMDL(2)	Allocations for Direct Loads to the Segment	Allocations for Upstream Loads to the Segment(4)	Allocations for Tributary Loads to the Segment(5)	MOS(6)
	LA(3)			
$Q_S \times WQC \times CF$	$\sum(Q_{LA} \times WQC \times CF)$	$\sum(Q_{Upstream} \times WQC \times CF)$	$\sum(Q_{Tributary} \times WQC \times CF)$	Implicit

(1)All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2)Q_S is the flow (ft^3/s) in the segment.

(3)Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(4)$Q_{Upstream}$ is the flow contribution (ft^3/s) from upstream of the segment. This load includes both WLA and LA sources upstream of the impaired segment.

(5)$Q_{Tributary}$ is the flow contribution (ft^3/s) from a tributary to the segment. This load includes both WLA and LA sources on tributaries to the impaired segment.

(6)The following assumptions provide an implicit MOS:

(a)Upstream and tributary bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b)There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

Figure H.9-2 shows the segment is located in an area where karst features such as sinkholes, sinking streams, and springs exist. The sink features may capture surface drainage and channel it underground to resurface later at one or more springs. These discharging springs may occur outside the watershed where the drainage originated. However, unless karst dye trace studies indicate otherwise, groundwater catchment is presumed to correspond to the topographic watershed boundaries of surface drainage. Dye tracing in Kentucky identified a small area from the Brush Creek watershed of the Green River basin, east of the Pleasant Grove Creek-Red River watershed boundary, that may contribute drainage to tributaries of Red River.

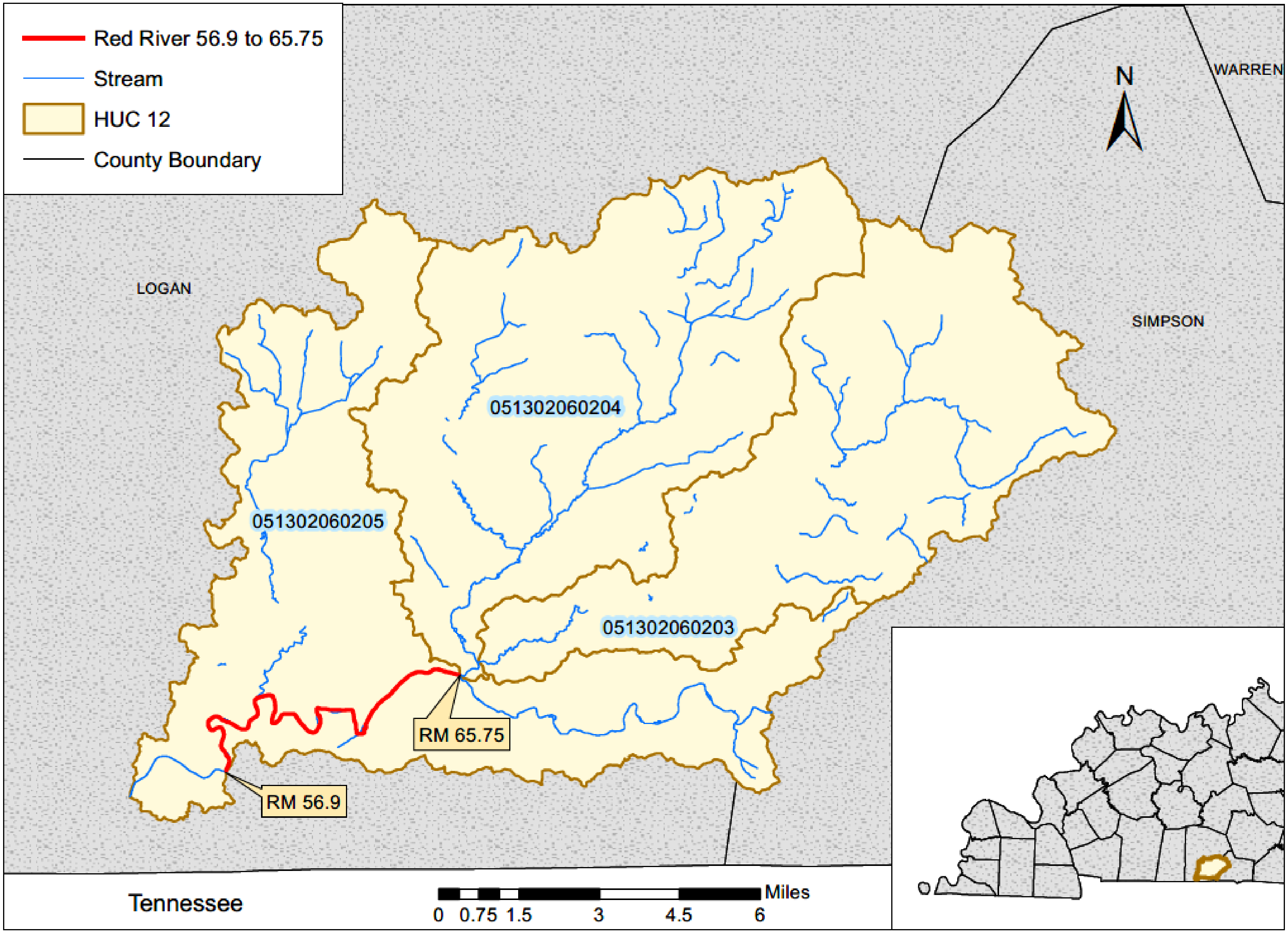


Figure H.9-1 Location of Red River 56.9 to 65.75

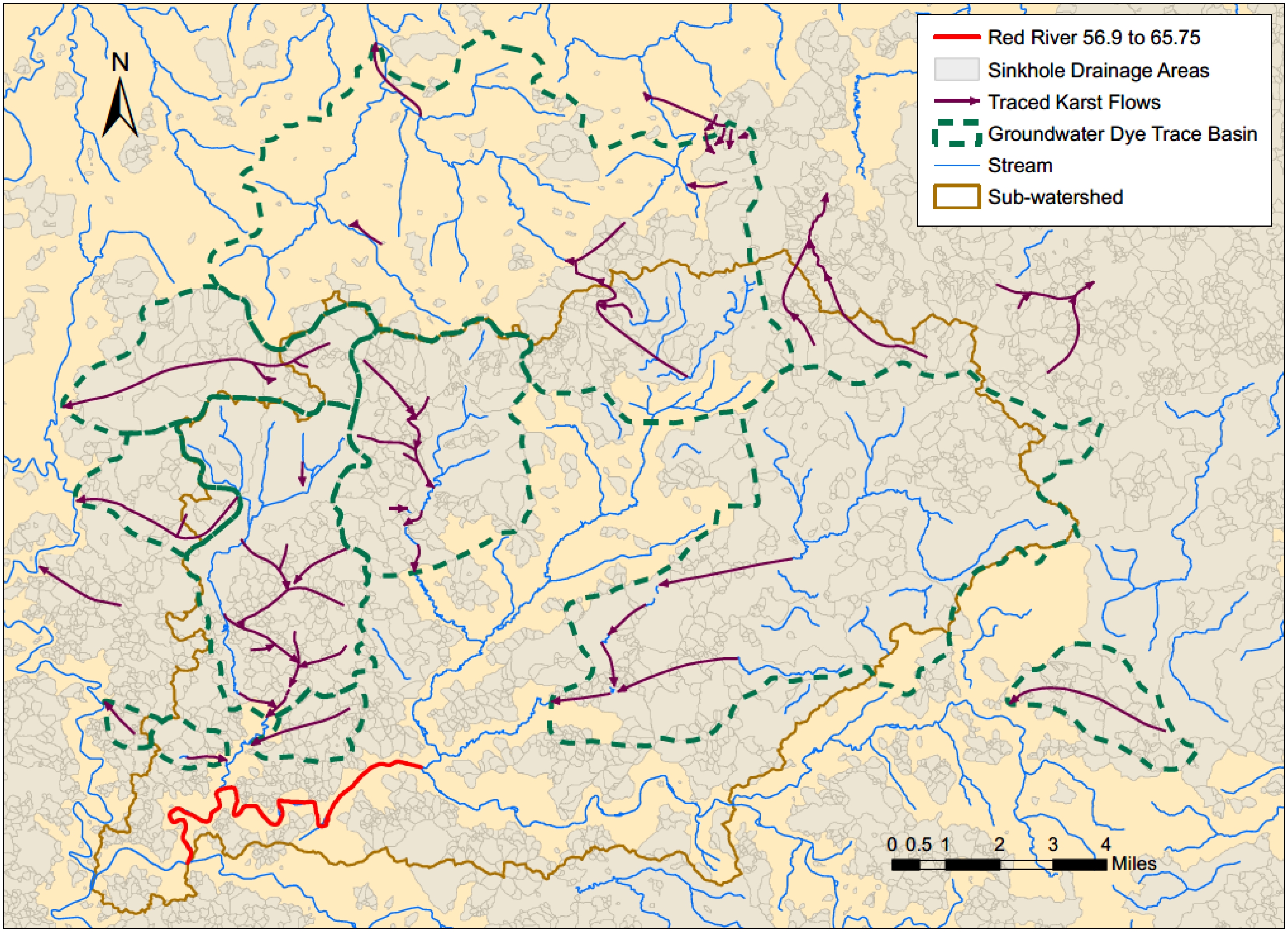


Figure H.9-2 Karst Influence in the Region of Red River 56.9 to 65.75

Section H.10 Red River 74.3 to 81.3

Waterbody ID: KY-1563

Receiving Water: Cumberland River

Impaired Use: PCR

Support Status: nonsupport

Listed Pollutant/TMDL Pollutant: *E. coli*

HUC 12: 051302060102

County: Simpson

The Division of Water (DOW) collected samples from station SWD02120505, located near river mile 81.96, in 2010. The station was sampled twelve times during the PCR season. Table H.10-1 summarizes information about the sampling station; Table H.10-2 provides a summary of the data collected from this station.

Table H.10-1 DOW Sample Site Location

Station Name	Latitude	Longitude	Stream Segment	River Mile
SWD02120505	36.64362	-86.6795	Red River 74.3 to 81.3	81.96

Table H.10-2 DOW Sample Data Summary(1)

Station Name	Indicator Bacteria(2)	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
SWD02120505	*E. coli*	12	45	517	197

(1)The full data set for samples collected from SWD02120505 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.

(2)The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for Red River 74.3 to 81.3 are presented in Table H.10-3. As of September 2021, there are no KPDES-permitted discharges of bacteria into this segment of Red River. The location of the segment within the Sulphur Spring Creek-Red River watershed is shown in Figure E.10-1.

Table H.10-3 Red River 74.3 to 81.3 *E. coli* TMDL Allocations(1)

TMDL(2)	Allocations for Direct Loads to the Segment	Allocations for Upstream Loads to the Segment(4)	Allocations for Tributary Loads to the Segment(5)	MOS(6)
	LA(3)			
Q_S×WQC×CF	∑(Q_{LA}×WQC×CF)	∑($Q_{Upstream}$×WQC×CF)	∑($Q_{Tributary}$×WQC×CF)	Implicit

(1)All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2)Q_S is the flow (ft^3/s) in the segment.

(3)Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(4)$Q_{Upstream}$ is the flow contribution (ft^3/s) from upstream of the segment. This load includes both WLA and LA sources upstream of the impaired segment.

(5)$Q_{Tributary}$ is the flow contribution (ft^3/s) from a tributary to the segment. This load includes both WLA and LA sources on tributaries to the impaired segment.

(6)The following assumptions provide an implicit MOS:

(a)Upstream and tributary bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b)There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

Figure H.10-2 shows the segment is located in an area where karst features such as sinkholes, sinking streams, and springs exist. The sink features may capture surface drainage and channel it underground to resurface later at one or more springs. These discharging springs may occur outside the watershed where the drainage originated. However, unless karst dye trace studies indicate otherwise, groundwater catchment is presumed to correspond to the topographic watershed boundaries of surface drainage. Dye tracing in Kentucky has identified small areas of the Green River basin that contribute drainage to tributaries of Red River downstream of this segment. None of the Kentucky studies has identified areas outside the Red River watershed that are contributing drainage to this segment, however. Additional areas of sinkholes are located upstream of the segment in Tennessee.

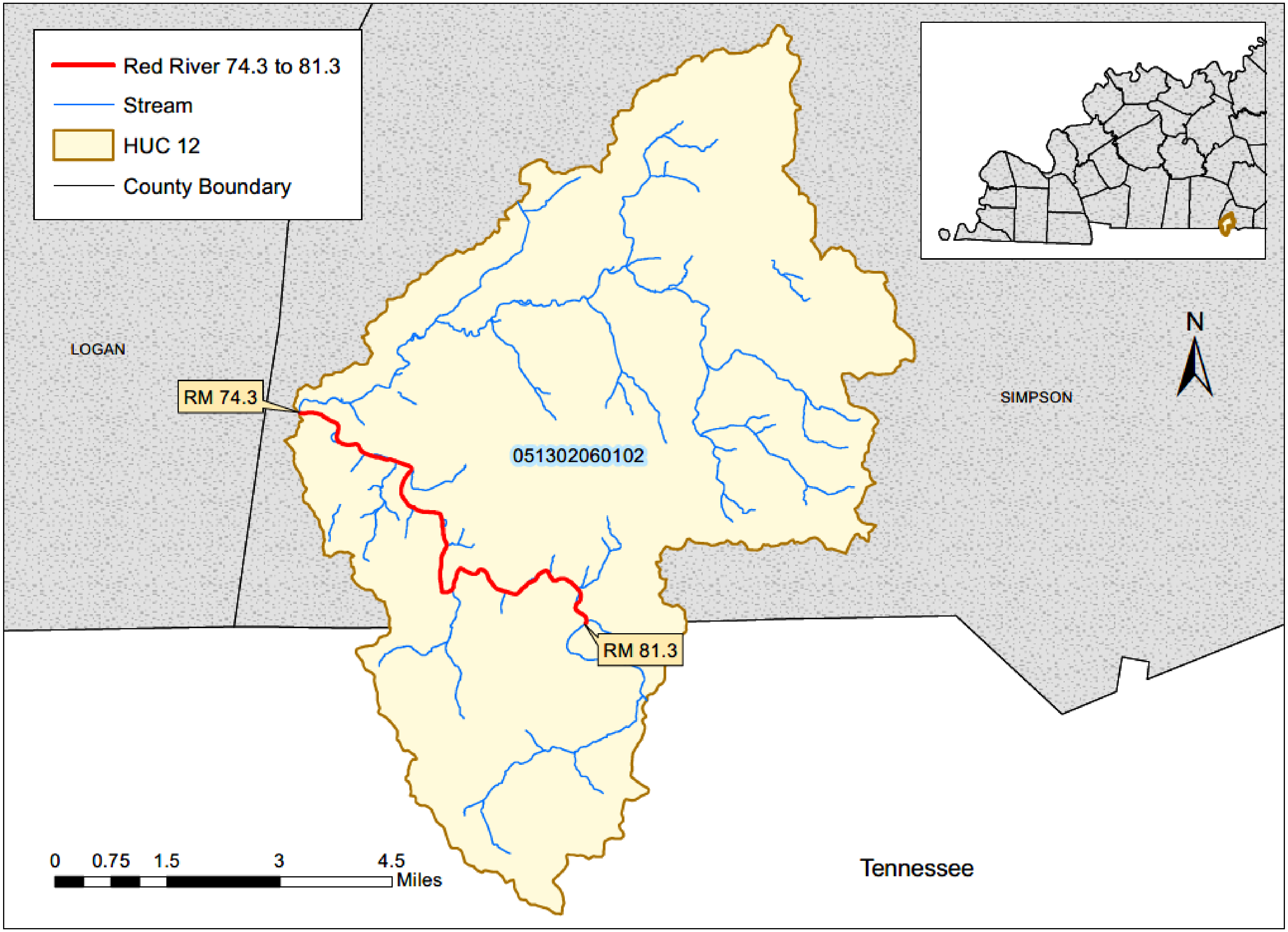


Figure H.10-1 Location of Red River 74.3 to 81.3

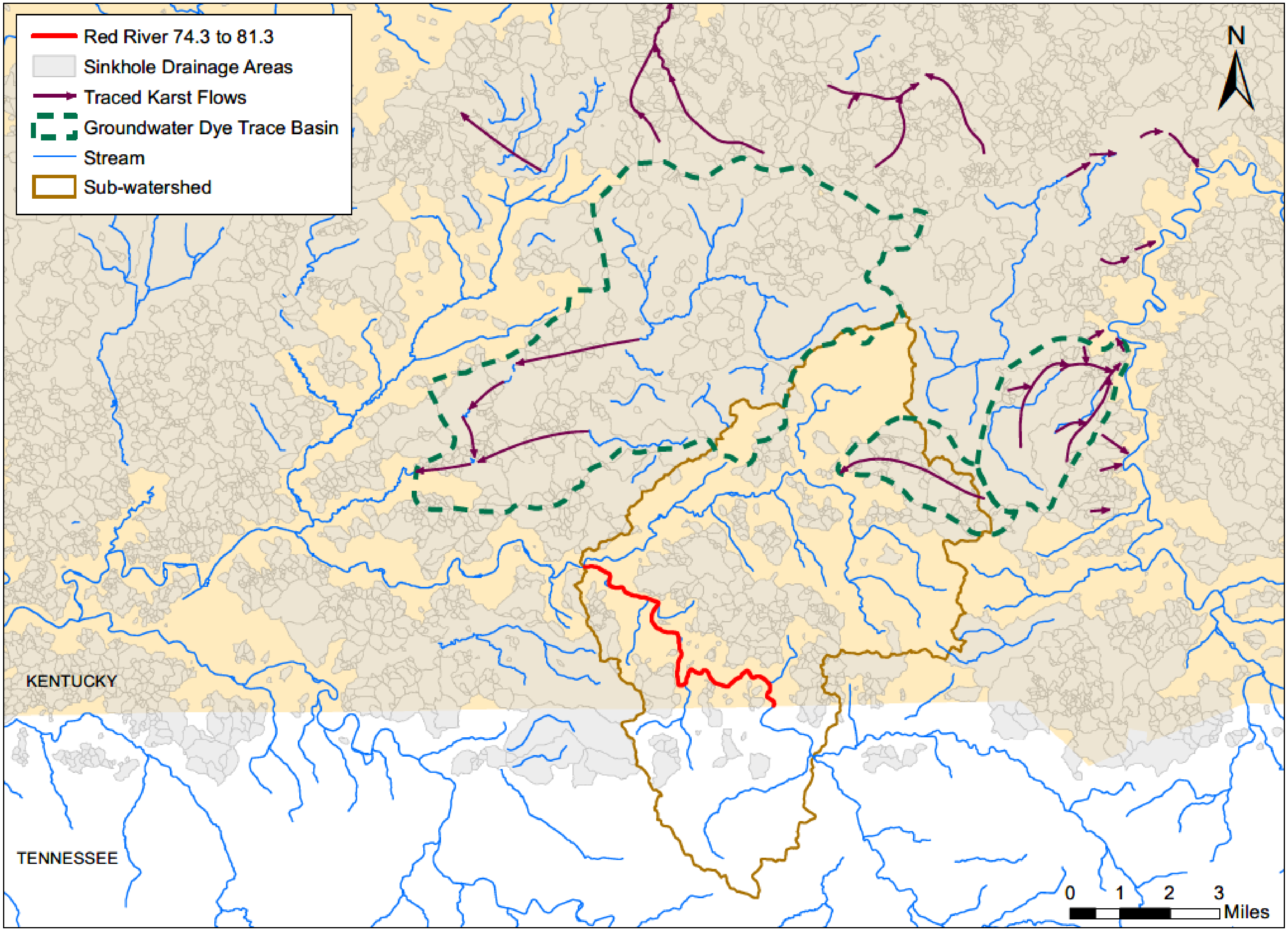


Figure H.10-2 Karst Influence in the Region of Red River 74.3 to 81.3

Section H.11 Sinking Creek 0.0 to 3.3

Waterbody ID: KY-1716

Receiving Water: Little Whippoorwill Creek

Impaired Use: PCR

Support Status: nonsupport

Listed Pollutant/TMDL Pollutant: *E. coli*

HUC 12: 051302060203

County: Logan

The Division of Water (DOW) collected samples from station DOW20020017, located near river mile 0.4, in 2010. The station was sampled twelve times during the PCR season. Table H.11-1 summarizes information about this sampling station; Table H.11-2 provides a summary of the data collected from this station.

Table H.11-1 DOW Sample Site Location

Station Name	Latitude	Longitude	Stream Segment	River Mile
DOW20020017	36.7028	-86.8412	Sinking Creek 0.0 to 3.3	0.4

Table H.11-2 DOW Sample Data Summary(1)

Station Name	Indicator Bacteria(2)	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
DOW20020017	*E. coli*	12	224	>2,420	1,449

(1)The full data set for samples collected from DOW20020017 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.

(2)The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for Sinking Creek 0.0 to 3.3 are presented in Table H.11-3. As of September 2021, there are no KPDES-permitted discharges of bacteria into this segment of Sinking Creek. The location of the segment within the Sinking Creek watershed is shown in Figure H.11-1.

Table H.11-3 Sinking Creek 0.0 to 3.3 *E. coli* TMDL Allocations(1)

TMDL(2)	Allocations for Direct Loads to the Segment	Allocations for Upstream Loads to the Segment(4)	MOS(5)
	LA(3)		
Q_S×WQC×CF	∑(Q_{LA}×WQC×CF)	∑($Q_{Upstream}$×WQC×CF)	Implicit

(1)All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2)Q_S is the flow (ft^3/s) in the segment.

(3)Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(4)$Q_{Upstream}$ is the flow contribution (ft^3/s) from upstream of the segment. This load includes both WLA and LA sources upstream of the impaired segment.

(5)The following assumptions provide an implicit MOS:

(a)Upstream bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b)There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

Figure H.11-2 shows the segment is located in an area where karst features such as sinkholes, sinking streams, and springs exist. The sink features may capture surface drainage and channel it underground to resurface later at one or more springs. These discharging springs may occur outside the watershed where the drainage originated. However, unless karst dye trace studies indicate otherwise, groundwater catchment is presumed to correspond to the topographic watershed boundaries of surface drainage. Dye tracing in the region identified areas east and west of the Sinking Creek watershed that contribute drainage to the segment. A small area from the Brush Creek watershed of the Green River basin, northeast of the Sinking Creek watershed boundary, may also contribute drainage to tributaries of Sinking Creek.

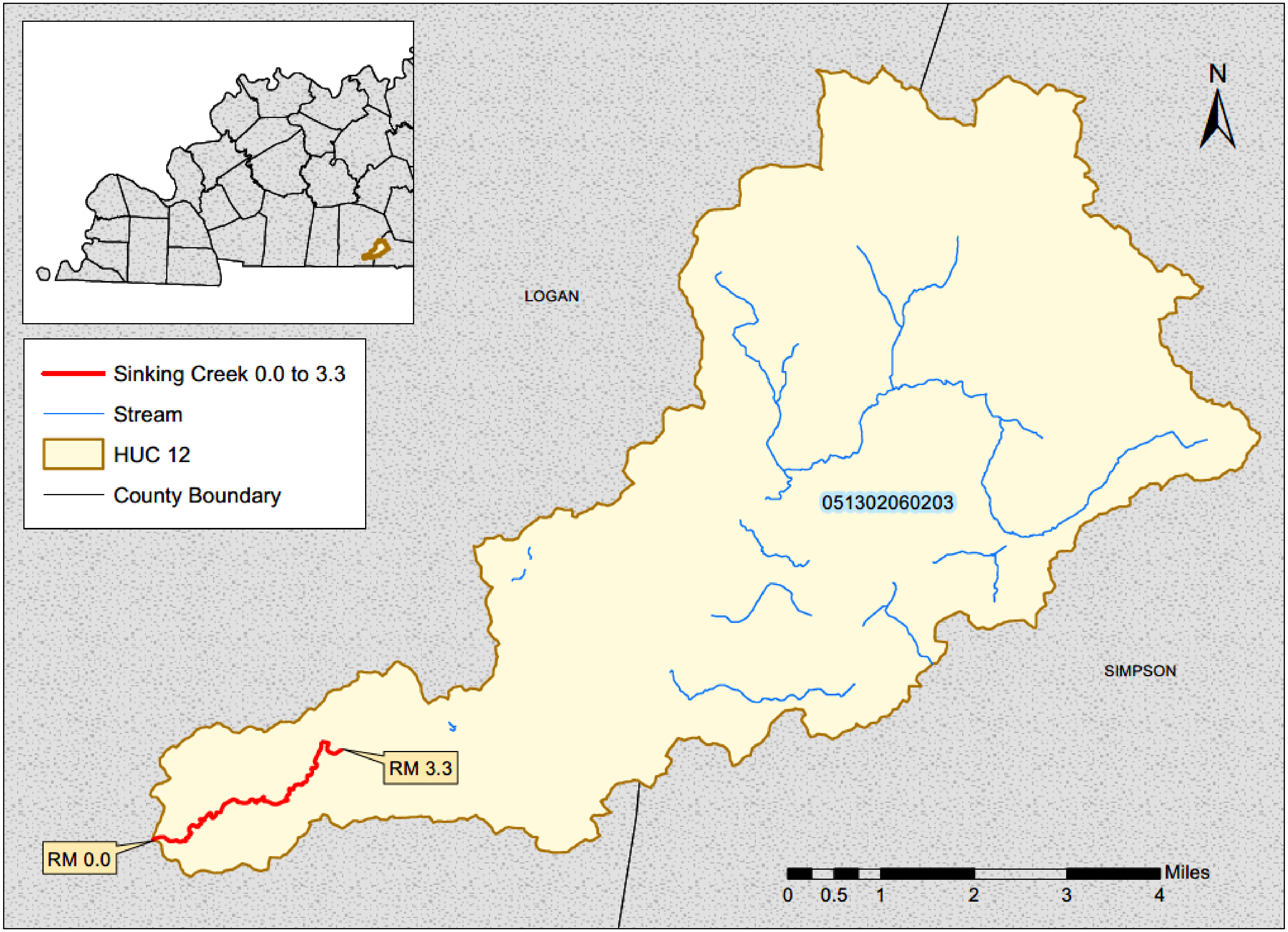


Figure H.11-1 Location of Sinking Creek 0.0 to 3.3

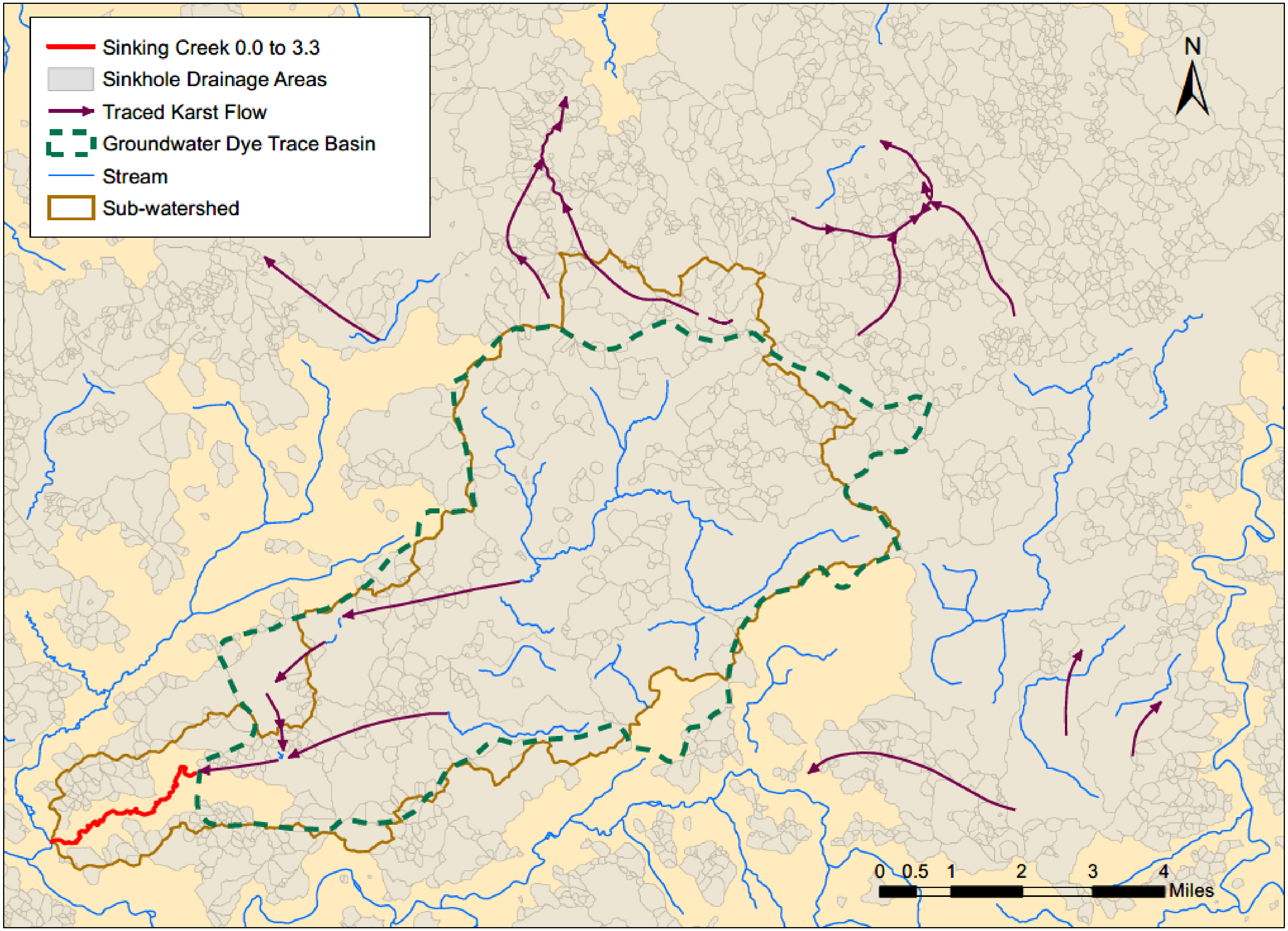


Figure H.11-2 Karst Influence in the Region of Sinking Creek 0.0 to 3.3

Section H.12 Sinking Fork 2.1 to 5.65

Waterbody ID: KY-1718

Receiving Water: Little River

Impaired Use: PCR

Support Status: nonsupport

Listed Pollutant/TMDL Pollutant: *E. coli*

HUC 12: 051302050607

County: Trigg

The Division of Water (DOW) has collected samples from station, CRW003, on this segment since 2000. The station is sampled every five years during the PCR season as part of the DOW five-year rotating schedule for basin monitoring (see also Section 7.2.1, Kentucky Watershed Management Framework). The station has typically been sampled six times during a monitoring year. Table H.12-1 summarizes information about this sampling station; Table H.12-2 provides a summary of the data collected from this station.

Table H.12-1 DOW Sample Site Location

Station Name	Latitude	Longitude	Stream Segment	River Mile
CRW003	36.84064	-87.740892	Sinking Fork 2.1 to 5.65	4.1

Table H.12-2 DOW Sample Data Summary(1)

Station Name	Indicator Bacteria(2)	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
CRW003	fecal coliform	12	42	530	131
CRW003	*E. coli*	13	131	1,986	508

(1)The full data set for samples collected from CRW003 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.

(2)The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for Sinking Fork 2.1 to 5.65 are presented in Table H.12-3. As of September 2021, there are no KPDES-permitted discharges of bacteria into this segment of Sinking Fork. The location of the segment within the Lower Sinking Fork watershed is shown in Figure H.12-1.

Table H.12-3 Sinking Fork 2.1 to 5.65 *E. coli* TMDL Allocations(1)

TMDL(2)	Allocations for Direct Loads to the Segment	Allocations for Upstream Loads to the Segment(4)	Allocations for Tributary Loads to the Segment(5)	MOS(6)
	LA(3)			
Q_S×WQC×CF	∑(Q_{LA}×WQC×CF)	∑($Q_{Upstream}$×WQC×CF)	∑($Q_{Tributary}$×WQC×CF)	Implicit

(1)All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2)Q_S is the flow (ft^3/s) in the segment.

(3)Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(4)$Q_{Upstream}$ is the flow contribution (ft^3/s) from upstream of the segment. This load includes both WLA and LA sources upstream of the impaired segment.

(5)$Q_{Tributary}$ is the flow contribution (ft^3/s) from a tributary to the segment. This load includes both WLA and LA sources on tributaries to the impaired segment.

(6)The following assumptions provide an implicit MOS:

(a)Upstream and tributary bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b)There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

Figure H.12-1 shows some karst features such as sinkholes exist in this watershed. The sink features may capture surface drainage and channel it underground to resurface later at one or more springs. These discharging springs may occur outside the watershed where the drainage originated. However, unless karst dye trace studies indicate otherwise, groundwater catchment is presumed to correspond to the topographic watershed boundaries of surface drainage. No dye tracing information is available from the area of the Lower Sinking Fork watershed. For more detailed information about karst geology, see Section 3.2, Karst, of the Core TMDL.

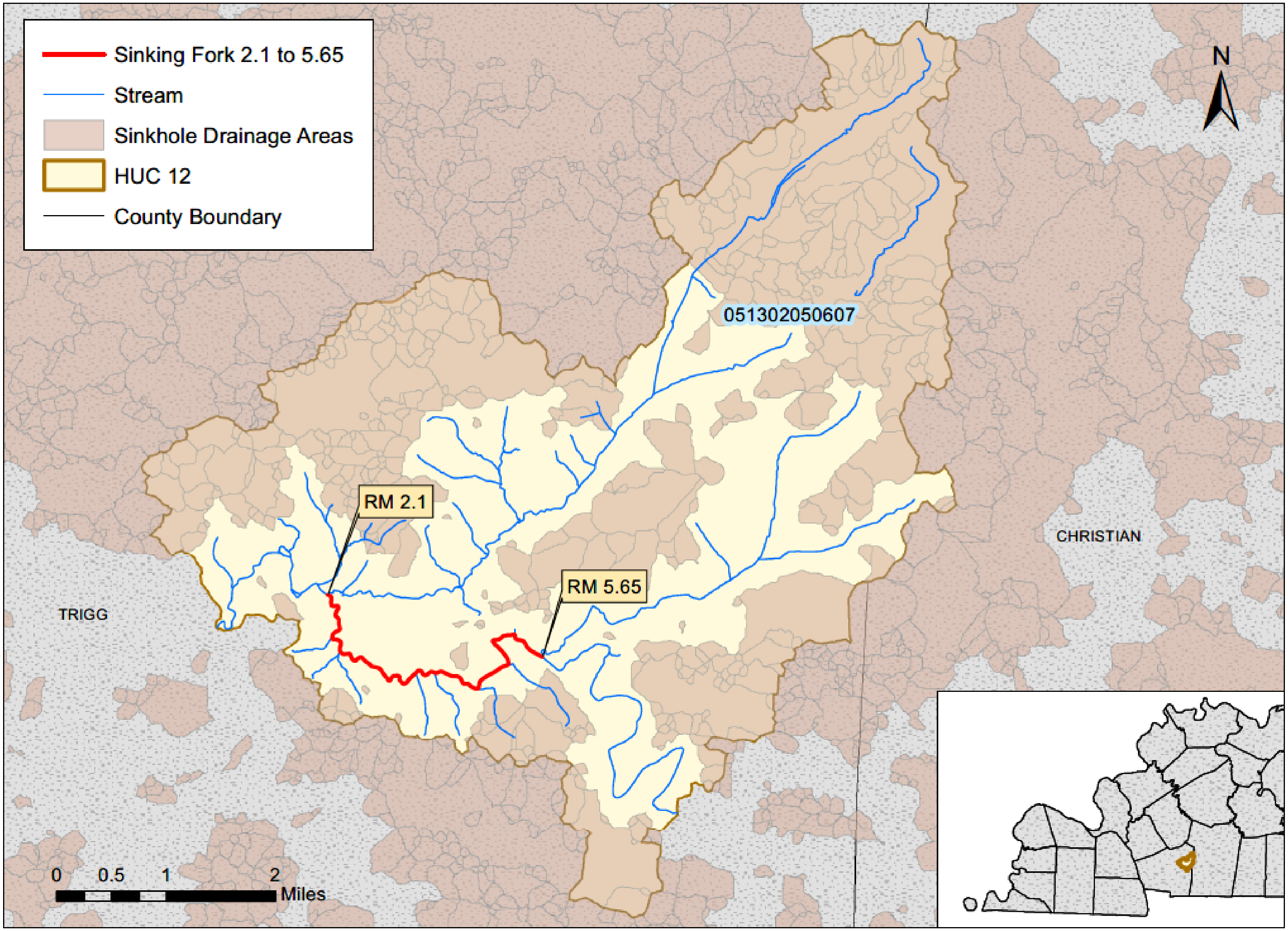


Figure H.12-1 Location of Sinking Fork 2.1 to 5.65

Section H.13 South Fork Red River 0.0 to 5.3

Waterbody ID: KY-1783

Receiving Water: Red River

Impaired Use: PCR

Support Status: nonsupport

Listed Pollutant/TMDL Pollutant: *E. coli*

HUC 12: 051302060202

County: Logan

The Division of Water (DOW) collected samples from station DOW20020003, located near river mile 2.65, in 2010. The station was sampled twelve times during the PCR season. Table H.13-1 summarizes information about this sampling station; Table H.13-2 provides a summary of the data collected from this station.

Table H.13-1 DOW Sample Site Location

Station Name	Latitude	Longitude	Stream Segment	River Mile
DOW20020003	36.66731	-86.89548	South Fork Red River 0.0 to 5.3	2.65

Table H.13-2 DOW Sample Data Summary(1)

Station Name	Indicator Bacteria(2)	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
DOW20020003	*E. coli*	12	60	>2,420	437

(1)The full data set for samples collected from DOW20020003 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.
(2)The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for South Fork Red River 0.0 to 5.3 are presented in Table H.13-3.

Table H.13-3 South Fork Red River 0.0 to 5.3 *E. coli* TMDL Allocations[1]

TMDL[2]	Allocations for Direct Loads to the Segment		Allocations for Upstream Loads to the Segment[5]	Allocations for Tributary Loads to the Segment[6]	MOS[7]
	SWS-WLA[3]	LA[4]			
Q_S×WQC×CF	∑(Q_{SWS}×WQC×CF)	∑(Q_{LA}×WQC×CF)	∑($Q_{Upstream}$×WQC×CF)	∑($Q_{Tributary}$×WQC×CF)	Implicit

[1] All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

[2] Q_S is the flow (ft^3/s) in the segment.

[3] Q_{SWS} is the flow (ft^3/s) in the segment due to a SWS entity. New or expanded SWS sources will be allowed to discharge to the segment contingent upon them meeting the PCR bacterial WQCs found in 401 KAR 10:031. SWS-WLAs will be translated into KPDES permit limits as an *E. coli* effluent gross limit of 130 colonies/100 ml as a monthly average (geometric mean) and 240 colonies/100 ml as a maximum weekly average (geometric mean).

[4] Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

[5] $Q_{Upstream}$ is the flow contribution (ft^3/s) from upstream of the segment. This load includes both WLA and LA sources upstream of the impaired segment.

[6] $Q_{Tributary}$ is the flow contribution (ft^3/s) from a tributary to the segment. This load includes both WLA and LA sources on tributaries to the impaired segment.

[7] The following assumptions provide an implicit MOS:

(a) Upstream and tributary bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b) Although all sources are provided an allocation at the Water Quality Standard, not all sources discharge at this maximum allocation at the same time.

(c) There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

Figure H.13-1 some karst features such as sinkholes exist in this watershed. The sink features may capture surface drainage and channel it underground to resurface later at one or more springs. These discharging springs may occur outside the watershed where the drainage originated. However, unless karst dye trace studies indicate otherwise, groundwater catchment is presumed to correspond to the topographic watershed boundaries of surface drainage. No dye tracing information is available from the area of the Lower South Fork Red River watershed. For more detailed information about karst geology, see Section 3.2, Karst, of the Core TMDL.

One facility permitted under the Kentucky Pollutant Discharge Elimination System (KPDES) discharges treated effluent directly into this segment of South Fork Red River. The directly discharging facility is a sanitary wastewater system. There are no MS4 communities or CSOs discharging directly to this segment of South Fork Red River. The definitions for MS4 and CSO are found in 401 KAR 5:002. The facility is identified in Table H.13-4 and the location of the segment within the Lower South Fork Red River watershed is shown in Figure H.13-1.

Table H.13-4 Summary of Active KPDES-permitted Sources as of March 2021

KPDES Permit Number	Facility Name	Design Flow (MGD)	Outfall Latitude	Outfall Longitude	Permit Expiration Date(1)	WLA(2) (colonies *E. coli* /day)
KY0020885	Adairville STP	0.26	36.660833	-86.858333	10/31/2023	Q_{SWS}×WQC×CF

(1)Permit expiration dates identify the permits in effect when the draft TMDL was written, including any permits that may be expired (but not terminated) or in administrative continuance. Permits issued after the approval of this TMDL will address the TMDL.

(2)Q_{SWS} is the flow in the segment due to a SWS entity. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day).

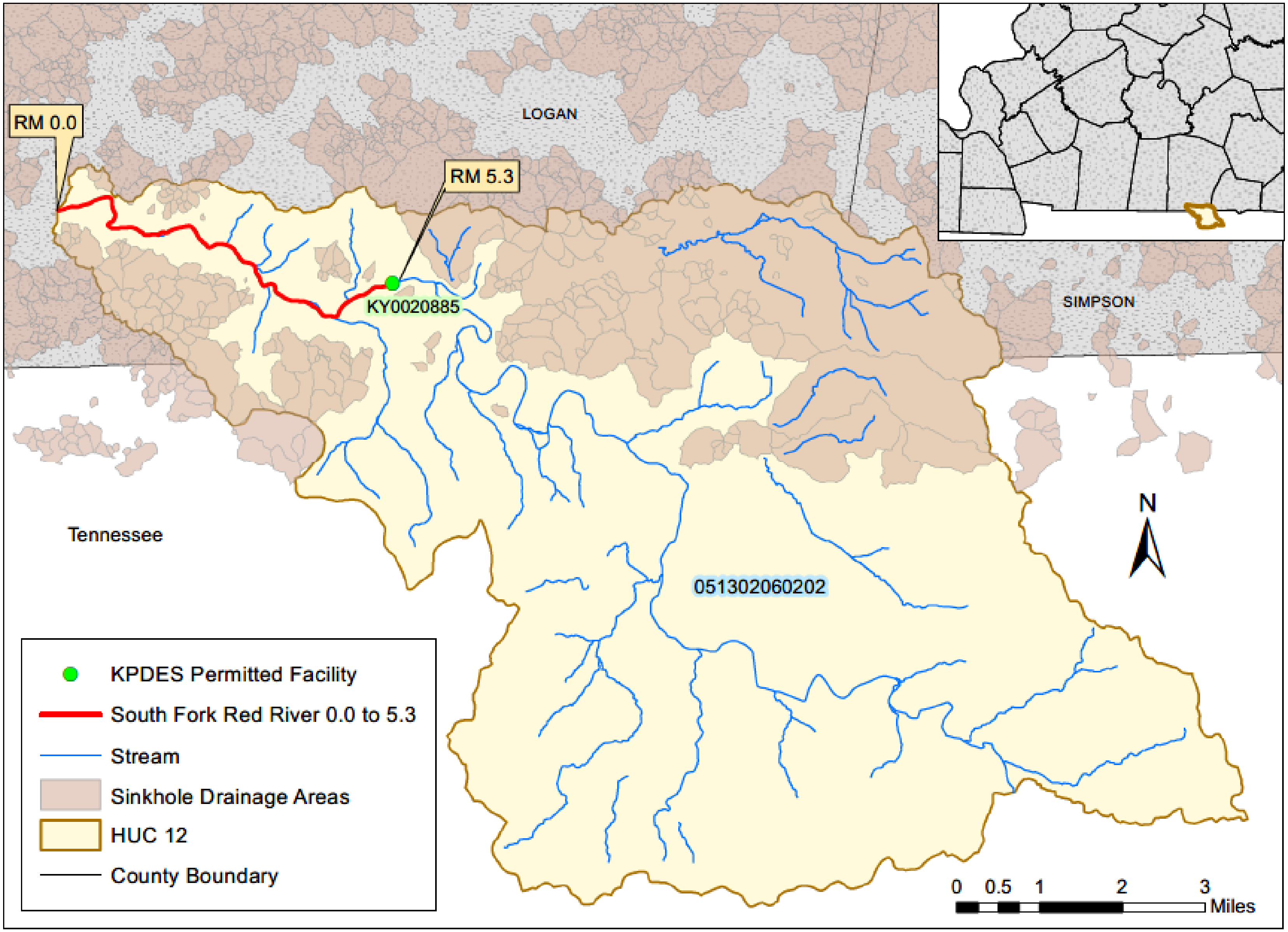


Figure H.13-1 Location of the KPDES-permitted Facility on South Fork Red River 0.0 to 5.3

Section H.14 Sulphur Spring Creek 0.0 to 6.6

Waterbody ID: KY-1868

Receiving Water: Red River

Impaired Use: PCR

Support Status: partial support

Listed Pollutant/TMDL Pollutant: *E. coli*

HUC 12: 051302060102

County: Simpson

The Division of Water (DOW) collected samples from station DOW20020018, located near river mile 1.4, in 2010. The station was sampled twelve times during the PCR season. Table H.14-1 summarizes information about this sampling station; Table H.14-2 provides a summary of the data collected from this station.

Table H.14-1 DOW Sample Site Location

Station Name	Latitude	Longitude	Stream Segment	River Mile
DOW20020018	36.6959	-86.729	Sulphur Spring Creek 0.0 to 6.6	1.4

Table H.14-2 DOW Sample Data Summary(1)

Station Name	Indicator Bacteria(2)	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
DOW20020018	*E. coli*	12	129	285	198

(1)The full data set for samples collected at DOW20020018 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.

(2)The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for Sulphur Spring Creek 0.0 to 6.6 are presented in Table H.14-3. As of September 2021, there are no KPDES-permitted discharges of bacteria into this segment of Sulphur Spring Creek. The location of the segment within the Sulphur Spring Creek-Red River watershed is shown in Figure H.14-1.

Table H.14-3 Sulphur Spring Creek 0.0 to 6.6 *E. coli* TMDL Allocations[1]

TMDL[2]	Allocations for Direct Loads to the Segment	Allocations for Upstream Loads to the Segment[4]	Allocations for Tributary Loads to the Segment[5]	MOS[6]
	LA[3]			
$Q_S \times WQC \times CF$	$\sum(Q_{LA} \times WQC \times CF)$	$\sum(Q_{Upstream} \times WQC \times CF)$	$\sum(Q_{Tributary} \times WQC \times CF)$	Implicit

[1] All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

[2] Q_S is the flow (ft^3/s) in the segment.

[3] Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

[4] $Q_{Upstream}$ is the flow contribution (ft^3/s) from upstream of the segment. This load includes both WLA and LA sources upstream of the impaired segment.

[5] $Q_{Tributary}$ is the flow contribution (ft^3/s) from a tributary to the segment. This load includes both WLA and LA sources on tributaries to the impaired segment.

[6] The following assumptions provide an implicit MOS:
(a) Upstream and tributary bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.
(b) There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

Figure H.14-2 shows the segment is located in an area where karst features such as sinkholes, sinking streams, and springs exist. The sink features may capture surface drainage and channel it underground to resurface later at one or more springs. These discharging springs may occur outside the watershed where the drainage originated. However, unless karst dye trace studies indicate otherwise, groundwater catchment is presumed to correspond to the topographic watershed boundaries of surface drainage. Dye tracing in Kentucky identified a small area from the West Fork Drakes Creek watershed of the Green River basin, east and northeast of the Sulphur Spring Creek sub-watershed boundary, that may contribute drainage to tributaries of Sulphur Spring Creek.

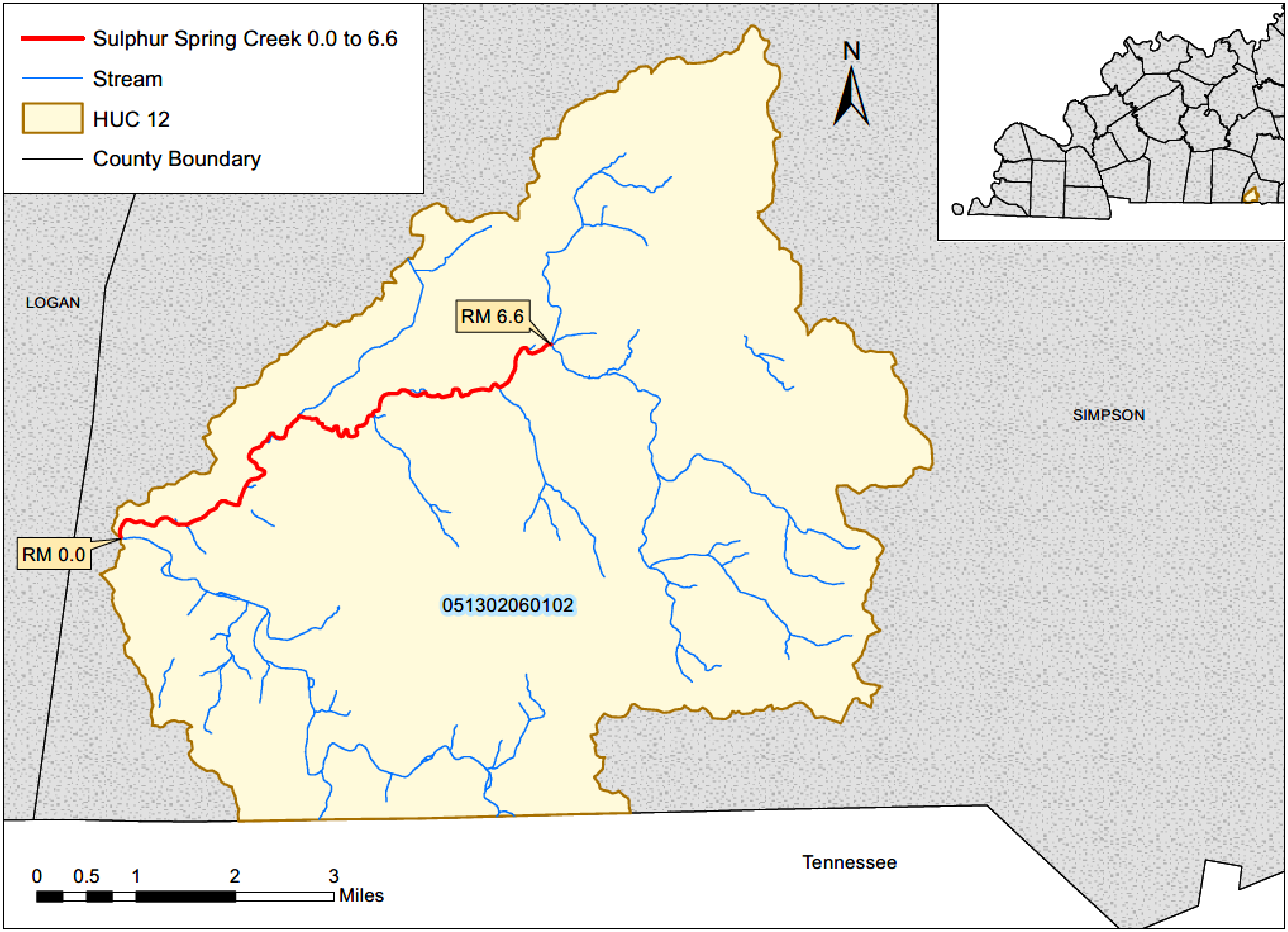


Figure H.14-1 Location of Sulphur Spring Creek 0.0 to 6.6

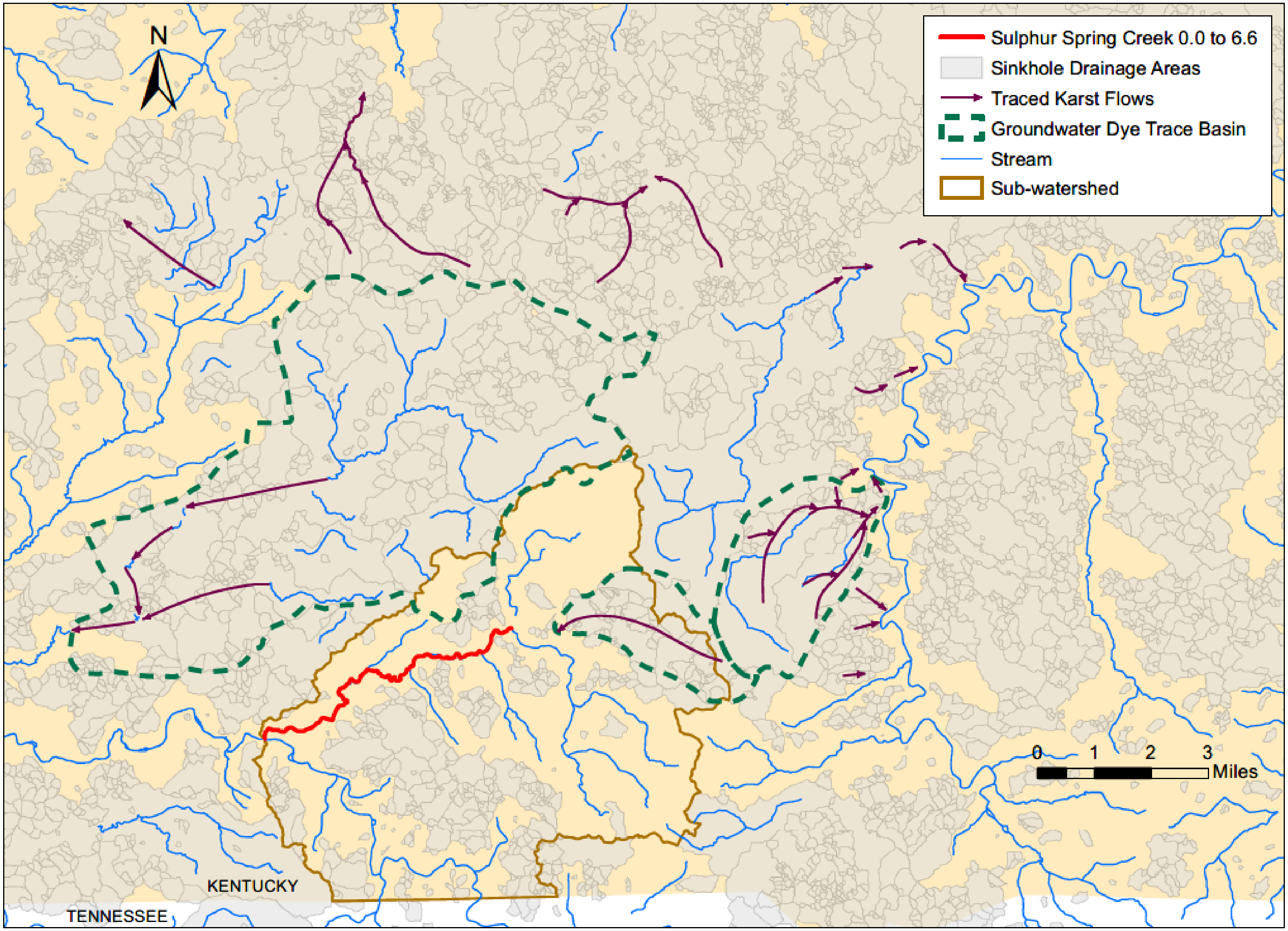


Figure H.14-2 Karst Influence in the Region of Sulphur Spring Creek 0.0 to 6.6

Section H.15 UT of Elk Fork Creek 0.0 to 4.8

Waterbody ID: KY-723

Receiving Water: Elk Fork Creek

Impaired Use: PCR

Support Status: partial support

Listed Pollutant/TMDL Pollutant: *E. coli*

HUC 12: 051302060703

County: Todd

The Division of Water (DOW) collected samples from station DOW20019007, located near river mile 0.19, in 2008. The station was sampled nine times during the PCR season. Table H.15-1 summarizes information about this sampling station; Table H.15-2 provides a summary of the data collected from this station.

Table H.15-1 DOW Sample Site Location

Station Name	Latitude	Longitude	Stream Segment	River Mile
DOW20019007	36.78152	-87.15059	UT of Elk Fork Creek 0.0 to 4.8	0.19

Table H.15-2 DOW Sample Data Summary(1)

Station Name	Indicator Bacteria(2)	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
DOW20019007	*E. coli*	9	84	2,240	407

(1)The full data set for samples collected at DOW20019007 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.

(2)The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for UT of Elk Fork Creek 0.0 to 4.8 are presented in Table H.15-3. As of September 2021, there are no KPDES-permitted discharges of bacteria into this segment of UT of Elk Fork Creek. The location within the Upper Elk Fork watershed is shown in Figure H.15-1.

Table H.15-3 UT of Elk Fork Creek 0.0 to 4.8 *E. coli* TMDL Allocations(1)

TMDL(2)	Allocations for Direct Loads to the Segment	Allocations for Tributary Loads to the Segment(4)	MOS(5)
	LA(3)		
Q_S×WQC×CF	∑(Q_{LA}×WQC×CF)	∑($Q_{Tributary}$×WQC×CF)	Implicit

(1)All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2)Q_S is the flow (ft^3/s) in the segment.

(3)Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(4)$Q_{Tributary}$ is the flow contribution (ft^3/s) from a tributary to the segment. This load includes both WLA and LA sources on tributaries to the impaired segment.

(5)The following assumptions provide an implicit MOS:

(a)Tributary bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b)There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

Figure H.15-1 shows some karst features such as sinkholes exist in this watershed. The sink features may capture surface drainage and channel it underground to resurface later at one or more springs. These discharging springs may occur outside the watershed where the drainage originated. However, unless karst dye trace studies indicate otherwise, groundwater catchment is presumed to correspond to the topographic watershed boundaries of surface drainage. No dye tracing information is available from the area of the Upper Elk Fork watershed. For more detailed information about karst geology, see Section 3.2, Karst, of the Core TMDL.

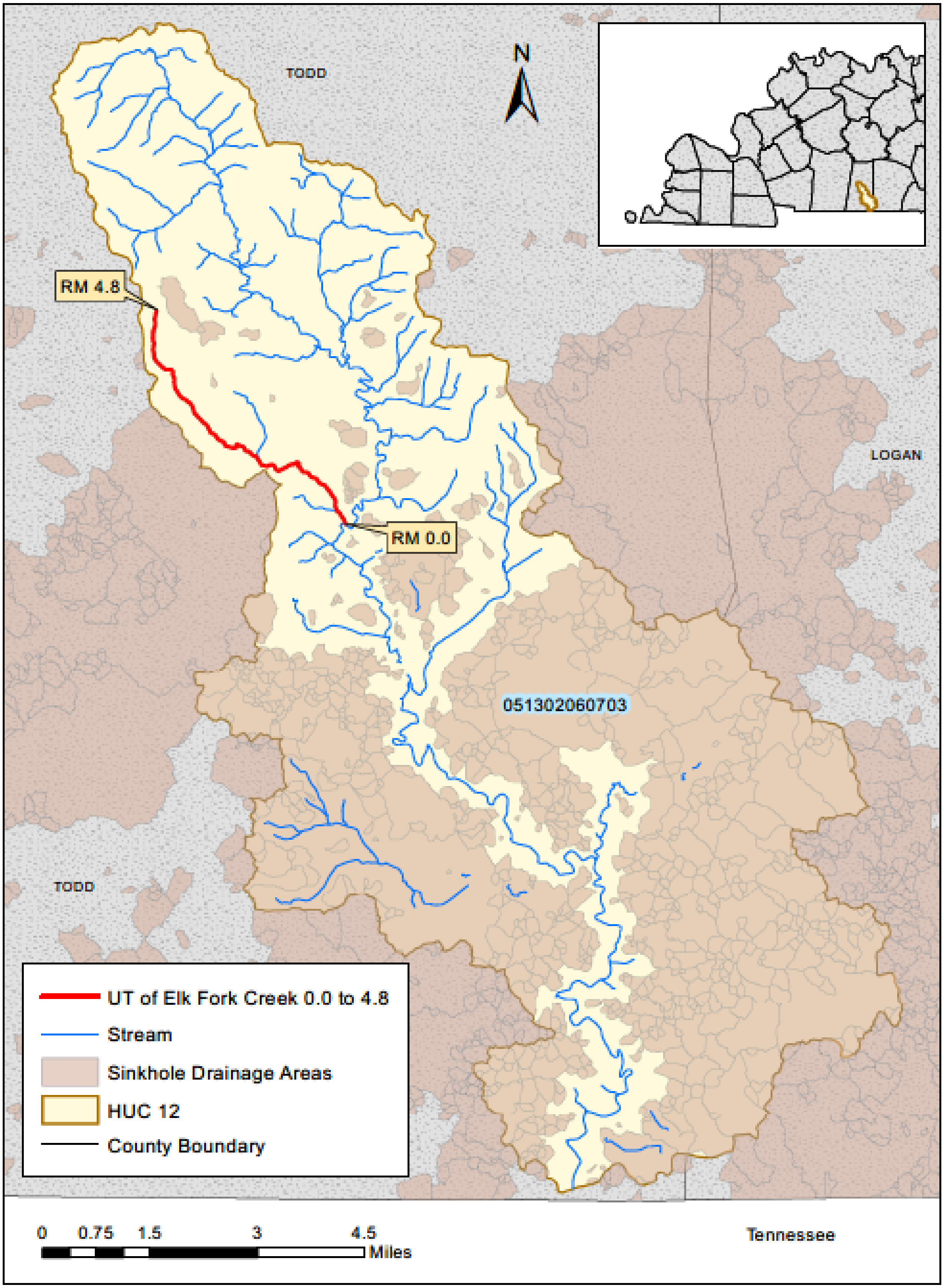


Figure H.15-1 Location of UT of Elk Fork Creek 0.0 to 4.8

Section H.16 West Fork Red River 14.65 to 26.8

Waterbody ID: KY-4

Receiving Water: Red River

Impaired Use: PCR

Support Status: partial support

Listed Pollutant/TMDL Pollutant: *E. coli*

HUC 12: 051302060604

County: Christian

The Division of Water (DOW) has collected samples from station, CRW005, on this segment since 2000. The station is sampled every five years during the PCR season as part of the DOW five-year rotating schedule for basin monitoring (see also Section 7.2.1, Kentucky Watershed Management Framework). The station has typically been sampled six times during a monitoring year. Table H.16-1 summarizes information about this sampling station; Table H.16-2 provides a summary of the data collected from this station.

Table H.16-1 DOW Sample Site Location

Station Name	Latitude	Longitude	Stream Segment	River Mile
CRW005	36.696901	-86.963335	West Fork Red River 14.65 to 26.8	4.5

Table H.16-2 DOW Sample Data Summary(1)

Station Name	Indicator Bacteria(2)	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
CRW005	fecal coliform	13	57	2,000	273
CRW005	*E. coli*	14	62	1,733	299

(1)The full data set for samples collected at CRW005 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.

(2)The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for West Fork Red River 14.65 to 26.8 are presented in Table H.16-3.

Table H.16-3 West Fork Red River 14.65 to 26.8 *E. coli* TMDL Allocations(1)

TMDL(2)	Allocations for Direct Loads to the Segment		Allocations for Upstream Loads to the Segment(5)	Allocations for Tributary Loads to the Segment(6)	MOS(7)
	SWS-WLA(3)	LA(4)			
$Q_S \times WQC \times CF$	$\sum(Q_{SWS} \times WQC \times CF)$	$\sum(Q_{LA} \times WQC \times CF)$	$\sum(Q_{Upstream} \times WQC \times CF)$	$\sum(Q_{Tributary} \times WQC \times CF)$	Implicit

(1)All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2)Q_S is the flow (ft^3/s) in the segment.

(3)Q_{SWS} is the flow (ft^3/s) in the segment due to a SWS entity. New or expanded SWS sources will be allowed to discharge to the segment contingent upon them meeting the PCR bacterial WQCs found in 401 KAR 10:031. SWS-WLAs will be translated into KPDES permit limits as an *E. coli* effluent gross limit of 130 colonies/100 ml as a monthly average (geometric mean) and 240 colonies/100 ml as a maximum weekly average (geometric mean).

(4)Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(5)$Q_{Upstream}$ is the flow contribution (ft^3/s) from upstream of the segment. This load includes both WLA and LA sources upstream of the impaired segment.

(6)$Q_{Tributary}$ is the flow contribution (ft^3/s) from a tributary to the segment. This load includes both WLA and LA sources on tributaries to the impaired segment.

(7)The following assumptions provide an implicit MOS:

(a)Upstream and tributary bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b)Although all sources are provided an allocation at the Water Quality Standard, not all sources discharge at this maximum allocation at the same time.

(c)There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

One facility permitted under the Kentucky Pollutant Discharge Elimination System (KPDES) discharges treated effluent directly into this segment of West Fork Red River. The directly discharging facility is a sanitary wastewater system. There are no MS4 communities or CSOs discharging directly to this segment of West Fork Red River. The definitions for MS4 and CSO are found in 401 KAR 5:002. The facility is identified in Table H.16-4 and the location of the segment within the City of Oak Grove-West Fork Red River watershed is shown in Figure H.16-1.

Table H.16-4 Summary of Active KPDES-permitted Sources as of March 2021

KPDES Permit Number	Facility Name	Design Flow (MGD)	Outfall Latitude	Outfall Longitude	Permit Expiration Date(1)	WLA(2) (colonies *E. coli* /day)
KY0094056	City of Oak Grove	0.72	36.65	-87.375833	07/31/2021	Q_{SWS}×WQC×CF

(1)Permit expiration dates identify the permits in effect when the draft TMDL was written, including any permits that may be expired (but not terminated) or in administrative continuance. Permits issued after the approval of this TMDL will address the TMDL.

(2)Q_{SWS} is the flow in the segment due to a SWS entity. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day).

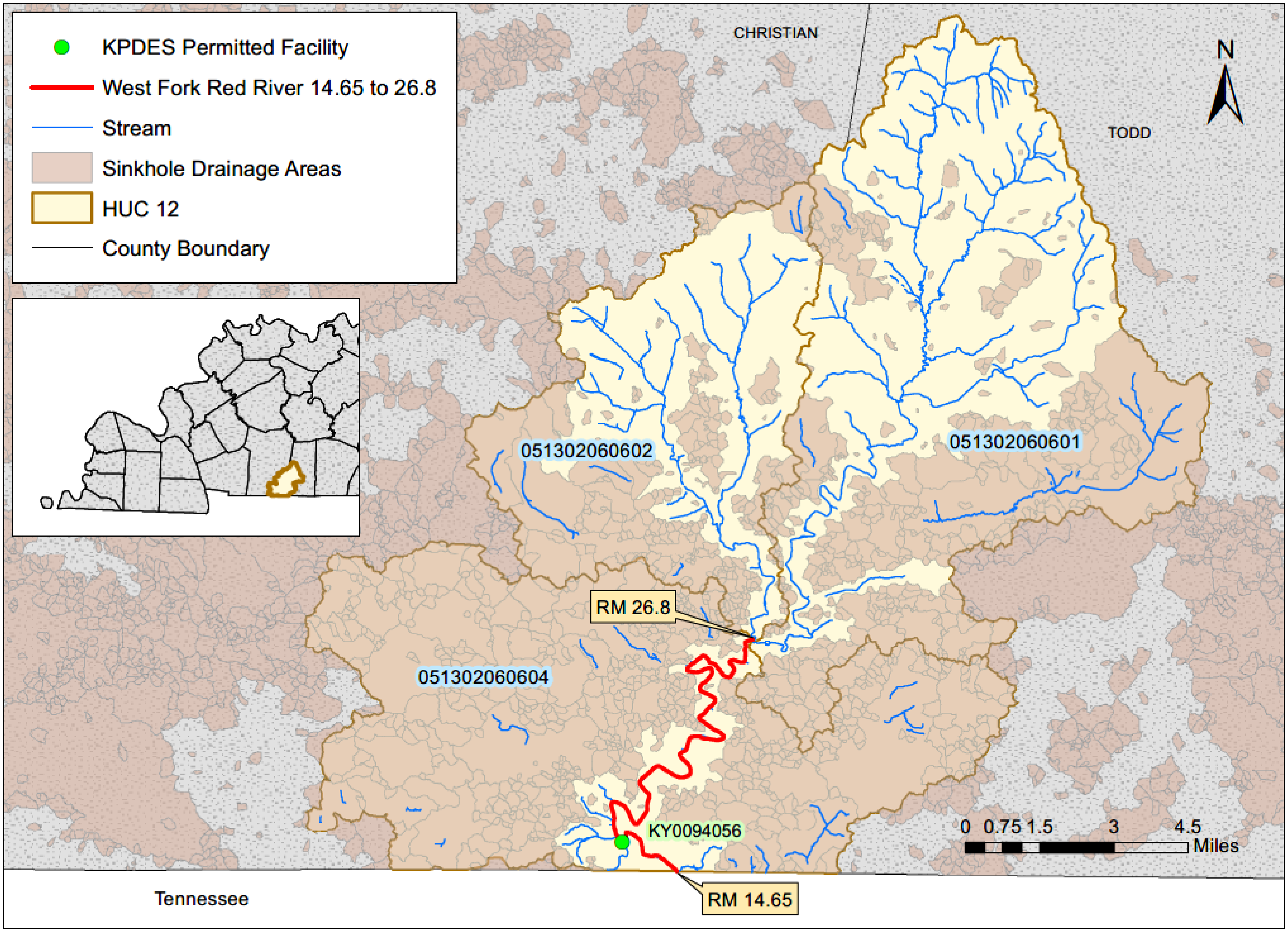


Figure H.16-1 Location of the KPDES-permitted Facility on West Fork Red River 14.65 to 26.8

APPENDIX I

Appendix I
Mississippi River Minor Tributary Watersheds

HUC 8s: 08010100, 08010201, 08010202

Level IV Ecoregions: Wabash-Ohio Bottomlands, Northern Holocene Meander Belts, Bluff Hills, Loess Plains

Drainage Area Within Kentucky: 1,300.77 square miles

Counties: Ballard, Calloway, Carlisle, Fulton, Graves, Hickman, McCracken

Major Cities: Mayfield, Fulton, Hickman, Bardwell, Clinton, Columbus, Wickliffe

The Ohio River joins the Mississippi River near Wickliffe, Ky. From here the Mississippi River flows south and forms the majority of the border between Missouri and Kentucky, along Ballard, Carlisle, Hickman, and Fulton counties, and then meanders north then south again at the Kentucky Bend. The Kentucky Bend is an exclave of Fulton Co., Kentucky and is encircled by Missouri and Tennessee. Several tributaries drain into the Mississippi River and not to one of Kentucky's other major river basins. This group of minor Mississippi River tributary watersheds is in the Jackson Purchase physiographic region and drains approximately 1,300 square miles within Kentucky.

Table I.1 provides a summary of the stream segments within the minor tributary watersheds of the Mississippi River that have been included on the Kentucky 2018/2020 303(d) list for impairment due to fecal coliform, *E. coli* and/or pathogens. Segments addressed by a TMDL in this report are listed in the table with the TMDL pollutant. Segments not addressed by a TMDL in this report have a footnote explaining why they are not included. Note that stream segments listed for the first time for a bacteria-related cause on the 2018/2020 303(d) list have not yet been prioritized for TMDL development. Table I.1 also provides a crosswalk between the waterbody IDs on the 2016 303(d) list and the corresponding waterbody IDs on the 2018/2020 303(d) list. This information is provided to assist with cross-referencing waterbodies to prior lists following the implementation of a new system of waterbody IDs with the 2018/2020 list. Figure I.1 shows the location of all segments within minor tributary watersheds of the Mississippi River addressed by a TMDL in this report.

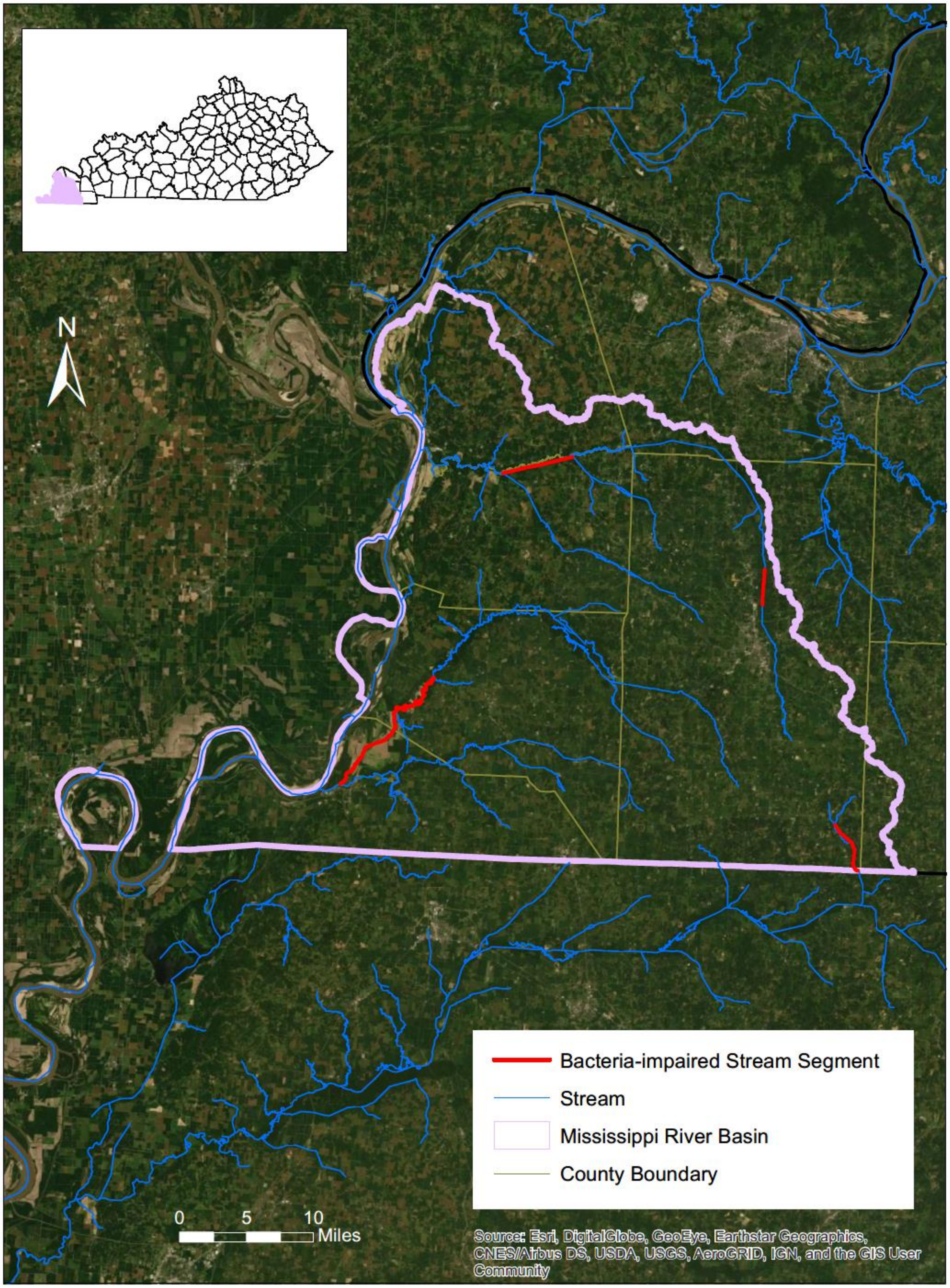
The river miles for each TMDL segment in this appendix match the 2018/2020 303(d) list. Since the National Hydrography Dataset (NHD) is continually updated to maintain accurate waterbody information, the river mile information in this appendix may not reflect the current 1:24,000 NHD for Kentucky. River mile information for stream segments is updated in each new 303(d) list submitted to EPA.

Table I.1 2018/2020 303(d) Listed Bacteria-impaired Stream Segments Within the Minor Tributary Watersheds of the Mississippi River

Waterbody Name	Waterbody ID	2016 Waterbody ID	Impaired Use (Support Status)	Listed Pollutant	TMDL Pollutant	Suspected Source(s)	County
Bayou de Chien 8.8 to 13.3[1]	KY-2858	KY486489_02	PCR (nonsupport)	*E. coli*	TMDL not included in this document	Non-Point Source	Fulton, Hickman
Mayfield Creek 10.65 to 16.0	KY-1245	KY497717_02	PCR (nonsupport)	*E. coli*	*E. coli*	Agriculture, Non-Point Source	Ballard, Carlisle
Mayfield Creek 37.7 to 40.4	KY-1248	KY497717_08	PCR (nonsupport)	*E. coli*	*E. coli*	Agriculture, Non-Point Source	Graves
Obion Creek 1.35 to 16.5	KY-1417	KY499767_01	PCR (nonsupport)	*E. coli*	*E. coli*	Agriculture, Non-Point Source	Fulton, Hickman
Shawnee Creek 0.0 to 3.4[2]	KY-1698	KY503285_01	PCR (partial support)	Pathogens	TMDL not included in this document	Municipal Point Source Discharges	Ballard
Terrapin Creek 2.8 to 7.0	KY-1882	KY505081_01	PCR (nonsupport)	*E. coli*	*E. coli*	Agriculture, Non-Point Source	Graves
Wilson Creek 0.0 to 2.15[1]	KY-2031	KY506898_01	PCR (partial support)	*E. coli*	TMDL not included in this document	Non-Point Source	Carlisle

[1] TMDLs for these segments will be developed in a future TMDL report. These are new 2018/2020 bacteria listings. These segments may have a 2016 waterbody ID listed in the table if they had any assessed use prior to the 2018/2020 IR reporting cycle.

[2] A TMDL is not included because this segment will be proposed for delisting on a future 303(d) list.



Source: Esri, DigitalGlobe, GeoEye, Earthstar Geographics, CNES/Airbus DS, USDA, USGS, AeroGRID, IGN, and the GIS User Community

Figure I.1 Location of Bacteria-impaired Streams within Mississippi River Minor Tributary Watersheds Addressed by TMDL in This Report (October 2021)

Land cover data is summarized in Table I.2, and its geographic distribution is shown in Figure I.2. Cultivated crops is the predominant class of land cover in the Mississippi River Minor Tributary Watersheds, accounting for approximately 48 percent. The next three classes by magnitude are deciduous forest, pasture/hay, and woody wetlands. Land cover classes are described in Appendix P of the core TMDL document.

Table I.2 Land Cover Classes in the Mississippi River Minor Tributary Watersheds (NLCD 2011)

Land Cover	Percent of Total Area	Square Miles	Acres
Open Water	3.95	51.42	32,906.77
Developed, Open	4.54	59.01	37,764.11
Developed, Low Intensity	0.52	6.77	4,334.58
Developed, Medium Intensity	0.17	2.28	1,456.27
Developed, High Intensity	0.08	1.09	695.02
Barren Land (Rock, Sand, Clay)	0.08	0.98	626.56
Deciduous Forest	20.97	272.75	174,556.81
Evergreen Forest	0.53	6.93	4,436.60
Shrub/Scrub	0.21	2.78	1,778.55
Grassland/Herbaceous	0.59	7.61	4,872.46
Pasture/Hay	11.75	152.89	97,848.36
Cultivated Crops	47.65	619.88	396,722.00
Woody Wetlands	7.95	103.36	66,150.04
Emergent Herbaceous Wetlands	1.00	13.04	8,344.66

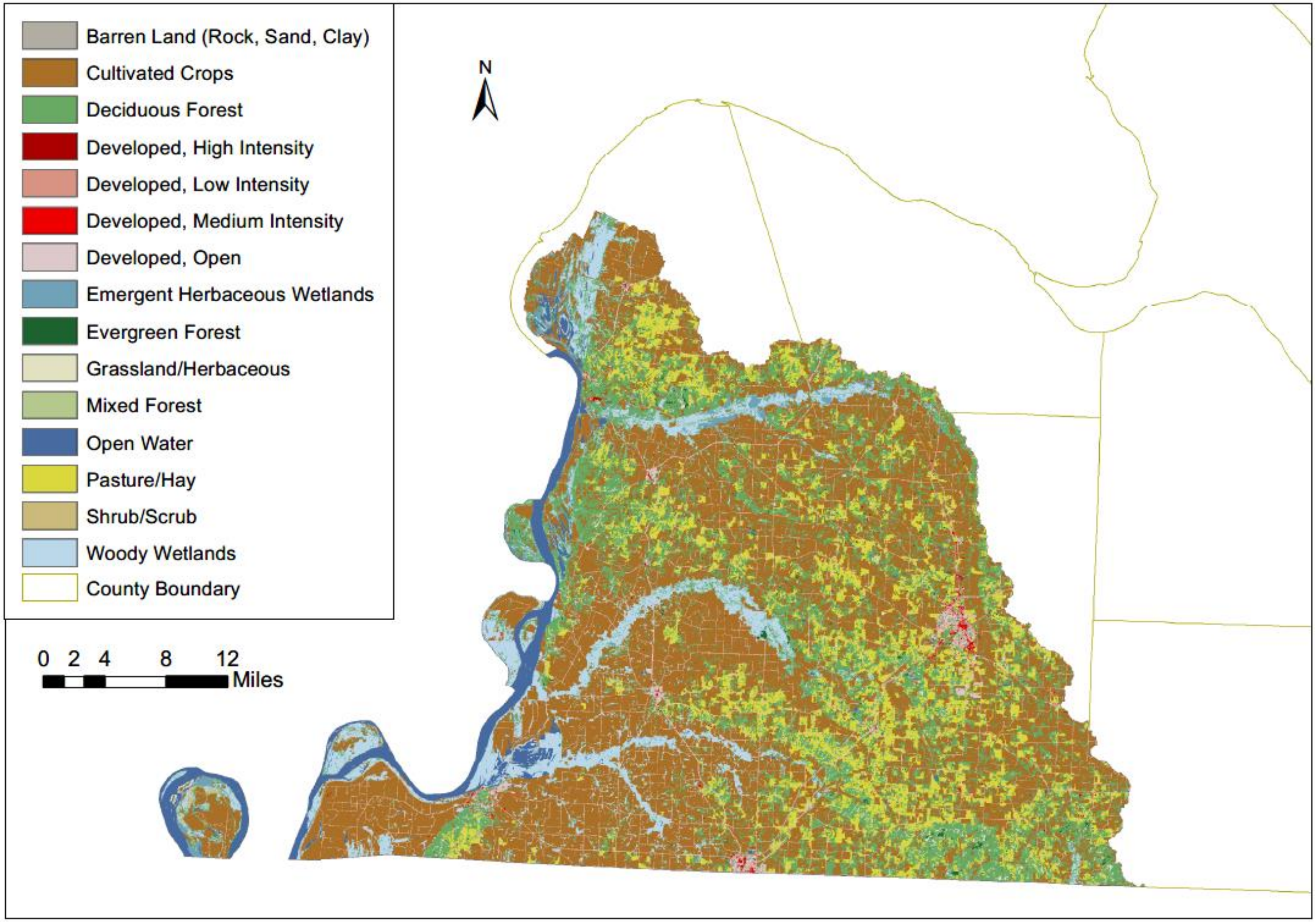


Figure I.2 Land Cover Classes in the Mississippi River Minor Tributary Watersheds

Section I.1 Mayfield Creek 10.65 to 16.0

Waterbody ID: KY-1245

Receiving Water: Mississippi River

Impaired Use: PCR

Support Status: nonsupport

Listed Pollutant/TMDL Pollutant: *E. coli*

HUC 12: 080102010205

Counties: Carlisle, Ballard

The Division of Water (DOW) has collected samples from station PRI042, located near river mile 13.2, since 2000. The station typically has been sampled two to six times during the PCR season. Table I.1-1 summarizes information about this sampling station; Table I.1-2 provides a summary of the data collected from this station.

Table I.1-1 DOW Sample Site Location

Station Name	Latitude	Longitude	Stream Segment	River Mile
PRI042	36.929874	-88.943046	Mayfield Creek 10.65 to 16.0	13.2

Table I.1-2 DOW Sample Data Summary(1)

Station Name	Indicator Bacteria(2)	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
PRI042	*E. coli*	49	13	>2,420	462
PRI042	fecal coliform	36	20	5,500	731

(1)The full data set for samples collected at PRI042 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.
(2)The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for Mayfield Creek 10.65 to 16.0 are presented in Table I.1-3. As of September 2021, there are no KPDES-permitted discharges of bacteria into this segment of Mayfield Creek. The location within the Hurricane Creek-Mayfield Creek watershed is shown in Figure I.1-1.

Table I.1-3 Mayfield Creek 10.65 to 16.0 *E. coli* TMDL Allocations(1)

TMDL(2)	Allocations for Direct Loads to the Segment	Allocations for Upstream Loads to the Segment(4)	Allocations for Tributary Loads to the Segment(5)	MOS(6)
	LA(3)			
$Q_S \times WQC \times CF$	$\sum(Q_{LA} \times WQC \times CF)$	$\sum(Q_{Upstream} \times WQC \times CF)$	$\sum(Q_{Tributary} \times WQC \times CF)$	Implicit

(1)All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2)Q_S is the flow (ft^3/s) in the segment.

(3)Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(4)$Q_{Upstream}$ is the flow contribution (ft^3/s) from upstream of the segment. This load includes both WLA and LA sources upstream of the impaired segment.

(5)$Q_{Tributary}$ is the flow contribution (ft^3/s) from a tributary to the segment. This load includes both WLA and LA sources on tributaries to the impaired segment.

(6)The following assumptions provide an implicit MOS:

(a)Upstream and tributary bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b)There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

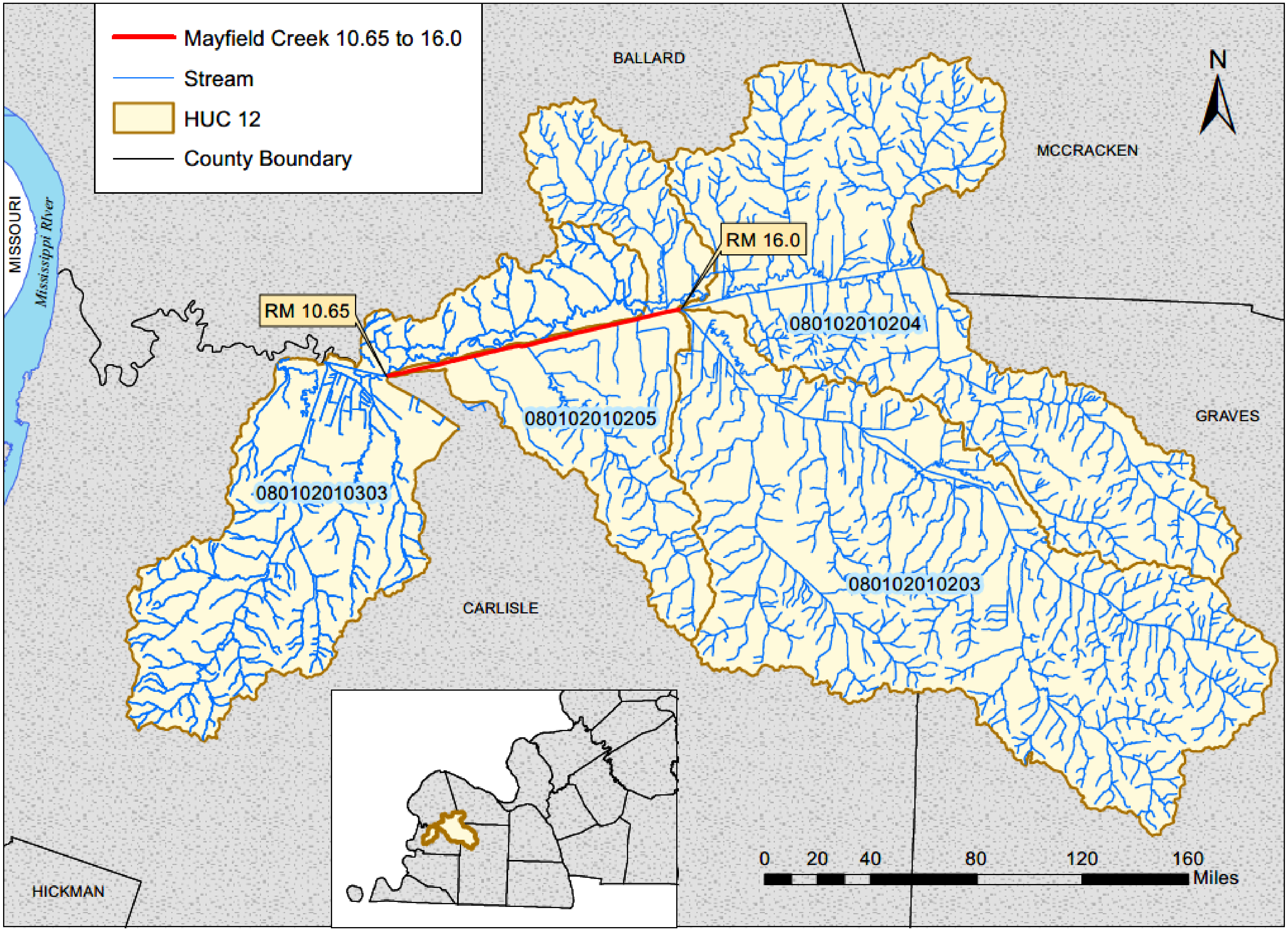


Figure I.1-1 Location of Mayfield Creek 10.65 to 16.0

Section I.2 Mayfield Creek 37.7 to 40.4

Waterbody ID: KY-1248

Receiving Water: Mississippi River

Impaired Uses: PCR

Support Status: nonsupport

Listed Pollutant/TMDL Pollutant: *E. coli*

HUC 12s: 080102010104, 080102010105

County: Graves

The Division of Water (DOW) has collected samples from station, MRW001, on this segment since 2000. The station is sampled every five years during the PCR season as part of the DOW five-year rotating schedule for basin monitoring (see also Section 7.2.1, Kentucky Watershed Management Framework). The station has typically been sampled six times during a monitoring year. Table I.2-1 summarizes information about this sampling station; Table I.2-2 provides a summary of the data collected from this station.

Table I.2-1 DOW Sample Site Location

Station Name	Latitude	Longitude	Stream Segment	River Mile
MRW001	36.818889	-88.630446	Mayfield Creek 37.7 to 40.4	38.2

Table I.2-2 DOW Sample Data Summary(1)

Station Name	Indicator Bacteria(2)	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
MRW001	*E. coli*	15	20	>2,420	745
MRW001	fecal coliform	6	10	200	103

(1)The full data set for samples collected at MRW001 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.

(2)The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for Mayfield Creek 37.7 to 40.4 are presented in Table I.2-3. As of September 2021, there are no KPDES-permitted discharges of bacteria into this segment of Mayfield Creek. The location within the Gilbert Creek-Mayfield Creek and Key Creek-Mayfield Creek watersheds is shown in Figure I.2-1.

Table I.2-3 Mayfield Creek 37.7 to 40.4 *E. coli* TMDL Allocations(1)

TMDL(2)	Allocations for Direct Loads to the Segment	Allocations for Upstream Loads to the Segment(4)	Allocations for Tributary Loads to the Segment(5)	MOS(6)
	LA(3)			
$Q_S \times WQC \times CF$	$\sum(Q_{LA} \times WQC \times CF)$	$\sum(Q_{Upstream} \times WQC \times CF)$	$\sum(Q_{Tributary} \times WQC \times CF)$	Implicit

(1)All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2)Q_S is the flow (ft^3/s) in the segment.

(3)Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(4)$Q_{Upstream}$ is the flow contribution (ft^3/s) from upstream of the segment. This load includes both WLA and LA sources upstream of the impaired segment.

(5)$Q_{Tributary}$ is the flow contribution (ft^3/s) from a tributary to the segment. This load includes both WLA and LA sources on tributaries to the impaired segment.

(6)The following assumptions provide an implicit MOS:

(a)Upstream and tributary bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b)There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

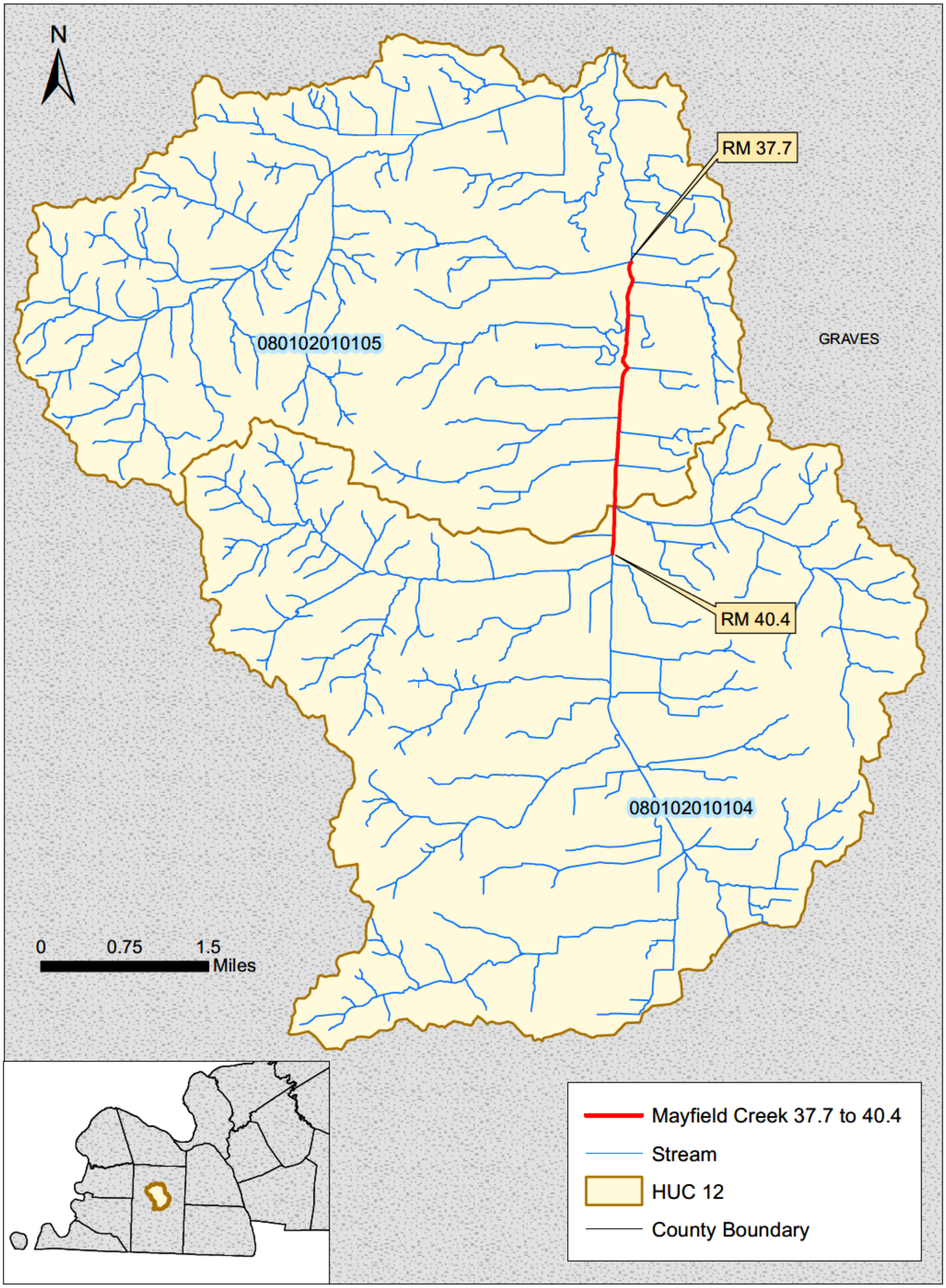


Figure I.2-1 Location of Mayfield Creek 37.7 to 40.4

Section I.3 Obion Creek 1.35 to 16.5

Waterbody ID: KY-1417

Receiving Water: Mississippi River

Impaired Use: PCR

Support Status: nonsupport

Listed Pollutant/TMDL Pollutant: *E. coli*

HUC 12: 080102010507

Counties: Hickman, Fulton

The Division of Water (DOW) has collected samples from station, MRW003, on this segment since 2000. The station is sampled every five years during the PCR season as part of the DOW five-year rotating schedule for basin monitoring (see also Section 7.2.1, Kentucky Watershed Management Framework). The station has typically been sampled three to six times during a monitoring year. Table I.3-1 summarizes information about this sampling station; Table I.3-2 summarizes the data collected from this station.

Table I.3-1 DOW Sample Site Location

Station Name	Latitude	Longitude	Stream Segment	River Mile
MRW003	36.649393	-89.122679	Obion Creek 1.35 to 16.5	8.6

Table I.3-2 DOW Sample Data Summary(1)

Station Name	Indicator Bacteria(2)	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
MRW003	*E. coli*	12	23	1,733	475
MRW003	fecal coliform	6	40	200	100

(1)The full data set for samples collected at MRW003 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.
(2)The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for Obion Creek 1.35 to 16.5 are presented in Table I.3-3. As of September 2021, there are no KPDES-permitted discharges of bacteria into this segment of Obion Creek. The location within the Cane Creek-Obion Creek watershed is shown in Figure I.3-1.

Table I.3-3 Obion Creek 1.35 to 16.5 *E. coli* TMDL Allocations(1)

TMDL(2)	Allocations for Direct Loads to the Segment	Allocations for Upstream Loads to the Segment(4)	Allocations for Tributary Loads to the Segment(5)	MOS(6)
	LA(3)			
Q_S×WQC×CF	$\sum(Q_{LA}$×WQC×CF)	$\sum(Q_{Upstream}$×WQC×CF)	$\sum(Q_{Tributary}$×WQC×CF)	Implicit

(1) All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2) Q_S is the flow (ft^3/s) in the segment.

(3) Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(4) $Q_{Upstream}$ is the flow contribution (ft^3/s) from upstream of the segment. This load includes both WLA and LA sources upstream of the impaired segment.

(5) $Q_{Tributary}$ is the flow contribution (ft^3/s) from a tributary to the segment. This load includes both WLA and LA sources on tributaries to the impaired segment.

(6) The following assumptions provide an implicit MOS:

(a)Upstream and tributary bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b)There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

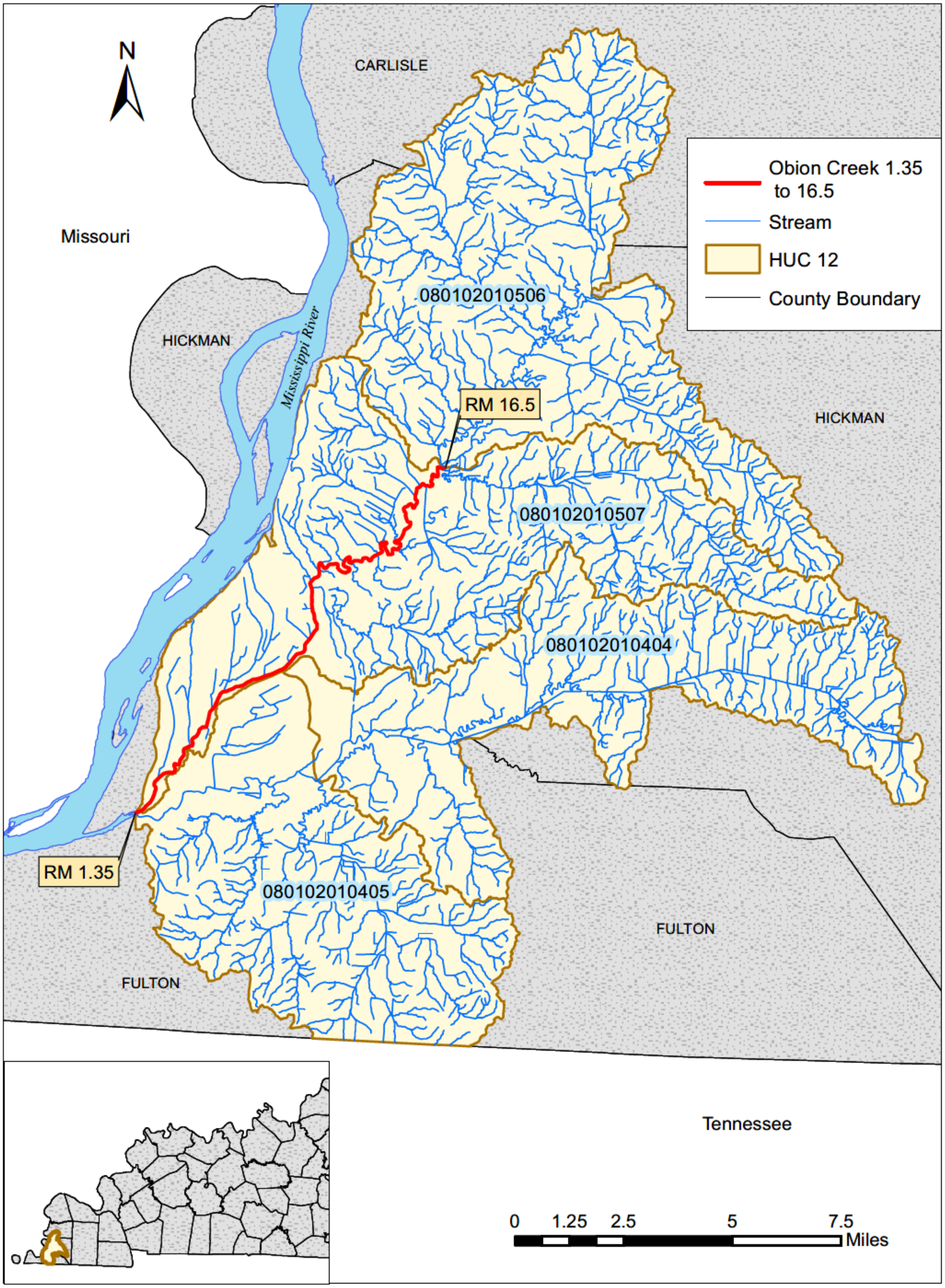


Figure I.3-1 Location of Obion Creek 1.35 to 16.5

Section I.4 Terrapin Creek 2.8 to 7.0

Waterbody ID: KY-1882

Receiving Water: North Fork Obion River

Impaired Use: PCR

Support Status: nonsupport

Listed Pollutant/ TMDL Pollutant: *E. coli*

HUC 12: 080102020103

County: Graves

The Division of Water (DOW) has collected samples from station, MRW004, on this segment since 2000. The station is sampled every five years during the PCR season as part of the DOW five-year rotating schedule for basin monitoring (see also Section 7.2.1, Kentucky Watershed Management Framework). The station has typically been sampled three to six times during a monitoring year. Table I.4-1 summarizes information about this sampling station; Table I.4-2 summarizes the data collected from this station.

Table I.4-1 DOW Sample Site Location

Station Name	Latitude	Longitude	Stream Segment	River Mile
MRW004	36.508659	-88.498949	Terrapin Creek 2.8 to 7.0	3.5

Table I.4-2 DOW Sample Data Summary(1)

Station Name	Indicator Bacteria(2)	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
MRW004	*E. coli*	14	71	2,420	521
MRW004	fecal coliform	5	10	370	206

(1)The full data set for samples collected from MRW004 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.

(2)The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for Terrapin Creek 2.8 to 7.0 are presented in Table I.4-3. As of September 2021, there are no KPDES-permitted discharges of bacteria into this segment of Terrapin Creek. The location within the Terrapin Creek watershed is shown in Figure I.4-1.

Table I.4-3 Terrapin Creek 2.8 to 7.0 *E. coli* TMDL Allocations(1)

TMDL(2)	Allocations for Direct Loads to the Segment	Allocations for Upstream Loads to the Segment(4)	Allocations for Tributary Loads to the Segment(5)	MOS(6)
	LA(3)			
Q_S×WQC×CF	∑(Q_{LA}×WQC×CF)	∑($Q_{Upstream}$×WQC×CF)	∑($Q_{Tributary}$×WQC×CF)	Implicit

(1)All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2)Q_S is the flow (ft^3/s) in the segment.

(3)Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(4)$Q_{Upstream}$ is the flow contribution (ft^3/s) from upstream of the segment. This load includes both WLA and LA sources upstream of the impaired segment.

(5)$Q_{Tributary}$ is the flow contribution (ft^3/s) from a tributary to the segment. This load includes both WLA and LA sources on tributaries to the impaired segment.

(6)The following assumptions provide an implicit MOS:

(a)Upstream and tributary bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b)There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

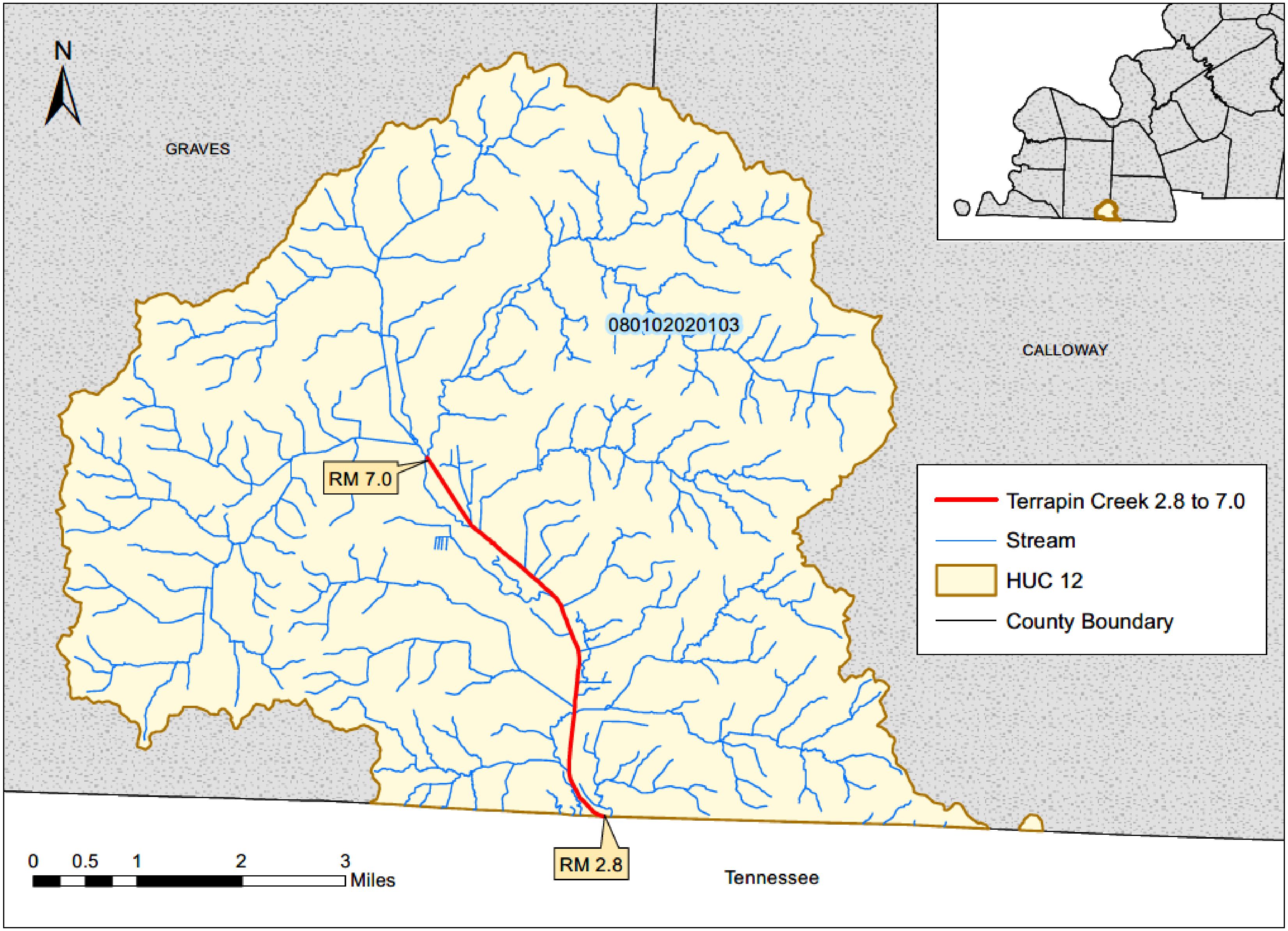


Figure I.4-1 Location of Terrapin Creek 2.8 to 7.0

APPENDIX L

Appendix L
Tennessee River Basin

HUC 8s: 06040005, 06040006

Level IV Ecoregions: Western Highland Rim, Wabash-Ohio Bottomlands, Loess Plains

Drainage Area Within Kentucky: 1,040.74 square miles

Counties: Calloway, Graves, Livingston, Lyon, McCracken, Marshall, Trigg

Major Cities: Paducah, Murray, Benton, Calvert City, Hardin, Hazel

The Tennessee River basin is located in western Kentucky. A majority of the Tennessee River basin lies within the Jackson Purchase physiographic region, with a small sliver in the north and east extending into the Western Pennyroyal physiographic region. The basin extends from the southern border near Kentucky Lake to the northern border near Paducah, Kentucky.

In 1944, the Kentucky Dam was completed at Gilbertsville, Ky., impounding the Tennessee River for 184 miles to create Kentucky Lake. Kentucky Lake lies at the border between Calloway Co., Kentucky and Tennessee and then the lake continues north into Kentucky for approximately 38 miles. Kentucky Lake extends nearly the entire length of the Tennessee River Basin in Kentucky. From the Kentucky Dam at Gilbertsville, the Tennessee River continues north and then west joining the Ohio River near Paducah, Ky. The Tennessee River basin drains an area of nearly 1,041 square miles within Kentucky.

Table L.1 provides a summary of the stream segments in the Tennessee River basin that have been included on the Kentucky 2018/2020 303(d) list for impairment due to fecal coliform, *E. coli* and/or pathogens. Segments addressed by a TMDL in this report are listed in the table with the TMDL pollutant. Segments not addressed by a TMDL in this report have a footnote explaining why they are not included. Note that stream segments listed for the first time for a bacteria-related cause on the 2018/2020 303(d) list have not yet been prioritized for TMDL development. Table L.1 also provides a crosswalk between the waterbody IDs on the 2016 303(d) list and the corresponding waterbody IDs on the 2018/2020 303(d) list. This information is provided to assist with cross-referencing waterbodies to prior lists following the implementation of a new system of waterbody IDs with the 2018/2020 list. Figure L.1 shows the location of all segments in the Tennessee River basin addressed by a TMDL in this report.

The river miles for each TMDL segment in this appendix match the 2018/2020 303(d) list. Since the National Hydrography Dataset (NHD) is continually updated to maintain accurate waterbody information, the river mile information in this appendix may not reflect the current 1:24,000 NHD for Kentucky. River mile information for stream segments is updated in each new 303(d) list submitted to EPA.

Table L.1 2018/2020 303(d) Listed Bacteria-impaired Stream Segments in the Tennessee River Basin

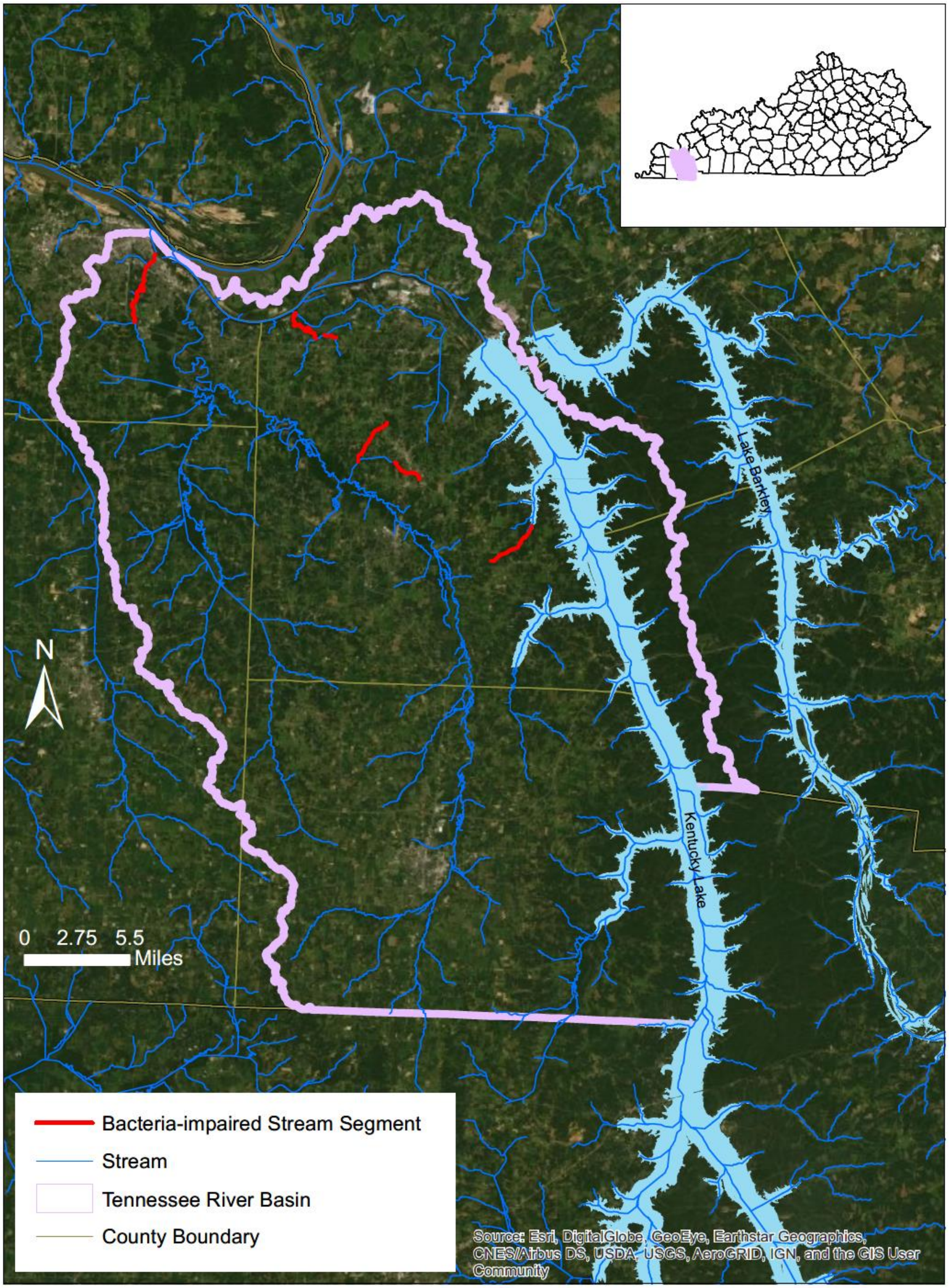
Waterbody Name	Waterbody ID	2016 Waterbody ID	Impaired Use (Support Status)	Listed Pollutant	TMDL Pollutant	Suspected Source(s)	County
Angle Creek 0.0 to 0.8	KY-135	KY485958_01	PCR (nonsupport)	Pathogens	*E. coli*	Source Unknown	Marshall
Bear Creek 3.4 to 6.7	KY-193	KY486553_02	PCR (nonsupport)	Pathogens	*E. coli*	On-site Treatment Systems (Septic Systems and Similar Decentralized Systems), Package Plant or Other Permitted Small Flows Discharges	Marshall
Chestnut Creek 3.2 to 5.05[1]	KY-475	KY489424_02	PCR (partial support)	*E. coli*	*E. coli*	Non-Point Source, Package Plant or Other Permitted Small Flows Discharges	Marshall
Clarks River 52.1 to 55.5[2]	KY-487	KY489552_07	PCR (nonsupport)	*E. coli*	TMDL not included in this document	Source Unknown	Calloway
Cypress Creek 0.0 to 6.25[3]	KY-617	KY490528_01	PCR (partial support)	*E. coli*	TMDL not included in this document	Municipal (Urbanized High Density Area), Non-Point Source, Unspecified Urban Stormwater	Marshall
Cypress Creek 11.5 to 12.8[3]	KY-3279	n/a	PCR (partial support)	*E. coli*	TMDL not included in this document	Agriculture, Municipal Point Source Discharges, Non-Point Source	Marshall
Cypress Creek 13.7 to 14.85[3]	KY-3281	n/a	PCR (nonsupport)	*E. coli*	TMDL not included in this document	Agriculture, Non-Point Source, Residential Districts	Marshall
Damon Creek 2.1 to 4.65[3]	KY-3271	n/a	PCR (partial support)	*E. coli*	TMDL not included in this document	Non-Point Source	Calloway
Island Creek 0.0 to 5.6	KY-985	KY495045_01	PCR (nonsupport)	Pathogens	*E. coli*	Source Unknown	McCracken
Little Cypress Creek 0.0 to 3.4	KY-1110	KY496700_01	PCR (partial support)	Pathogens	*E. coli*	Source Unknown	Marshall
Stice Creek 1.3 to 5.1[3]	KY-3272	n/a	PCR (nonsupport)	*E. coli*	TMDL not included in this document	Agriculture, Non-Point Source, Residential Districts	Marshall
UT of Chestnut Creek 0.0 to 2.9	KY-476	KY489424-1.05_01	PCR (nonsupport)	*E. coli*	*E. coli*	Non-Point Source, Upstream Source	Marshall
UT of Cypress Creek 0.1 to	KY-3275	n/a	PCR (partial support)	*E. coli*	TMDL not included	Non-Point Source, Urban	Marshall

1.3[3]					in this document	Runoff/Storm Sewers	

[1] Prior to the 2018/2020 303(d) list, this segment was incorrectly associated to a TMDL and should have been listed on the 2016 303(d) list. This segment will be addressed with a TMDL in this document.

[2] Prior to the 2018/2020 303(d) list, this segment was incorrectly associated to a TMDL and should have been listed on the 2016 303(d) list. This segment will be addressed in a future TMDL report.

[3] TMDLs for these segments will be developed in a future TMDL report. These are new 2018/2020 bacteria listings. These segments may have a 2016 waterbody ID listed in the table if they had any assessed use prior to the 2018/2020 IR reporting cycle.



Source: Esri, DigitalGlobe, GeoEye, Earthstar Geographics, CNES/Airbus DS, USDA, USGS, AeroGRID, IGN, and the GIS User Community

Figure L.1 Location of the Tennessee River Basin and Bacteria-impaired Streams Addressed in This TMDL (October 2021)

Land cover data is summarized in Table L.2, and its geographic distribution is shown in Figure L.2. Deciduous forest is the predominant class of land cover in the Tennessee River basin, accounting for approximately 39 percent. The next three classes by magnitude are cultivated crops, pasture/hay, and open water. Land cover classes are described in Appendix P of the core TMDL document.

Table L.2 Land Cover Classes in the Tennessee River Basin (NLCD 2011)

Land Cover	Percent of Total Area	Square Miles	Acres
Open Water	8.11	84.40	54,014.13
Developed, Open	4.95	51.48	32,944.94
Developed, Low Intensity	1.13	11.78	7,537.92
Developed, Medium Intensity	0.49	5.10	3,265.88
Developed, High Intensity	0.30	3.17	2,027.20
Barren Land (Rock, Sand, Clay)	0.11	1.14	732.05
Deciduous Forest	39.12	407.13	260,566.00
Evergreen Forest	3.20	33.29	21,307.05
Mixed Forest	0.00	0.00	2.22
Shrub/Scrub	0.06	0.65	416.16
Grassland/Herbaceous	1.38	14.34	9,175.20
Pasture/Hay	11.30	117.58	75,248.71
Cultivated Crops	25.27	262.95	168,286.50
Woody Wetlands	3.99	41.49	26,554.56
Emergent Herbaceous Wetlands	0.60	6.24	3,994.16

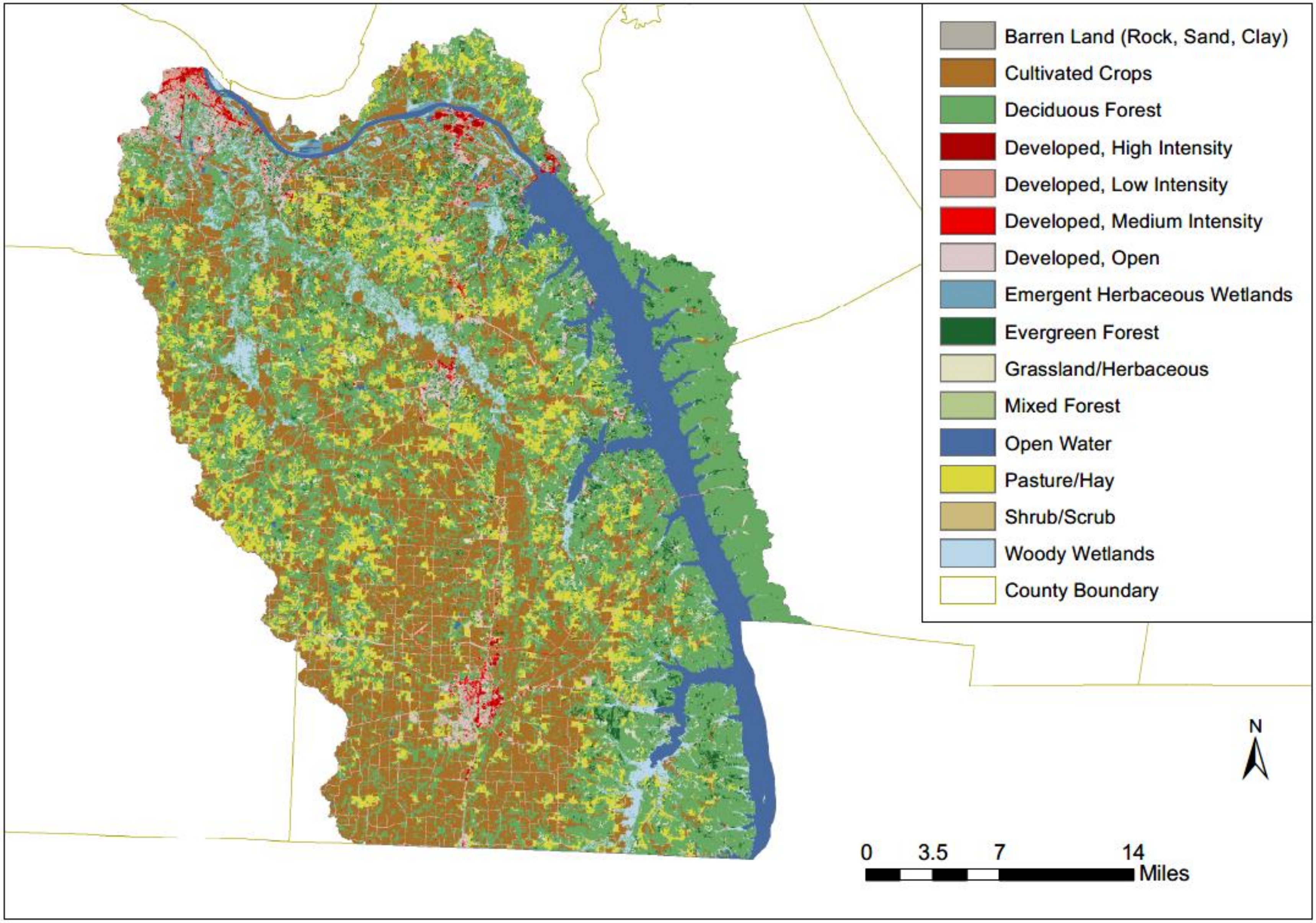


Figure L.2 Land Cover Classes in the Tennessee River Basin

Section L.1 Angle Creek 0.0 to 0.8

Waterbody ID: KY-135

Receiving Water: Barrett Branch

Impaired Use: PCR

Support Status: nonsupport

Listed Pollutant: pathogens **TMDL Pollutant:** *E. coli*

HUC 12: 060400060503

County: Marshall

Murray State University collected samples at station CRR090013, located near river mile 0.1, as part of a 319(h) nonpoint source project conducted in the Lower Cumberland, Tennessee, and Mississippi River watersheds. This station was sampled six times during the PCR season in 2000. Table L.1-1 summarizes information about this sampling station; Table L.1-2 provides a summary of the data collected from this station.

Table L.1-1 Sample Site Location

Station Name	Latitude	Longitude	Stream Segment	River Mile
CRR090013	37.01356	-88.42278	Angle Creek 0.0 to 0.8	0.1

Table L.1-2 Sample Data Summary(1)

Station Name	Indicator Bacteria(2)	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
CRR090013	*E. coli*	6	50	37,000	6,455

(1)The full data set for samples collected at CRR090013 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.

(2)The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for Angle Creek 0.0 to 0.8 are presented in Table L.1-3. As of September 2021, there are no KPDES-permitted discharges of bacteria into this segment of Angle Creek. The location within the Lower Cypress Creek watershed is shown in Figure L.1-1.

Table L.1-3 Angle Creek 0.0 to 0.8 *E. coli* TMDL Allocations(1)

TMDL(2)	Allocations for Direct Loads to the Segment	Allocations for Upstream Loads to the Segment(4)	MOS(5)
	LA(3)		
Q_S×WQC×CF	∑(Q_{LA}×WQC×CF)	∑($Q_{Upstream}$×WQC×CF)	Implicit

(1)All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2)Q_S is the flow (ft^3/s) in the segment.

(3)Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(4)$Q_{Upstream}$ is the flow contribution (ft^3/s) from upstream of the segment. This load includes both WLA and LA sources upstream of the impaired segment.

(5)The following assumptions provide an implicit MOS:

(a)Upstream bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b)There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

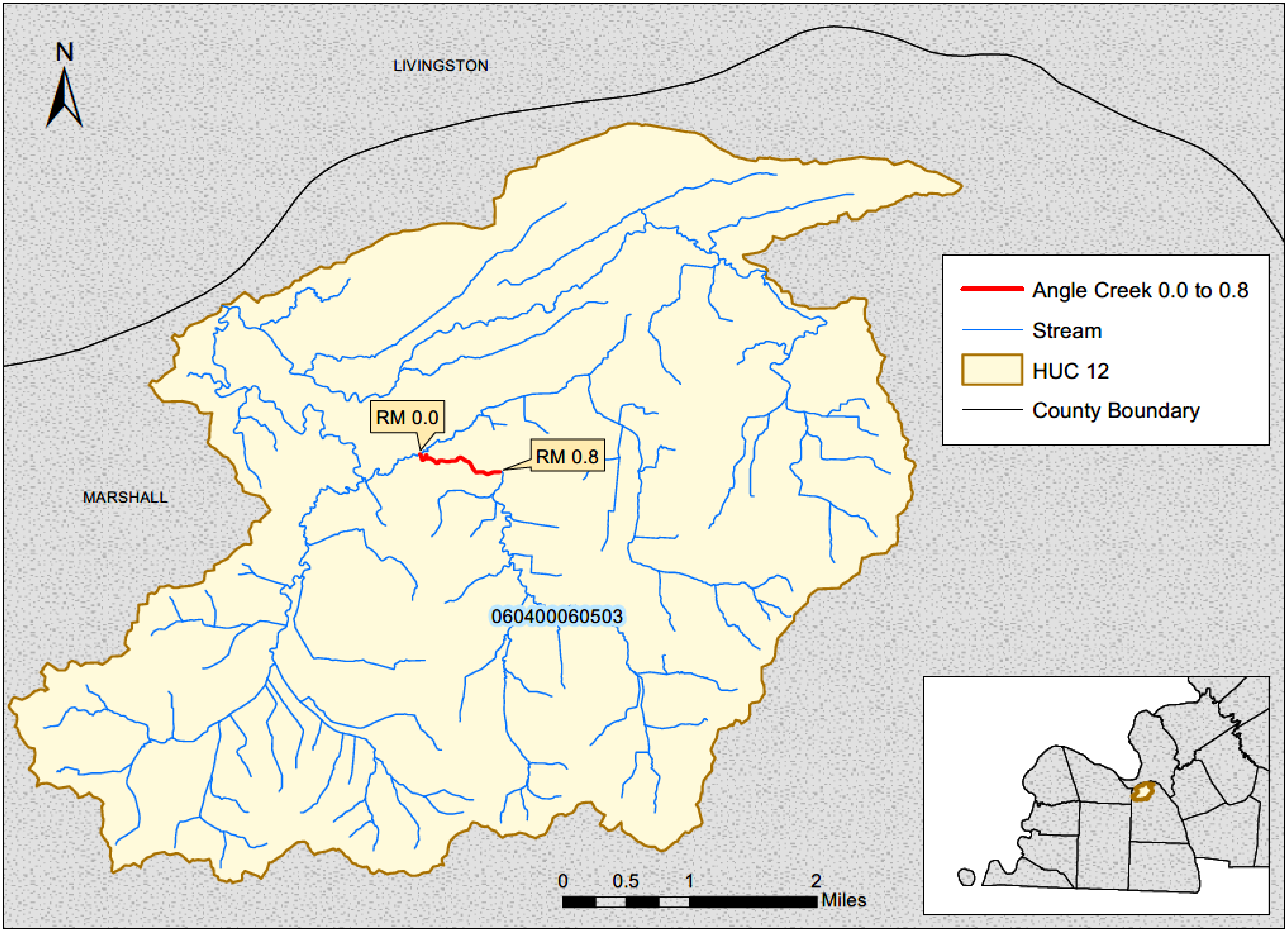


Figure L.1-1 Location of Angle Creek 0.0 to 0.8

Section L.2 Bear Creek 3.4 to 6.7

Waterbody ID: KY-193

Receiving Water: Tennessee River

Impaired Uses: PCR

Support Status: nonsupport

Listed Pollutant: pathogens **TMDL Pollutant:** *E. coli*

HUC 12: 060400051005

County: Marshall

Murray State University collected samples at station ADB_HIST_321, located near river mile 5.6, as part of a 319(h) nonpoint source project conducted in the Lower Cumberland, Tennessee, and Mississippi River watersheds. This station was sampled three times during the PCR season in 2000. Table L.2-1 summarizes information about this sampling station; Table L.2-2 provides a summary of the data collected from this station.

Table L.2-1 Sample Site Location

Station Name	Latitude	Longitude	Stream Segment	River Mile
ADB_HIST_321	36.8578	-88.2332	Bear Creek 3.4 to 6.7	5.6

Table L.2-2 Sample Data Summary(1)

Station Name	Indicator Bacteria(2)	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
ADB_HIST_321	*E. coli*	3	70	15,600	9,023

(1)The full data set for samples collected at ADB_HIST_321 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.

(2)The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for Bear Creek 3.4 to 6.7 are presented in Table L.2-3. As of September 2021, there are no KPDES-permitted discharges of bacteria into this segment of Bear Creek. The location within the Bear Creek-Kentucky Lake watershed is shown in Figure L.2-1.

Table L.2-3 Bear Creek 3.4 to 6.7 *E. coli* TMDL Allocations(1)

TMDL(2)	Allocations for Direct Loads to the Segment	Allocations for Tributary Loads to the Segment(4)	MOS(5)
	LA(3)		
Q_S×WQC×CF	∑(Q_{LA}×WQC×CF)	∑($Q_{Tributary}$×WQC×CF)	Implicit

(1)All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2)Q_S is the flow (ft^3/s) in the segment.

(3)Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(4)$Q_{Tributary}$ is the flow contribution (ft^3/s) from a tributary to the segment. This load includes both WLA and LA sources on tributaries to the impaired segment.

(5)The following assumptions provide an implicit MOS:

(a)Tributary bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b)There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

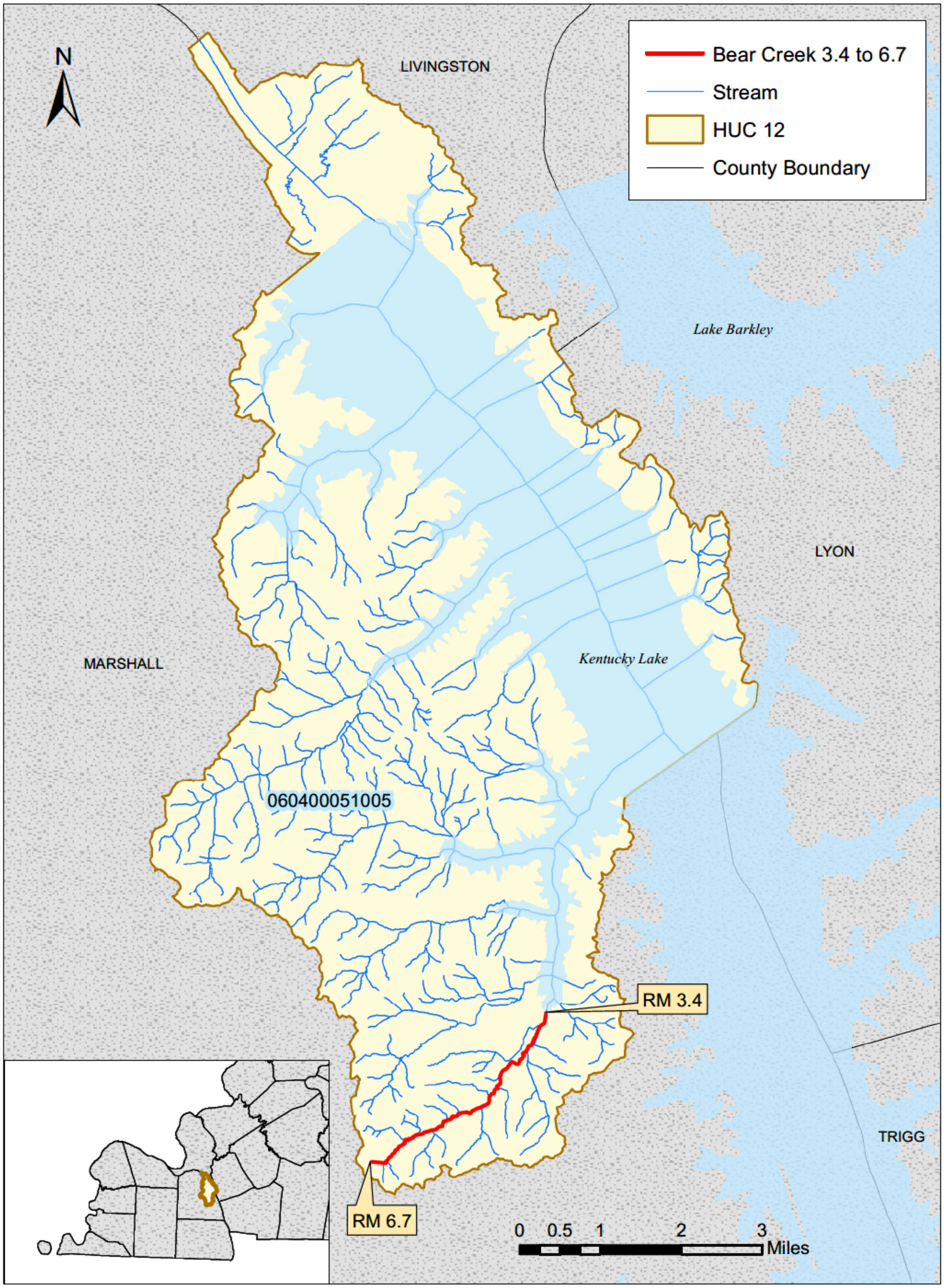


Figure L.2-1 Location of Bear Creek 3.4 to 6.7

Section L.3 Chestnut Creek 3.2 to 5.05

Waterbody ID: KY-475

Receiving Water: Clarks River

Impaired Use: PCR

Support Status: partial support

Listed Pollutant/TMDL Pollutant: *E. coli*

HUC 12: 060400060404

County: Marshall

The Division of Water (DOW) collected samples from station NPSCHESTERC01, located near river mile 3.9, for a Watershed Based Plan in Chestnut Creek. The station was sampled three times in 2013 and five times in 2014 during the PCR season. Table L.3-1 summarizes information about this sampling station; Table L.3-2 summarizes the data collected from this station.

Table L.3-1 DOW Sample Site Location

Station Name	Latitude	Longitude	Stream Segment	River Mile
NPSCHESTERC01	36.91225	-88.34538	Chestnut Creek 3.2 to 5.05	3.9

Table L.3-2 DOW Sample Data Summary(1)

Station Name	Indicator Bacteria(2)	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
NPSCHESTC01	*E. coli*	5	56	488	234

(1)The full data set for samples collected at NPSCHESTC01 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.

(2)The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for Chestnut Creek 3.2 to 5.05 are presented in Table L.3-3. As of September 2021, there are no KPDES-permitted discharges of bacteria into this segment of Chestnut Creek. The location within the Chestnut Creek-Clarks River watershed is shown in Figure L.3-1.

Table L.3-3 Chestnut Creek 3.2 to 5.05 *E. coli* TMDL Allocations(1)

TMDL(2)	Allocations for Direct Loads to the Segment	Allocations for Tributary Loads to the Segment(4)	MOS(5)
	LA(3)		
$Q_S \times WQC \times CF$	$\sum(Q_{LA} \times WQC \times CF)$	$\sum(Q_{Tributary} \times WQC \times CF)$	Implicit

(1) All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2) Q_S is the flow (ft^3/s) in the segment.

(3) Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(4) $Q_{Tributary}$ is the flow contribution (ft^3/s) from a tributary to the segment. This load includes both WLA and LA sources on tributaries to the impaired segment.

(5) The following assumptions provide an implicit MOS:

(a) Tributary bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b) There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

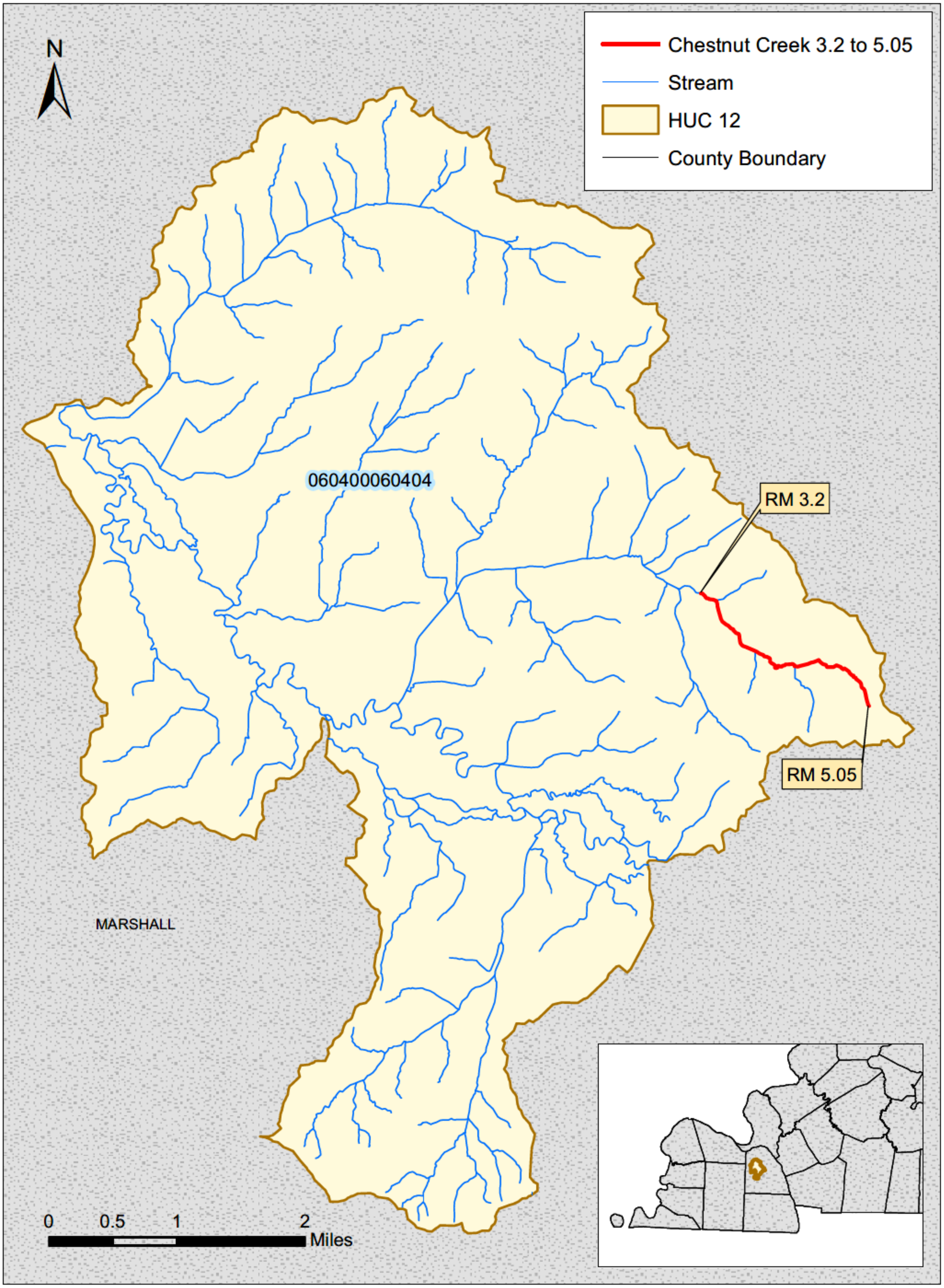


Figure L.3-1 Location of Chestnut Creek 3.2 to 5.05

Section L.4 Island Creek 0.0 to 5.6

Waterbody ID: KY-985

Receiving Water: Tennessee River

Impaired Use: PCR

Support Status: nonsupport

Listed Pollutant: pathogens **TMDL Pollutant:** *E. coli*

HUC 12s: 060400060504, 060400060505

County: McCracken

Murray State University collected samples at station ADB_HIST_337, located near river mile 1.1, as part of a 319(h) nonpoint source project conducted in the Lower Cumberland, Tennessee, and Mississippi River watersheds. This station was sampled six times during the PCR season in 2000. Table L.4-1 summarizes information about this sampling station; Table L.4-2 summarizes the data collected from this station.

Table L.4-1 Sample Site Location

Station Name	Latitude	Longitude	Stream Segment	River Mile
ADB_HIST_337	37.0604	-88.5937	Island Creek 0.0 to 5.6	1.1

Table L.4-2 Sample Data Summary(1)

Station Name	Indicator Bacteria(2)	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
ADB_HIST_337	*E. coli*	6	40	21,000	4,343

(1)The full data set for samples collected at ADB_HIST_337 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.

(2)The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for Island Creek 0.0 to 5.6 are presented in Table L.4-3.

Table L.4-3 Island Creek 0.0 to 5.6 *E. coli* TMDL Allocations(1)

TMDL(2)	Allocations for Direct Loads to the Segment		Allocations for Upstream Loads to the Segment(5)	Allocations for Tributary Loads to the Segment(6)	MOS(7)
	MS4-WLA(3)	LA(4)			
Q_S×WQC×CF	∑(Q_{MS4}×WQC×CF)	∑(Q_{LA}×WQC×CF)	∑($Q_{Upstream}$×WQC×CF)	∑($Q_{Tributary}$×WQC×CF)	Implicit

(1)All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2)Q_S is the flow (ft^3/s) in the segment.

(3)Q_{MS4} is the flow (ft^3/s) in the segment due to an MS4 entity. The MS4-WLA is not an end-of-pipe limit. The MS4-WLA is an aggregate of the in-stream contribution of all MS4 outfalls within the MS4 jurisdiction, not the storm water contribution from individual MS4 outfalls. The MS4-WLA will be addressed through the MS4 permit and implemented through the Storm Water Quality Management Plan (SWQMP). An MS4 permittee is compliant with its MS4-WLA if it is compliant with its KPDES permit.

(4)Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(5)$Q_{Upstream}$ is the flow contribution (ft^3/s) from upstream of the segment. This load includes both WLA and LA sources upstream of the impaired segment.

(6)$Q_{Tributary}$ is the flow contribution (ft^3/s) from a tributary to the segment. This load includes both WLA and LA sources on tributaries to the impaired segment.

(7)The following assumptions provide an implicit MOS:

(a)Upstream and tributary bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b)There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

The City of Paducah and Kentucky Department of Transportation have Municipal Separate Storm Sewer System (MS4) permit coverage for this segment of Island Creek. Information about MS4 permits is summarized in Table L.4-4. There are no other Kentucky Pollutant Discharge Elimination System (KPDES) permitted discharges of bacteria into the segment. The definitions for MS4 and CSO are found in 401 KAR 5:002. The location of the MS4 area and the segment within the Island Creek and White Oak Creek-Tennessee River watersheds is shown in Figure L.4-1.

Table L.4-4 Summary of Active KPDES-permitted Sources as of April 2021

KPDES Permit Number	Facility Name	Permit Expiration Date[1]	WLA[2] (colonies *E. coli* /day)
KYG200021	City of Paducah	04/30/2023	Q_{MS4}×WQC×CF
KYS000003	Kentucky Department of Transportation	09/30/2017	Q_{MS4}×WQC×CF

[1] Permit expiration dates identify the permits in effect when the draft TMDL was written, including any permits that may be expired (but not terminated) or in administrative continuance. Permits issued after the approval of this TMDL will address the TMDL.

[2] Q_{MS4} is the flow in the segment due to an MS4 entity. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day).

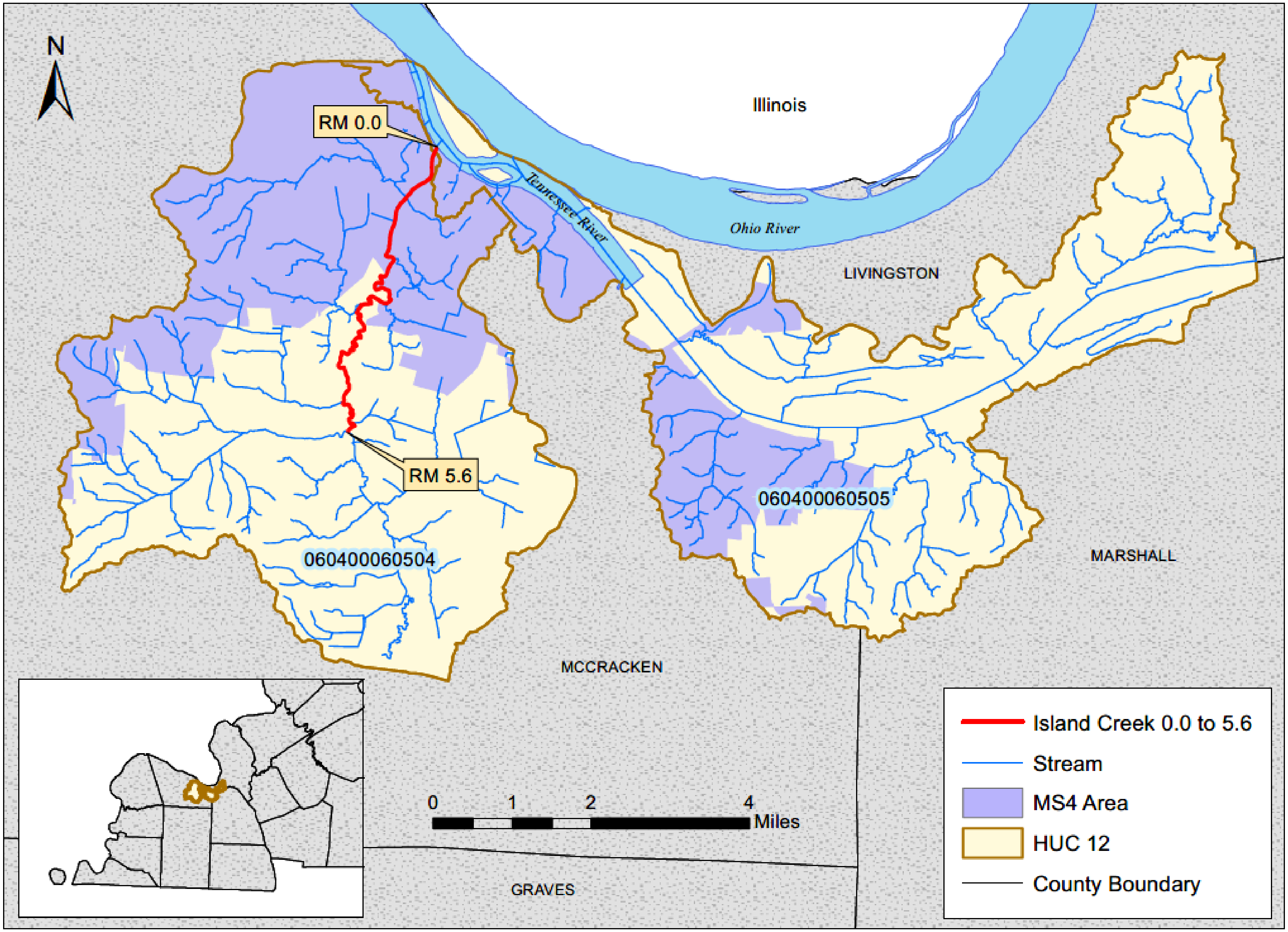


Figure L.4-1 Location of Island Creek 0.0 to 5.6

Section L.5 Little Cypress Creek 0.0 to 3.4

Waterbody ID: KY-1110

Receiving Water: Cypress Creek

Impaired Use: PCR

Support Status: partial support

Listed Pollutant: pathogens **TMDL Pollutant:** *E. coli*

HUC 12: 060400060503

County: Marshall

Murray State University collected samples at station CRR090014, located near river mile 2.07, as part of a 319(h) nonpoint source project conducted in the Lower Cumberland, Tennessee, and Mississippi River watersheds. This station was sampled six samples times during the PCR season in 2000. Table L.5-1 summarizes information about this sampling station; Table L.5-2 summarizes the data collected from this station.

Table L.5-1 Sample Site Location

Station Name	Latitude	Longitude	Stream Segment	River Mile
CRR090014	37.01738	-88.44224	Little Cypress Creek 0.0 to 3.4	2.07

Table L.5-2 Sample Data Summary(1)

Station Name	Indicator Bacteria(2)	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
CRR090014	*E. coli*	6	10	19,200	3,867

(1)The full data set for samples collected from CRR090014 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.
(2)The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for Little Cypress Creek 0.0 to 3.4 are presented in Table L.5-3. As of September 2021, there are no KPDES-permitted discharges of bacteria into this segment of Little Cypress Creek. The location within the Lower Cypress Creek watershed is shown in Figure L.5-1.

Table L.5-3 Little Cypress Creek 0.0 to 3.4 *E. coli* TMDL Allocations(1)

TMDL(2)	Allocations for Direct Loads to the Segment	Allocations for Upstream Loads to the Segment(4)	Allocations for Tributary Loads to the Segment(5)	MOS(6)
	LA(3)			
$Q_S \times WQC \times CF$	$\sum(Q_{LA} \times WQC \times CF)$	$\sum(Q_{Upstream} \times WQC \times CF)$	$\sum(Q_{Tributary} \times WQC \times CF)$	Implicit

(1)All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2)Q_S is the flow (ft^3/s) in the segment.

(3)Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(4)$Q_{Upstream}$ is the flow contribution (ft^3/s) from upstream of the segment. This load includes both WLA and LA sources upstream of the impaired segment.

(5)$Q_{Tributary}$ is the flow contribution (ft^3/s) from a tributary to the segment. This load includes both WLA and LA sources on tributaries to the impaired segment.

(6)The following assumptions provide an implicit MOS:

(a)Upstream and tributary bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b)There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

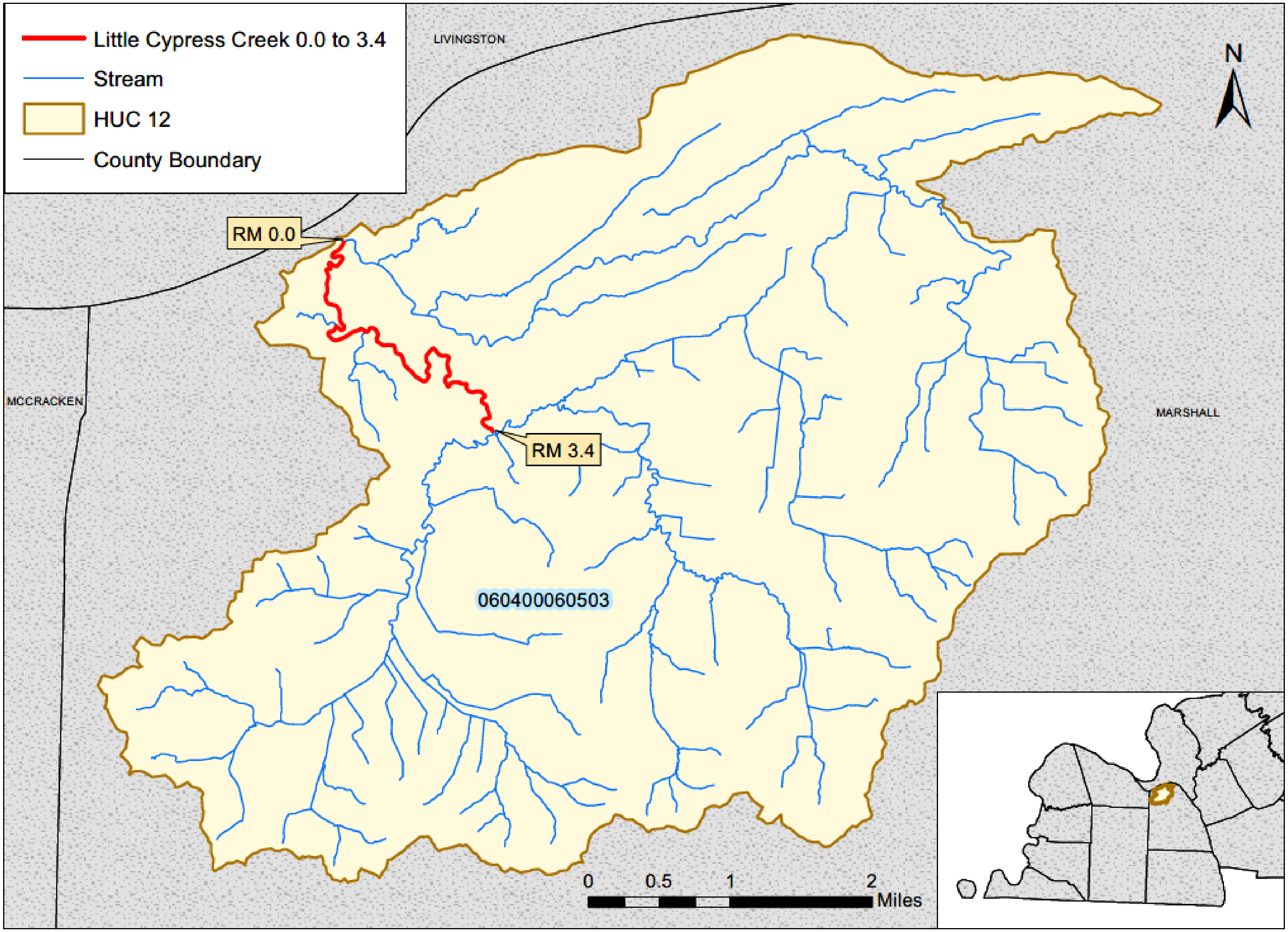


Figure L.5-1 Location of Little Cypress Creek 0.0 to 3.4

Section L.6 UT of Chestnut Creek 0.0 to 2.9

Waterbody ID: KY-476

Receiving Water: Chestnut Creek

Impaired Uses: PCR

Support Status: nonsupport

Listed Pollutant/TMDL Pollutant: *E. coli*

HUC 12: 060400060404

County: Marshall

The Division of Water (DOW) collected samples from station DOW09004005, located near river mile 0.1, in 2013. The station was sampled four times during the PCR season. Table L.6-1 summarizes information about this sampling station; Table L.6-2 provides a summary of the data collected from this station.

Table L.6-1 DOW Sample Site Location

Station Name	Latitude	Longitude	Stream Segment	River Mile
DOW09004005	36.92003	-88.38763	UT of Chestnut Creek 0.0 to 2.9	0.1

Table L.6-2 DOW Sample Data Summary(1)

Station Name	Indicator Bacteria(2)	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
DOW09004005	*E. coli*	4	50	613	228

(1)The full data set for samples collected at DOW09004005 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.

(2)The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for UT of Chestnut Creek 0.0 to 2.9 are presented in Table L.6-3. As of September 2021, there are no KPDES-permitted discharges of bacteria into this segment of UT of Chestnut Creek. The location within the Chestnut Creek-Clarks River watershed is shown in Figure L.6-1

Table L.6-3 UT of Chestnut Creek 0.0 to 2.9 *E. coli* TMDL Allocations(1)

TMDL(2)	Allocations for Direct Loads to the Segment	Allocations for Tributary Loads to the Segment(4)	MOS(5)
	LA(3)		
Q_S×WQC×CF	∑(Q_{LA}×WQC×CF)	∑($Q_{Tributary}$×WQC×CF)	Implicit

(1)All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2)Q_S is the flow (ft^3/s) in the segment.

(3)Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(4)$Q_{Tributary}$ is the flow contribution (ft^3/s) from a tributary to the segment. This load includes both WLA and LA sources on tributaries to the impaired segment.

(5)The following assumptions provide an implicit MOS:

(a)Tributary bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b)There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

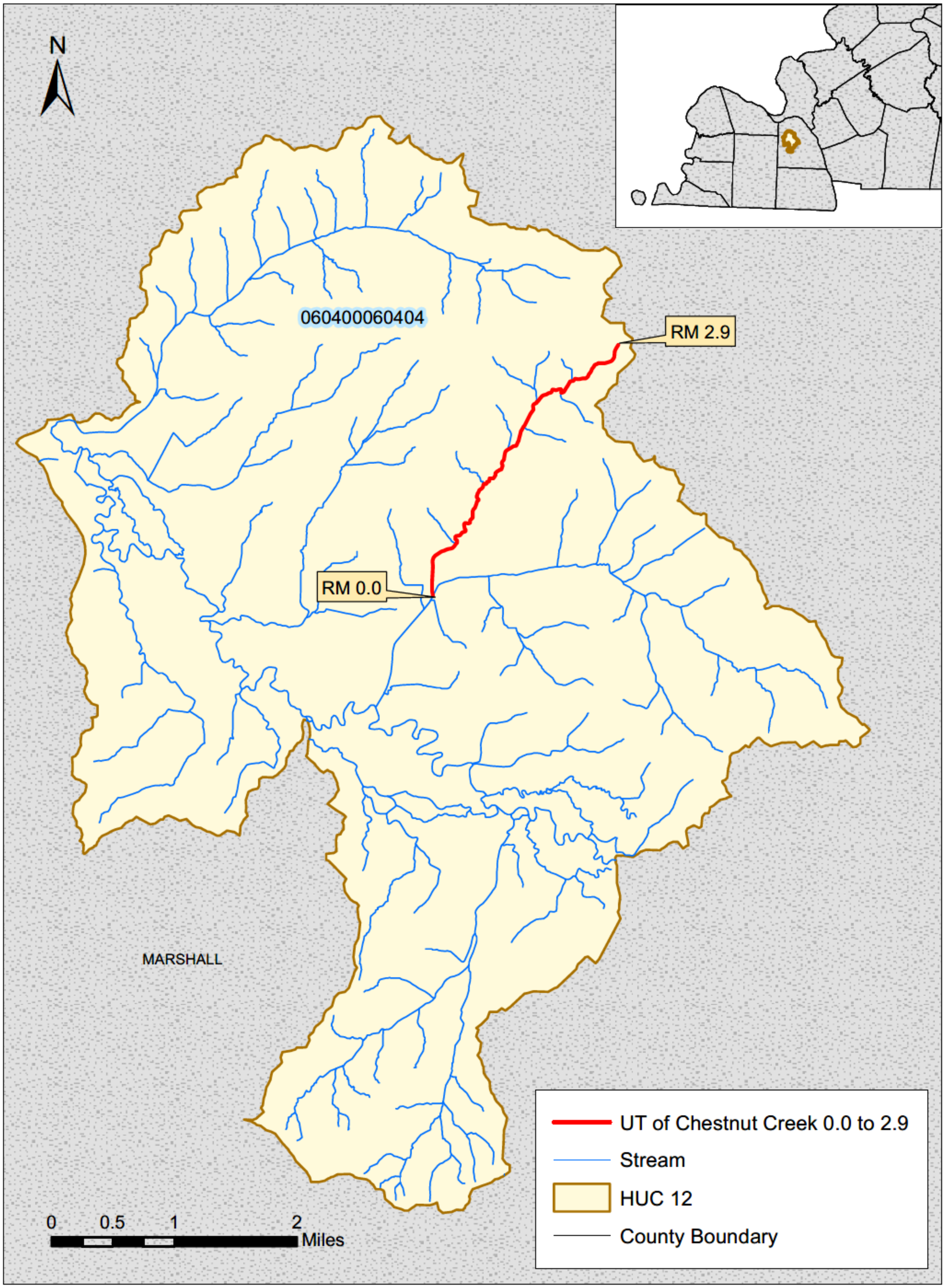


Figure L.6-1 Location of UT of Chestnut Creek 0.0 to 2.9

APPENDIX O

Appendix O
Upper Cumberland River Basin

HUC 8s: 05130101, 05130102, 05130103, 05130104, 05130105

Level IV Ecoregions: Cumberland Plateau, Plateau Escarpment, Dissected Appalachian Plateau, Cumberland Mountain Thrust Block, Knobs-Lower Scioto Dissected Plateau, Ohio/Kentucky Carboniferous Plateau, Northern Forested Plateau Escarpment, Knobs-Norman Upland, Eastern Highland Rim, Outer Nashville Basin

Drainage Area Within Kentucky: 5,179.93 square miles

Counties: Adair, Bell, Casey, Clay, Clinton, Garrard, Harlan, Jackson, Knox, Laurel, Leslie, Letcher, Lincoln, McCreary, Madison, Metcalfe, Monroe, Pulaski, Rockcastle, Russell, Wayne, Whitley

Major Cities: Corbin, Middlesboro, Somerset, Barbourville, Cumberland, Harlan, London, Pineville, Williamsburg, Monticello

The Upper Cumberland River basin is located in southeast Kentucky. A majority of the Upper Cumberland River basin lies within the Eastern Coal Field physiographic region. The far southeastern area of the Upper Cumberland River basin extends into the Cumberland Escarpment physiographic region and a very small portion in the north extends into the Knobs physiographic region. In the west, the Upper Cumberland River basin extends into the Eastern Pennyroyal physiographic region.

The basin is oriented east to west, generally along the axis of the Cumberland River. The Cumberland River originates in Harlan Co. and is formed where the headwaters, Martin's Fork, Clover Fork, and Poor Fork, converge in Baxter, Ky. The Cumberland River flows west and meanders south through Monroe Co., Ky. before entering Tennessee. The Cumberland River flows west through middle Tennessee and then north back into the Lower Cumberland River Basin in Kentucky, joining the Ohio River near Smithland, Kentucky. The Upper Cumberland River Basin drains an area of nearly 5,180 square miles in Kentucky.

Table O.1 provides a summary of the stream segments in the Upper Cumberland River basin that have been included on the Kentucky 2018/2020 303(d) list for impairment due to fecal coliform, *E. coli* and/or pathogens. Segments addressed by a TMDL in this report are listed in the table with the TMDL pollutant. Segments not addressed by a TMDL in this report have a footnote explaining why they are not included. Note that stream segments listed for the first time for a bacteria-related cause on the 2018/2020 303(d) list have not yet been prioritized for TMDL development. Table O.1 also provides a crosswalk between the waterbody IDs on the 2016 303(d) list and the corresponding waterbody IDs on the 2018/2020 303(d) list. This information is provided to assist with cross-referencing waterbodies to prior lists following the implementation of a new system of waterbody IDs with the 2018/2020 list. Figure O.1 shows the location of all segments in the Upper Cumberland River basin addressed by a TMDL in this report.

The river miles for each TMDL segment in this appendix match the 2018/2020 303(d) list. Since the National Hydrography Dataset (NHD) is continually updated to maintain accurate waterbody information, the river mile information in this appendix may not reflect the current 1:24,000 NHD for Kentucky. River mile information for stream segments is updated in each new 303(d) list submitted to EPA.

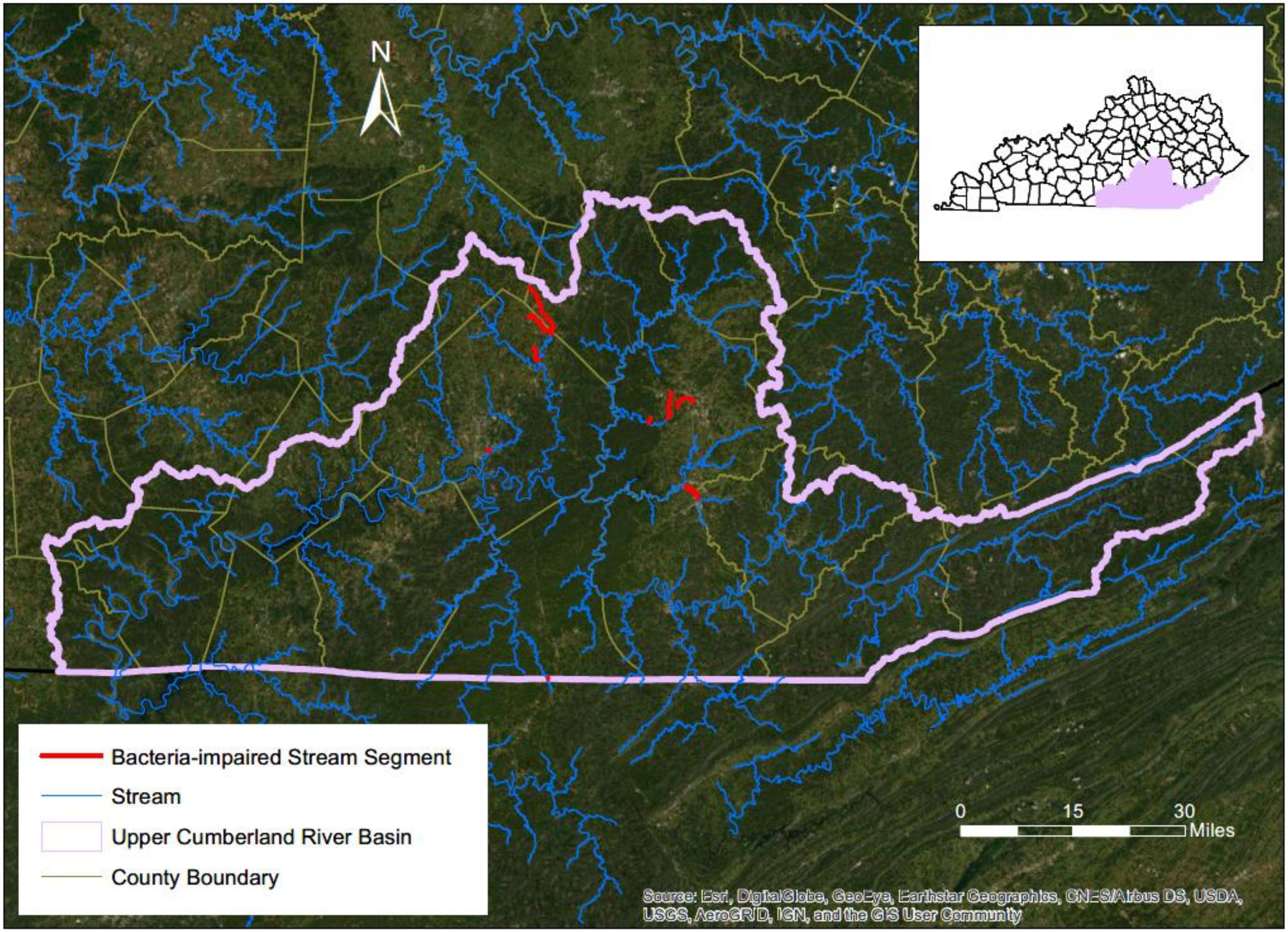
Table O.1 2018/2020 303(d) Listed Bacteria-impaired Stream Segments in the Upper Cumberland River Basin

Waterbody Name	Waterbody ID	2016 Waterbody ID	Impaired Use (Support Status)	Listed Pollutant	TMDL Pollutant	Suspected Source(s)	County
Bee Lick Creek 0.0 to 5.7	KY-212	KY486678_01	PCR (partial support)	*E. coli*	*E. coli*	Source Unknown	Pulaski
Brushy Creek 8.0 to 16.5	KY-2116	KY510974_02	PCR (partial support)	*E. coli*	*E. coli*	Agriculture	Pulaski, Rockcastle
Clifty Creek 0.0 to 2.7	KY-2171	KY511409_01	PCR (partial support)	*E. coli*	*E. coli*	Loss of Riparian Habitat, Managed Pasture Grazing, Non-Point Source	Pulaski
Clover Fork Cumberland River 0.0 to 8.65[1]	KY-2172	KY511423_01	PCR (nonsupport)	*E. coli*	TMDL not included in this document	Non-Point Source, Unknown Point Source	Harlan
Cumberland River 677 to 688.9[1]	KY-2641	KY517018_11	PCR (nonsupport)	*E. coli*	TMDL not included in this document	Municipal Point Source Discharges, Non-Point Source, Wet Weather Discharges (Point Source and Combination of Stormwater, SSO or CSO)	Harlan
Lynn Camp Creek 0.8 to 4.3	KY-2396	KY513739_01	PCR (nonsupport)	Pathogens	*E. coli*	Source Unknown, Urban Runoff/Storm Sewers	Laurel, Knox, Whitley
Martins Fork Cumberland River 17.7 to 27.3[2]	KY-1237	KY497628_03	PCR (nonsupport)	Pathogens	TMDL not included in this document	Source Unknown	Harlan
Mitchell Creek 0.0 to 3.85	KY-2422	KY514033_01	PCR (nonsupport)	*E. coli*	*E. coli*	Non-Point Source, Upstream Source	Laurel

Pitman Creek 5.4 to 6.0	KY-2462	KY514627_01	PCR (partial support)	*E. coli*	*E. coli*	Municipal Point Source Discharges	Pulaski
Poor Fork Cumberland River 1.2 to 14.9[1]	KY-3012	KY514707_01	PCR (partial support)	*E. coli*	TMDL not included in this document	On-site Treatment Systems (Septic Systems and Similar Decentralized Systems)	Harlan
Powder Mill Creek 0.0 to 4.95	KY-2476	KY514748_01	PCR (partial support)	*E. coli*	*E. coli*	Non-Point Source, Upstream Source, Urban Runoff/Storm Sewers	Laurel
Roaring Paunch Creek 15.6 to 15.75	KY-2503	KY514993_03	PCR (nonsupport)	*E. coli*	*E. coli*	Non-Point Source, Rural (Residential Areas)	McCreary
White Oak Creek 0.0 to 1.0	KY-2615	KY516320_01	PCR (partial support)	*E. coli*	*E. coli*	Non-Point Source, Upstream Source	Laurel

[1] TMDLs for these segments will be developed in a future TMDL report. These are new 2018/2020 bacteria listings. These segments may have a 2016 waterbody ID listed in the table if they had any assessed use prior to the 2018/2020 IR reporting cycle.

[2] A TMDL is not included because this segment will be proposed for delisting on a future 303(d) list.



Source: Esri, DigitalGlobe, GeoEye, Earthstar Geographics, CNES/Airbus DS, USDA, USGS, AeroGRID, IGN, and the GIS User Community

Figure O.1 Location of the Upper Cumberland River Basin and Bacteria-impaired Streams Addressed in This TMDL (October 2021)

Land cover data is summarized in Table O.2, and its geographic distribution is shown in Figure O.2. Deciduous forest is the predominant class of land cover in the Upper Cumberland River basin, accounting for approximately 60 percent. The next three classes by magnitude are pasture/hay, grassland/herbaceous, and mixed forest. Land cover classes are described in Appendix P of the core TMDL document.

Table O.2 Land Cover Classes in the Upper Cumberland River Basin (NLCD 2011)

Land Cover	Percent of Total Area	Square Miles	Acres
Open Water	1.85	95.94	61,402.46
Developed, Open	4.62	239.49	153,273.45
Developed, Low Intensity	2.12	109.68	70,194.06
Developed, Medium Intensity	0.58	30.29	19,383.37
Developed, High Intensity	0.16	8.54	5,466.09
Barren Land (Rock, Sand, Clay)	0.68	35.16	22,502.75
Deciduous Forest	59.71	3,092.81	1,979,397.99
Evergreen Forest	0.88	45.47	29,098.18
Mixed Forest	5.91	306.32	196,044.09
Shrub/Scrub	0.54	28.00	17,917.40
Grassland/Herbaceous	6.39	331.00	211,840.02
Pasture/Hay	14.96	775.16	496,104.07
Cultivated Crops	1.56	80.86	51,749.46
Woody Wetlands	0.01	0.39	252.15
Emergent Herbaceous Wetlands	0.02	0.82	527.87

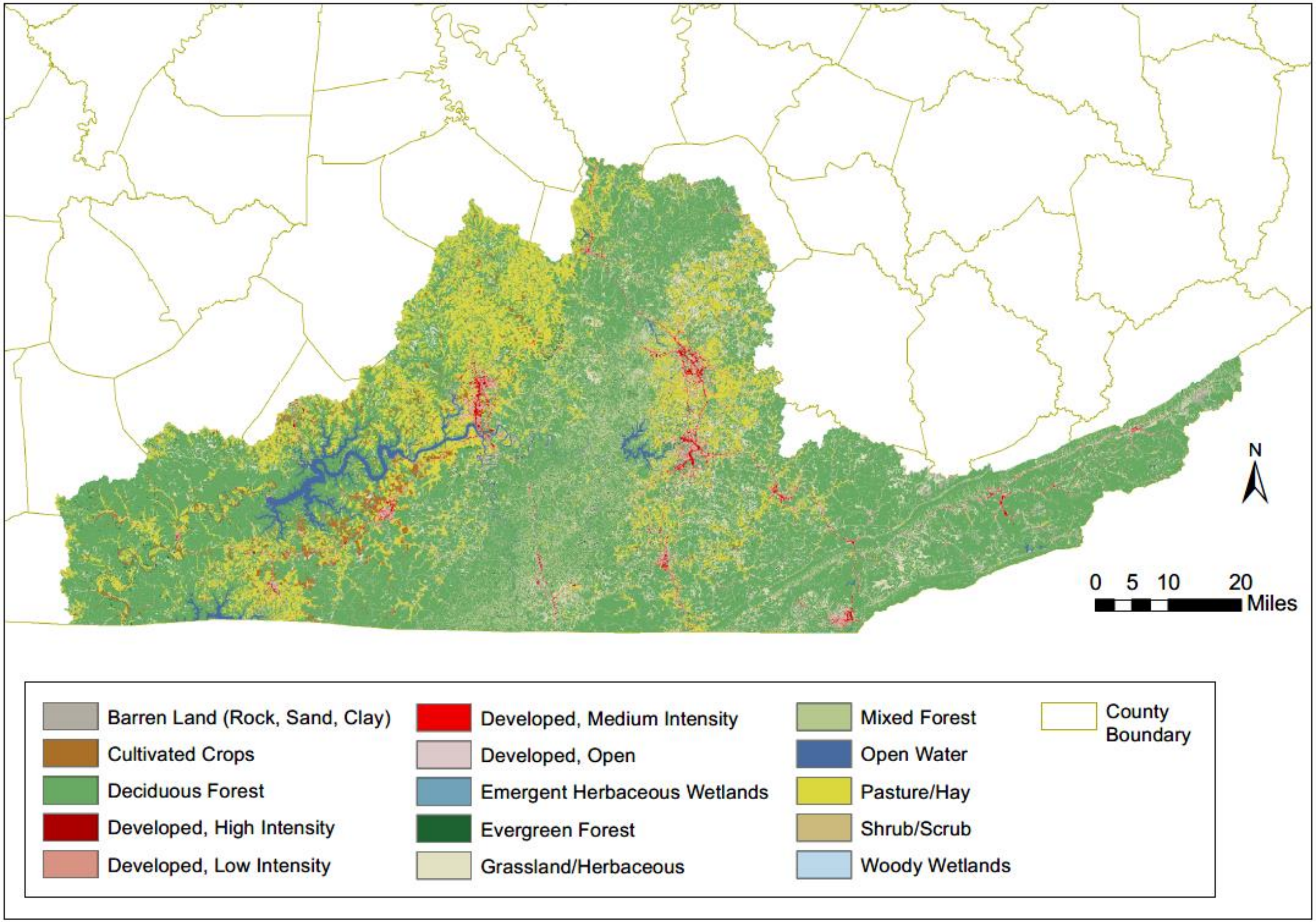


Figure O.2 Land Cover Classes in the Upper Cumberland River Basin

Section O.1 Bee Lick Creek 0.0 to 5.7

Waterbody ID: KY-212

Receiving Water: Brushy Creek

Impaired Use: PCR

Support Status: partial support

Listed Pollutant/TMDL Pollutant: *E. coli*

HUC 12: 051301030103

County: Pulaski

University of Louisville collected samples from two stations on this segment as part of the development of a watershed plan for Brushy Creek watershed. The stations were sampled eleven times during the PCR season from 2011 to 2012. Table O.1-1 summarizes information about these sampling stations; Table O.1-2 provides a summary of the data collected from these stations.

Table O.1-1 DOW Sample Site Locations

Station Name	Latitude	Longitude	Stream Segment	River Mile
BL 1	37.2743	-84.45103	Bee Lick Creek 0.0 to 5.7	1.25
BL 2	37.30178	-84.48912	Bee Lick Creek 0.0 to 5.7	5.3

Table O.1-2 DOW Sample Data Summary(1)

Station Name	Indicator Bacteria(2)	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
BL 1	*E. coli*	11	50	1,300	261
BL 2	*E. coli*	11	19	1,600	569

(1)The full data set for samples collected at BL 1 and BL 2 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.
(2)The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for Bee Lick Creek 0.0 to 5.7 are presented in Table O.1-3. As of September 2021, there are no KPDES-permitted discharges of bacteria into this segment of Bee Lick Creek. The location within the Brushy Creek watershed is shown in Figure O.1-1.

Table O.1-3 Bee Lick Creek 0.0 to 5.7 *E. coli* TMDL Allocations(1)

TMDL(2)	Allocations for Direct Loads to the Segment	Allocations for Upstream Loads to the Segment(4)	Allocations for Tributary Loads to the Segment(5)	MOS(6)
	LA(3)			
Q_S×WQC×CF	$\sum(Q_{LA}$×WQC×CF)	$\sum(Q_{Upstream}$×WQC×CF)	$\sum(Q_{Tributary}$×WQC×CF)	Implicit

(1)All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2)Q_S is the flow (ft^3/s) in the segment.

(3)Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(4)$Q_{Upstream}$ is the flow contribution (ft^3/s) from upstream of the segment. This load includes both WLA and LA sources upstream of the impaired segment.

(5)$Q_{Tributary}$ is the flow contribution (ft^3/s) from a tributary to the segment. This load includes both WLA and LA sources on tributaries to the impaired segment.

(6)The following assumptions provide an implicit MOS:

(a)Upstream and tributary bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b)There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

Figure O.1-2 shows the segment is located near an area where karst features such as sinkholes and springs exist. The sink features may capture surface drainage and channel it underground to resurface later at one or more springs. These discharging springs may occur outside the watershed where the drainage originated. However, unless karst dye trace studies indicate otherwise, groundwater catchment is presumed to correspond to the topographic watershed boundaries of surface drainage. Dye tracing in the region did not identify any areas outside the boundary of the Brushy Creek watershed that contribute drainage to the segment.

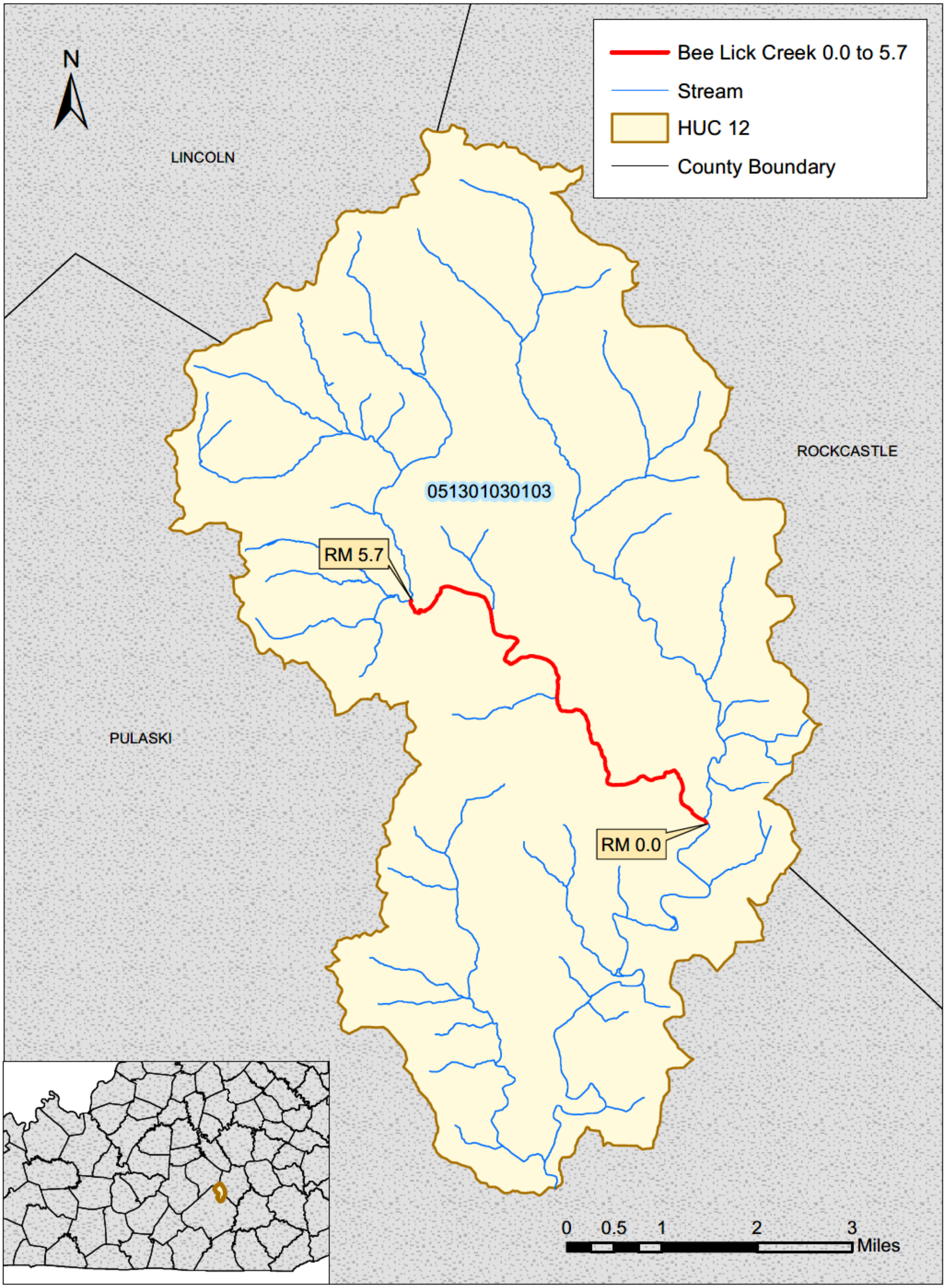


Figure O.1-1 Location of Bee Lick Creek 0.0 to 5.7

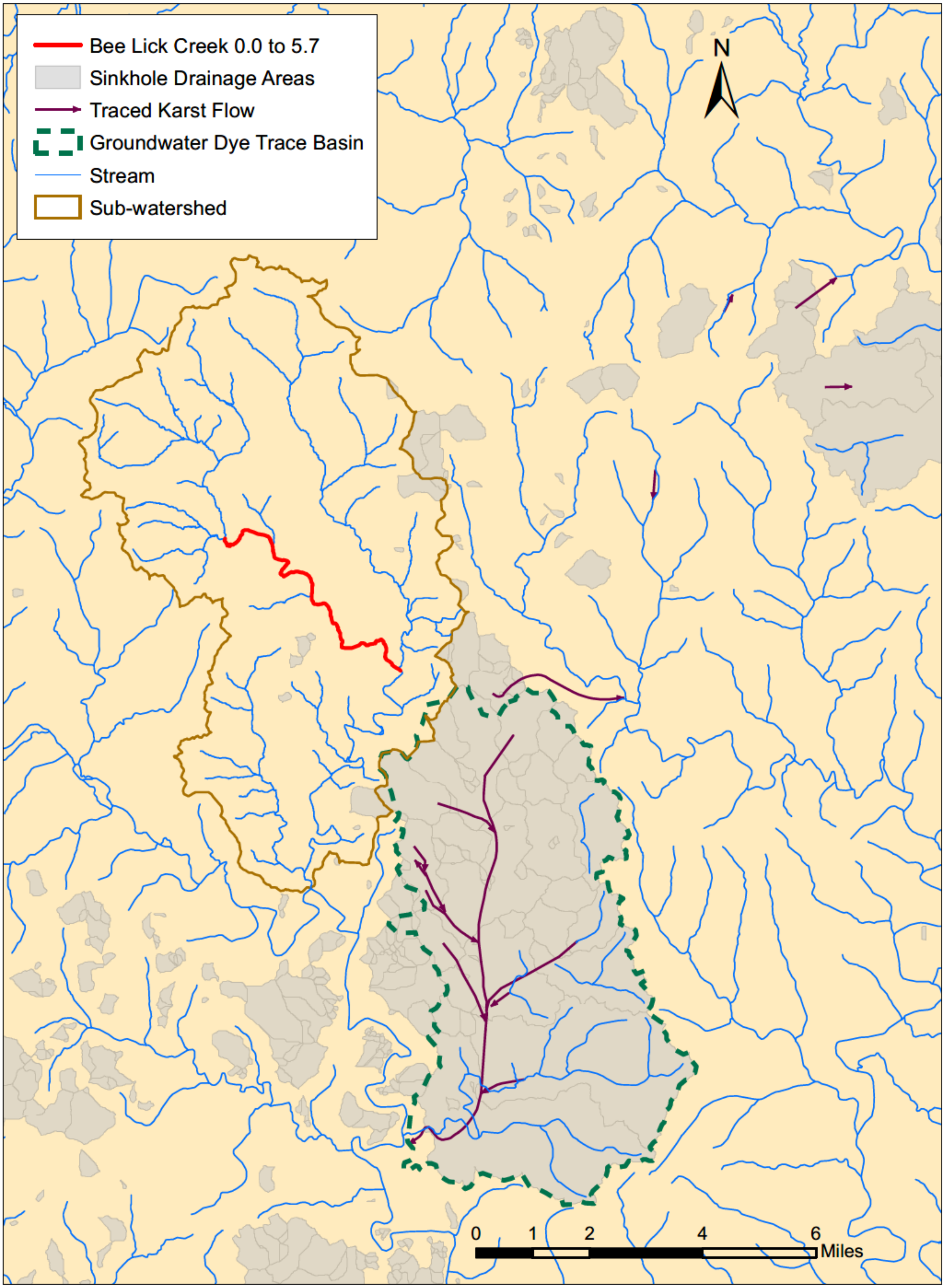


Figure O.1-2 Karst Influence in the Region of Bee Lick Creek 0.0 to 5.7

Section O.2 Brushy Creek 8.0 to 16.5

Waterbody ID: KY-2116

Receiving Water: Buck Creek

Impaired Uses: PCR

Support Status: partial support

Listed Pollutant/TMDL Pollutant: *E. coli*

HUC 12: 051301030103

Counties: Pulaski, Rockcastle

University of Louisville collected samples from two stations on this segment as part of the development of a watershed plan for Brushy Creek watershed. The stations were sampled eleven times during the PCR season from 2011 to 2012. Table O.2-1 summarizes information about these sampling stations; Table O.2-2 provides a summary of the data collected from these stations.

Table O.2-1 DOW Sample Site Locations

Station Name	Latitude	Longitude	Stream Segment	River Mile
BR 2	37.2761	-84.4373	Brushy Creek 8.0 to 16.5	8.6
BR 3	37.308502	-84.46064	Brushy Creek 8.0 to 16.5	12.1

Table O.2-2 DOW Sample Data Summary(1)

Station Name	Indicator Bacteria(2)	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
BR 2	*E. coli*	11	185	>2,420	648
BR 3	*E. coli*	11	610	24,200	3,362

(1)The full data set for samples collected at BR 2 and BR 3 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.

(2)The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for Brushy Creek 8.0 to 16.5 are presented in Table O.2-3. As of September 2021, there are no KPDES-permitted discharges of bacteria into this segment of Brushy Creek. The location within the Brushy Creek watershed is shown in Figure O.2-1.

Table O.2-3 Brushy Creek 8.0 to 16.5 *E. coli* TMDL Allocations(1)

TMDL(2)	Allocations for Direct Loads to the Segment	Allocations for Tributary Loads to the Segment(4)	MOS(5)
	LA(3)		
$Q_S \times WQC \times CF$	$\sum(Q_{LA} \times WQC \times CF)$	$\sum(Q_{Tributary} \times WQC \times CF)$	Implicit

(1)All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2)Q_S is the flow (ft^3/s) in the segment.

(3)Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(4)$Q_{Tributary}$ is the flow contribution (ft^3/s) from a tributary to the segment. This load includes both WLA and LA sources on tributaries to the impaired segment.

(5)The following assumptions provide an implicit MOS:

(a)Tributary bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b)There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

Figure O.2-2 shows the segment is located near an area where karst features such as sinkholes and springs exist. The sink features may capture surface drainage and channel it underground to resurface later at one or more springs. These discharging springs may occur outside the watershed where the drainage originated. However, unless karst dye trace studies indicate otherwise, groundwater catchment is presumed to correspond to the topographic watershed boundaries of surface drainage. Dye tracing in the region did not identify any areas outside the boundary of the Brushy Creek watershed that contribute drainage to the segment.

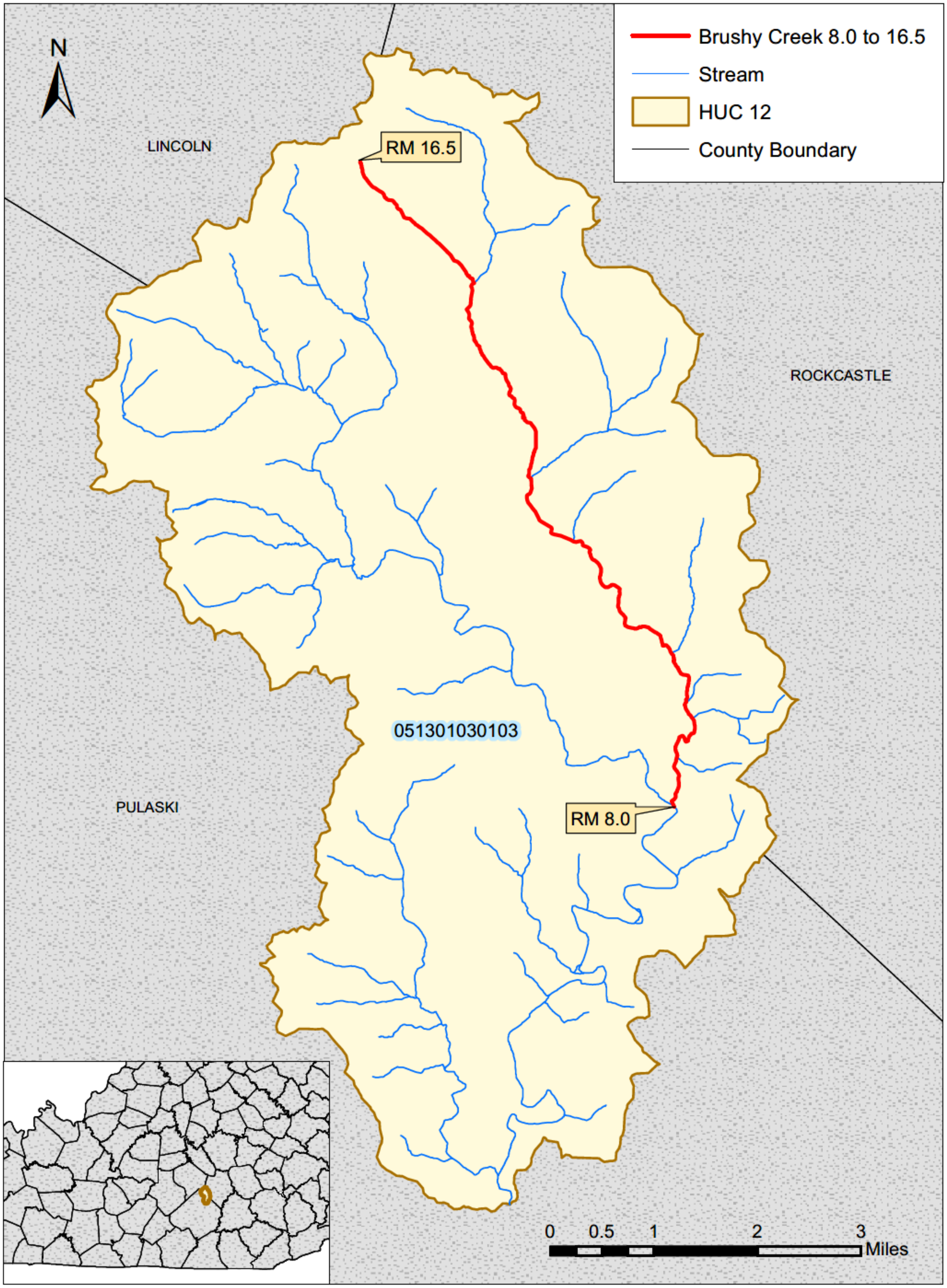


Figure O.2-1 Location of Brushy Creek 8.0 to 16.5

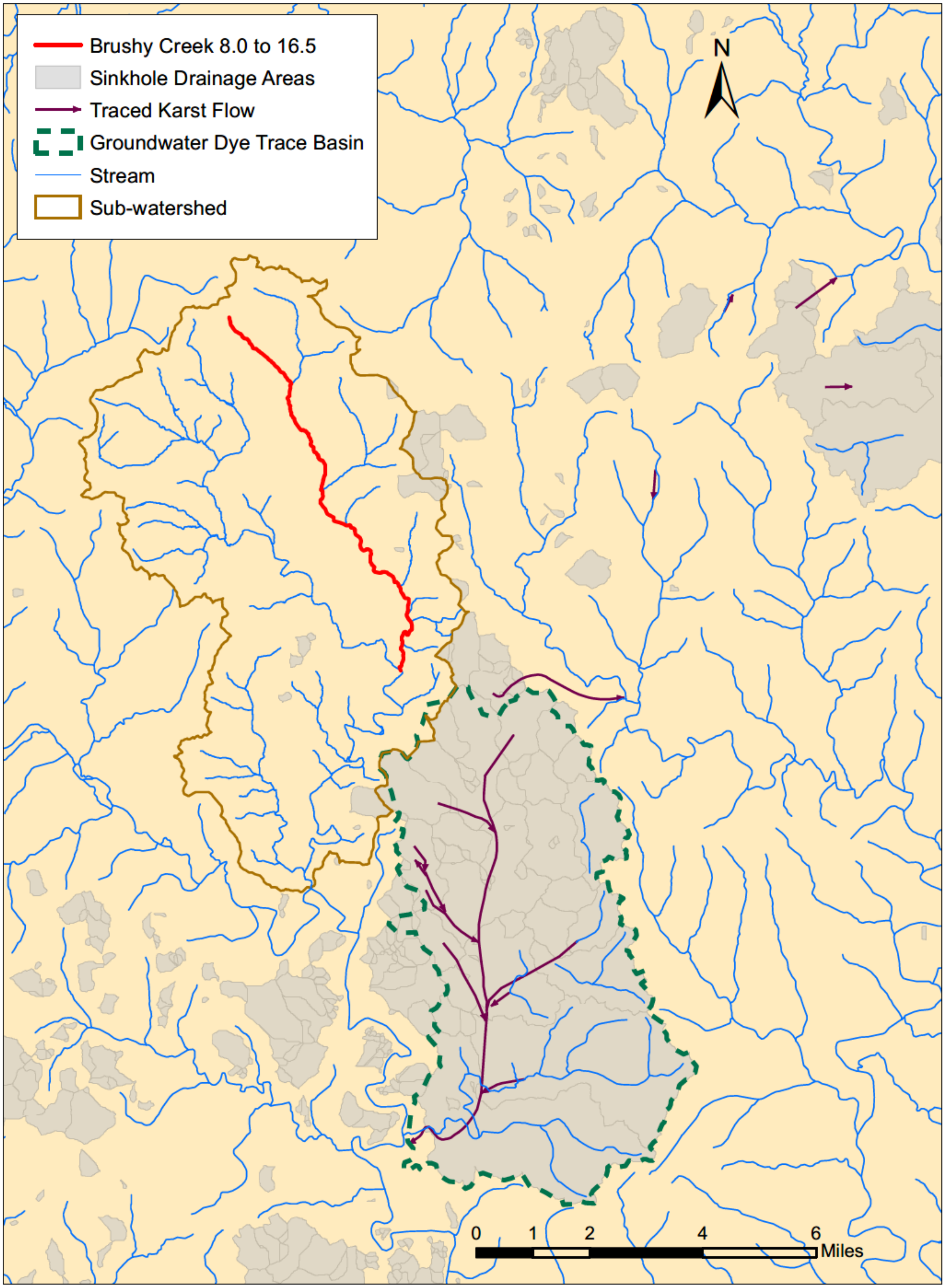


Figure O.2-2 Karst Influence in the Region of Brushy Creek 8.0 to 16.5

Section O.3 Clifty Creek 0.0 to 2.7

Waterbody ID: KY-2171

Receiving Water: Brushy Creek

Impaired Use: PCR

Support Status: partial support

Listed Pollutant/TMDL Pollutant: *E. coli*

HUC 12: 051301030103

County: Pulaski

University of Louisville collected samples from station CL 1, located near river mile 0.1, from 2011 to 2012 as part of the development of a watershed plan for Brushy Creek watershed. The station was sampled eleven times during the PCR season. Table O.3-1 summarizes information about this sampling station; Table O.3-2 summarizes the data collected from this station.

Table O.3-1 DOW Sample Site Location

Station Name	Latitude	Longitude	Stream Segment	River Mile
CL 1	37.21757	-84.47061	Clifty Creek 0.0 to 2.7	0.1

Table O.3-2 DOW Sample Data Summary(1)

Station Name	Indicator Bacteria(2)	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
CL 1	*E. coli*	11	2	2,420	470

(1)The full data set for samples collected at CL 1 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.
(2)The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for Clifty Creek 0.0 to 2.7 are presented in Table O.3-3. As of September 2021, there are no KPDES-permitted discharges of bacteria into this segment of Clifty Creek. The location within the Brushy Creek watershed is shown in Figure O.3-1.

Table O.3-3 Clifty Creek 0.0 to 2.7 *E. coli* TMDL Allocations(1)

TMDL(2)	Allocations for Direct Loads to the Segment	Allocations for Upstream Loads to the Segment(4)	Allocations for Tributary Loads to the Segment(5)	MOS(6)
	LA(3)			
$Q_S \times WQC \times CF$	$\sum(Q_{LA} \times WQC \times CF)$	$\sum(Q_{Upstream} \times WQC \times CF)$	$\sum(Q_{Tributary} \times WQC \times CF)$	Implicit

(1)All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2)Q_S is the flow (ft^3/s) in the segment.

(3)Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(4)$Q_{Upstream}$ is the flow contribution (ft^3/s) from upstream of the segment. This load includes both WLA and LA sources upstream of the impaired segment.

(5)$Q_{Tributary}$ is the flow contribution (ft^3/s) from a tributary to the segment. This load includes both WLA and LA sources on tributaries to the impaired segment.

(6)The following assumptions provide an implicit MOS:

(a)Upstream and tributary bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b)There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

Figure O.3-2 shows the segment is located near an area where karst features such as sinkholes and springs exist. The sink features may capture surface drainage and channel it underground to resurface later at one or more springs. These discharging springs may occur outside the watershed where the drainage originated. However, unless karst dye trace studies indicate otherwise, groundwater catchment is presumed to correspond to the topographic watershed boundaries of surface drainage. Dye tracing in the region did not identify any areas outside the boundary of the Brushy Creek watershed that contribute drainage to the segment.

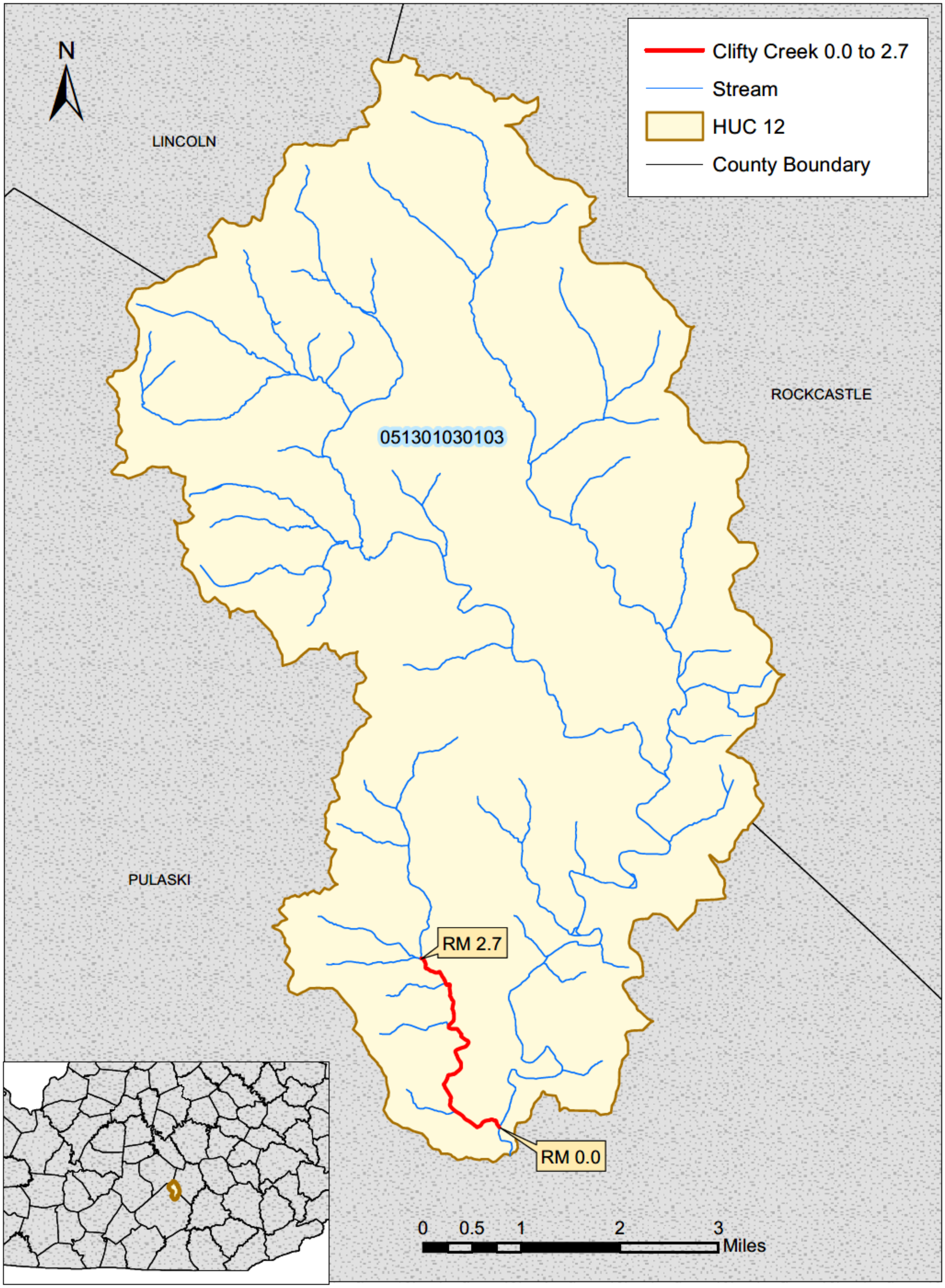


Figure O.3-1 Location of Clifty Creek 0.0 to 2.7

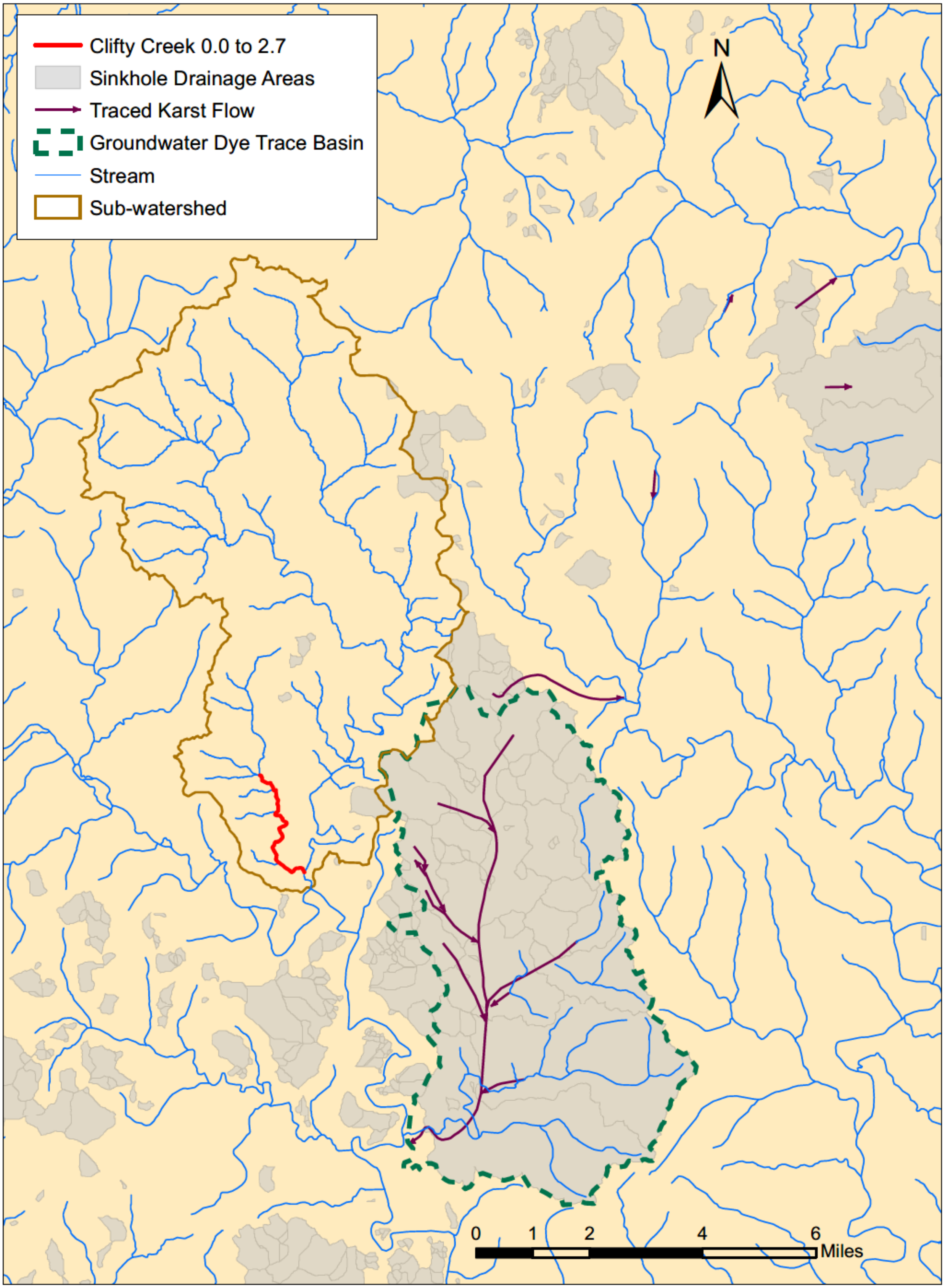


Figure O.3-2 Karst Influence in the Region of Clifty Creek 0.0 to 2.7

Section O.4 Lynn Camp Creek 0.8 to 4.3

Waterbody ID: KY-2396

Receiving Water: Laurel River

Impaired Use: PCR

Support Status: nonsupport

Listed Pollutant: pathogens **TMDL Pollutant:** *E. coli*

HUC 12: 051301010804

Counties: Laurel, Knox, Whitley

This segment was first listed on Kentucky's 1998 303(d) list. Assessment records indicate sampling occurred between 1996 and 1997, but the data could not be located as of this writing.

The TMDL allocations for Lynn Camp Creek 0.8 to 4.3 are presented in Table O.4-1.

Table O.4-1 Lynn Camp Creek 0.8 to 4.3 *E. coli* TMDL Allocations(1)

TMDL(2)	Allocations for Direct Loads to the Segment		Allocations for Upstream Loads to the Segment(5)	Allocations for Tributary Loads to the Segment(6)	MOS(7)
	SWS-WLA(3)	LA(4)			
$Q_S \times WQC \times CF$	$\sum(Q_{SWS} \times WQC \times CF)$	$\sum(Q_{LA} \times WQC \times CF)$	$\sum(Q_{Upstream} \times WQC \times CF)$	$\sum(Q_{Tributary} \times WQC \times CF)$	Implicit

(1)All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2)Q_S is the flow (ft^3/s) in the segment.

(3)Q_{SWS} is the flow (ft^3/s) in the segment due to a SWS entity. New or expanded SWS sources will be allowed to discharge to the segment contingent upon them meeting the PCR bacterial WQCs found in 401 KAR 10:031. SWS-WLAs will be translated into KPDES permit limits as an *E. coli* effluent gross limit of 130 colonies/100 ml as a monthly average (geometric mean) and 240 colonies/100 ml as a maximum weekly average (geometric mean).

(4)Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(5)$Q_{Upstream}$ is the flow contribution (ft^3/s) from upstream of the segment. This load includes both WLA and LA sources upstream of the impaired segment.

(6)$Q_{Tributary}$ is the flow contribution (ft^3/s) from a tributary to the segment. This load includes both WLA and LA sources on tributaries to the impaired segment.

(7)The following assumptions provide an implicit MOS:

(a)Upstream and tributary bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b)Although all sources are provided an allocation at the Water Quality Standard, not all sources discharge at this maximum allocation at the same time.

(c)There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

One facility permitted under the Kentucky Pollutant Discharge Elimination System (KPDES) discharges treated effluent directly into this segment of Lynn Camp Creek. The directly discharging facility is a sanitary wastewater system. There are no MS4 communities or CSOs discharging directly to this segment of Lynn Camp Creek. This facility is identified in Table O.4-2 and the location within the Lynn Camp Creek watershed is shown in Figure O.4-1.

Table O.4-2 Summary of Active KPDES-permitted Sources as of October 2021

KPDES Permit Number	Facility Name	Design Flow (MGD)	Outfall Latitude	Outfall Longitude	Permit Expiration Date(1)	WLA(2) (colonies *E. coli* /day)
KY0020133	Corbin STP	4.5	36.95525	-84.098278	09/30/2019	Q_{SWS}×WQC×CF

(1)Permit expiration dates identify the permits in effect when the draft TMDL was written, including any permits that may be expired (but not terminated) or in administrative continuance. Permits issued after the approval of this TMDL will address the TMDL.

(2)Q_{SWS} is the flow in the segment due to a SWS entity. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day).

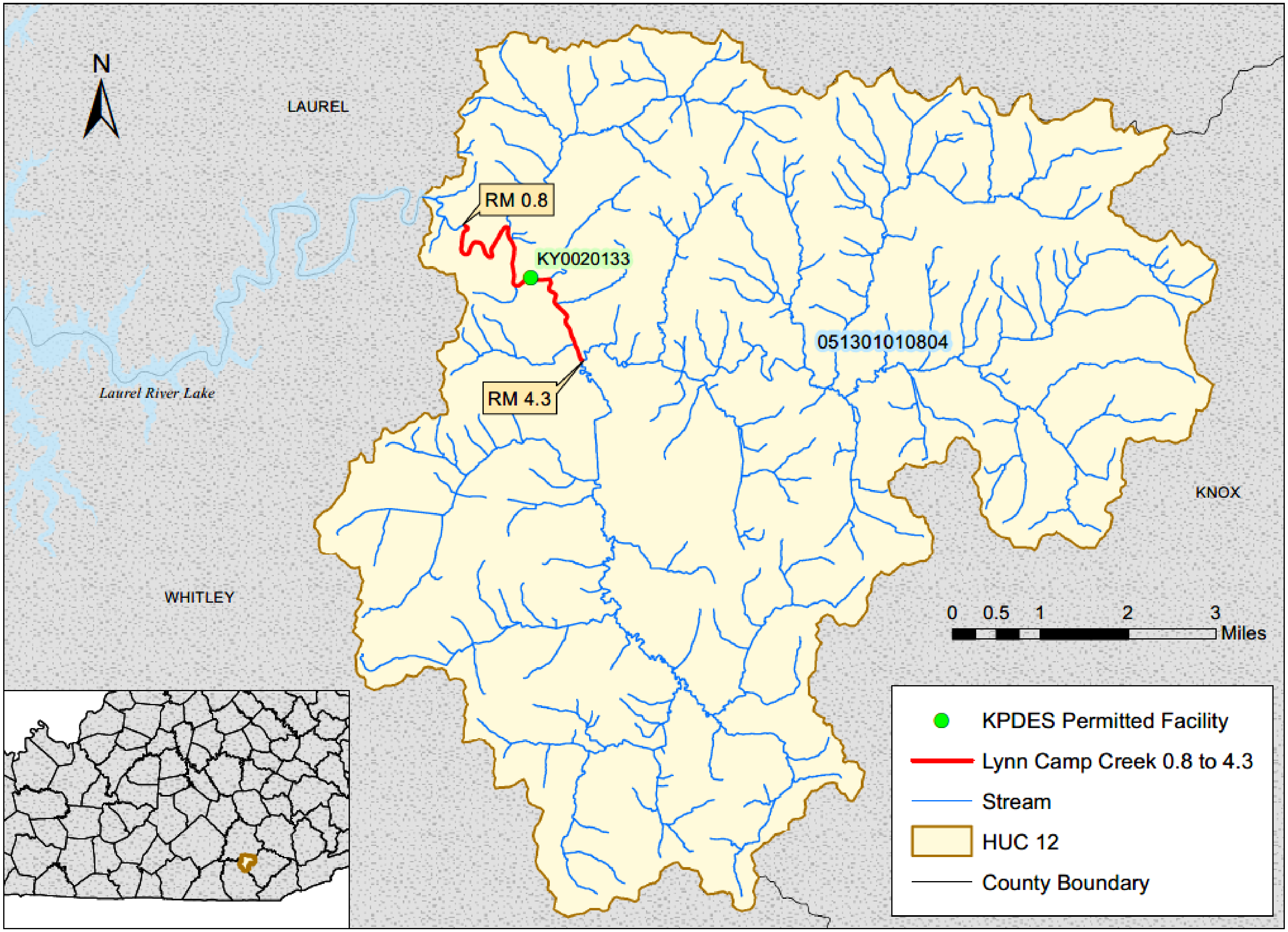


Figure O.4-1 Location of the KPDES-permitted Facility on Lynn Camp Creek 0.8 to 4.3

Section O.5 Mitchell Creek 0.0 to 3.85

Waterbody ID: KY-2422

Receiving Water: Sinking Creek

Impaired Use: PCR

Support Status: nonsupport

Listed Pollutant/TMDL Pollutant: *E. coli*

HUC 12: 051301020501

County: Laurel

University of Louisville collected samples from station MC, located near river mile 0.8, from 2012 to 2013 as part of a 319(h) nonpoint source project conducted in the Sinking Creek watershed. The station was sampled twelve times during the PCR season. Table O.5-1 summarizes information about this sampling station; Table O.5-2 summarizes the data collected from this station.

Table O.5-1 DOW Sample Site Location

Station Name	Latitude	Longitude	Stream Segment	River Mile
MC	37.12947	-84.13295	Mitchell Creek 0.0 to 3.85	0.8

Table O.5-2 DOW Sample Data Summary(1)

Station Name	Indicator Bacteria(2)	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
MC	*E. coli*	12	67	8,212	1,974

(1)The full data set for samples collected from MC may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.

(2)The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for Mitchell Creek 0.0 to 3.85 are presented in Table O.5-3. As of October 2021, there are no KPDES-permitted discharges of bacteria into this segment of Mitchell Creek. The location within the Sinking Creek watershed is shown in Figure O.5-1.

Table O.5-3 Mitchell Creek 0.0 to 3.85 *E. coli* TMDL Allocations(1)

TMDL(2)	Allocations for Direct Loads to the Segment	Allocations for Tributary Loads to the Segment(4)	MOS(5)
	LA(3)		
$Q_S \times WQC \times CF$	$\sum(Q_{LA} \times WQC \times CF)$	$\sum(Q_{Tributary} \times WQC \times CF)$	Implicit

(1)All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2)Q_S is the flow (ft^3/s) in the segment.

(3)Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(4)$Q_{Tributary}$ is the flow contribution (ft^3/s) from a tributary to the segment. This load includes both WLA and LA sources on tributaries to the impaired segment.

(5)The following assumptions provide an implicit MOS:

(a)Tributary bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b)There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

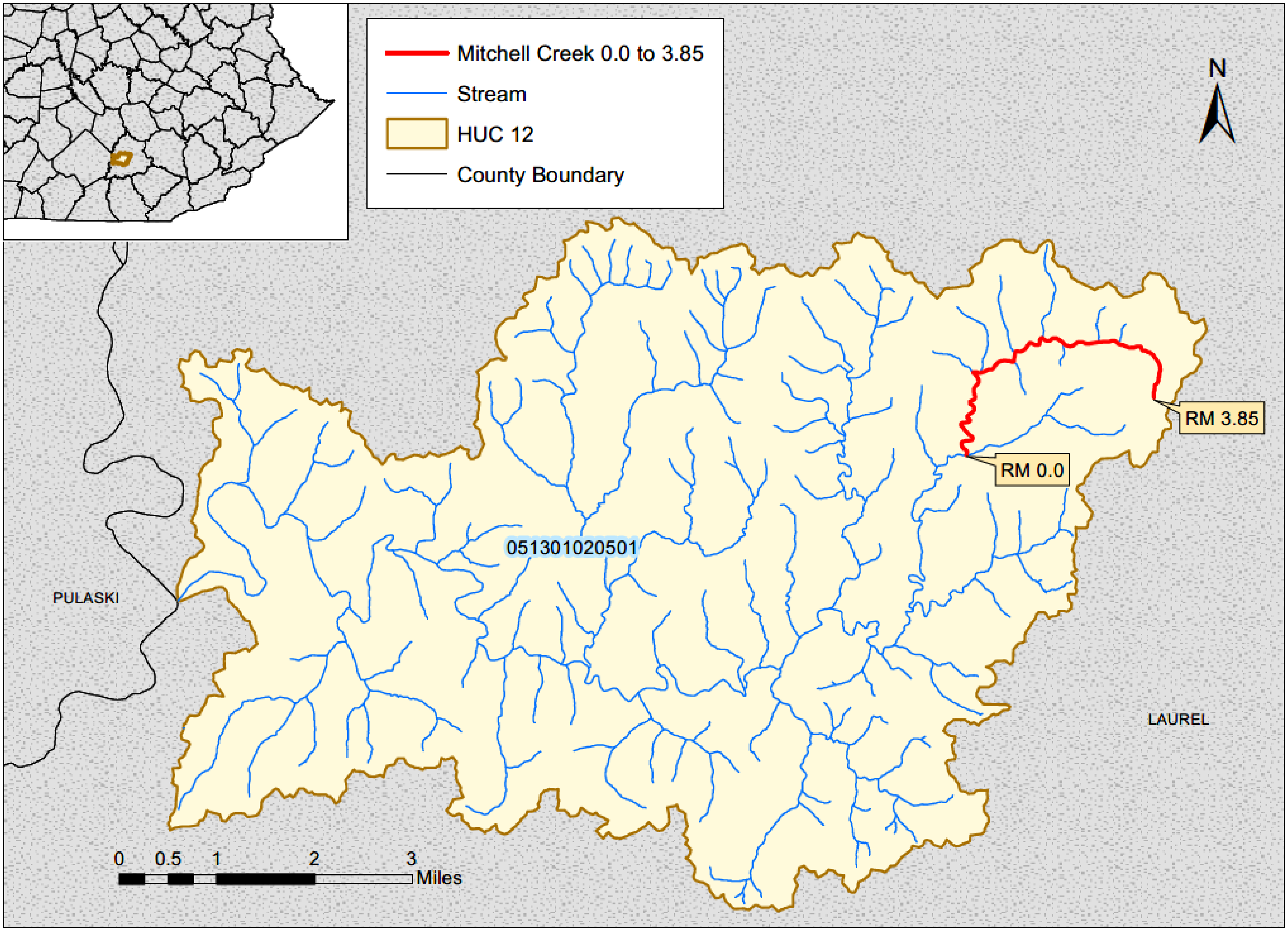


Figure O.5-1 Location of Mitchell Creek 0.0 to 3.85

Section O.6 Pitman Creek 5.4 to 6.0

Waterbody ID: KY-2462

Receiving Water: Cumberland River

Impaired Use: PCR

Support Status: partial support

Listed Pollutant/TMDL Pollutant: *E. coli*

HUC 12: 051301030204

County: Pulaski

The Division of Water (DOW) collected samples from station CRW024, located near river mile 5.8, in 2005. Assessment records give coordinates for the sampling location, but the data could not be located as of this writing. Table O.6-1 summarizes information about this sampling station.

Table O.6-1 DOW Sample Site Location

Station Name	Latitude	Longitude	Stream Segment	River Mile
CRW024	37.04391	-84.59591	Pitman Creek 5.4 to 6.0	5.8

The TMDL allocations for Pitman Creek 5.4 to 6.0 are presented in Table O.6-2.

Table O.6-2 Pitman Creek 5.4 to 6.0 *E. coli* TMDL Allocations[1]

TMDL[2]	Allocations for Direct Loads to the Segment		Allocations for Upstream Loads to the Segment[5]	MOS[6]
	SWS-WLA[3]	LA[4]		
$Q_S \times WQC \times CF$	$\sum(Q_{SWS} \times WQC \times CF)$	$\sum(Q_{LA} \times WQC \times CF)$	$\sum(Q_{Upstream} \times WQC \times CF)$	Implicit

(1)All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2)Q_S is the flow (ft^3/s) in the segment.

(3)Q_{SWS} is the flow (ft^3/s) in the segment due to a SWS entity. New or expanded SWS sources will be allowed to discharge to the segment contingent upon them meeting the PCR bacterial WQCs found in 401 KAR 10:031. SWS-WLAs will be translated into KPDES permit limits as an *E. coli* effluent gross limit of 130 colonies/100 ml as a monthly average (geometric mean) and 240 colonies/100 ml as a maximum weekly average (geometric mean).

(4)Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(5)$Q_{Upstream}$ is the flow contribution (ft^3/s) from upstream of the segment. This load includes both WLA and LA sources upstream of the impaired segment.

(6)The following assumptions provide an implicit MOS:

(a)Upstream bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b)Although all sources are provided an allocation at the Water Quality Standard, not all sources discharge at this maximum allocation at the same time.

(c)There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

Figure O.6-2 shows the segment is located in an area where karst features such as sinkholes, sinking streams, and springs exist. The sink features may capture surface drainage and channel it underground to resurface later at one or more springs. These discharging springs may occur outside the watershed where the drainage originated. However, unless karst dye trace studies indicate otherwise, groundwater catchment is presumed to correspond to the topographic watershed boundaries of surface drainage. Dye tracing in the region did not identify any areas outside the boundary of the Lower Pitman Creek watershed that contribute drainage to the segment.

One facility permitted under the Kentucky Pollutant Discharge Elimination System (KPDES) discharges treated effluent directly into this segment of Pitman Creek. The directly discharging facility is a sanitary wastewater system. There are no MS4 communities or CSOs discharging directly to this segment of Pitman Creek. This facility is identified in Table O.6-3 and the location within the Lower Pitman Creek watershed is shown in Figure O.6-1.

Table O.6-3 Summary of Active KPDES-permitted Sources as of October 2021

KPDES Permit Number	Facility Name	Design Flow (MGD)	Outfall Latitude	Outfall Longitude	Permit Expiration Date(1)	WLA(2) (colonies *E. coli*/day)
KY0026611	Somerset STP	4.4	37.04441	-84.59845	07/31/2014	Q_{SWS}×WQC×CF

(1)Permit expiration dates identify the permits in effect when the draft TMDL was written, including any permits that may be expired (but not terminated) or in administrative continuance. Permits issued after the approval of this TMDL will address the TMDL.

(2)Q_{SWS} is the flow in the segment due to a SWS entity. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day).

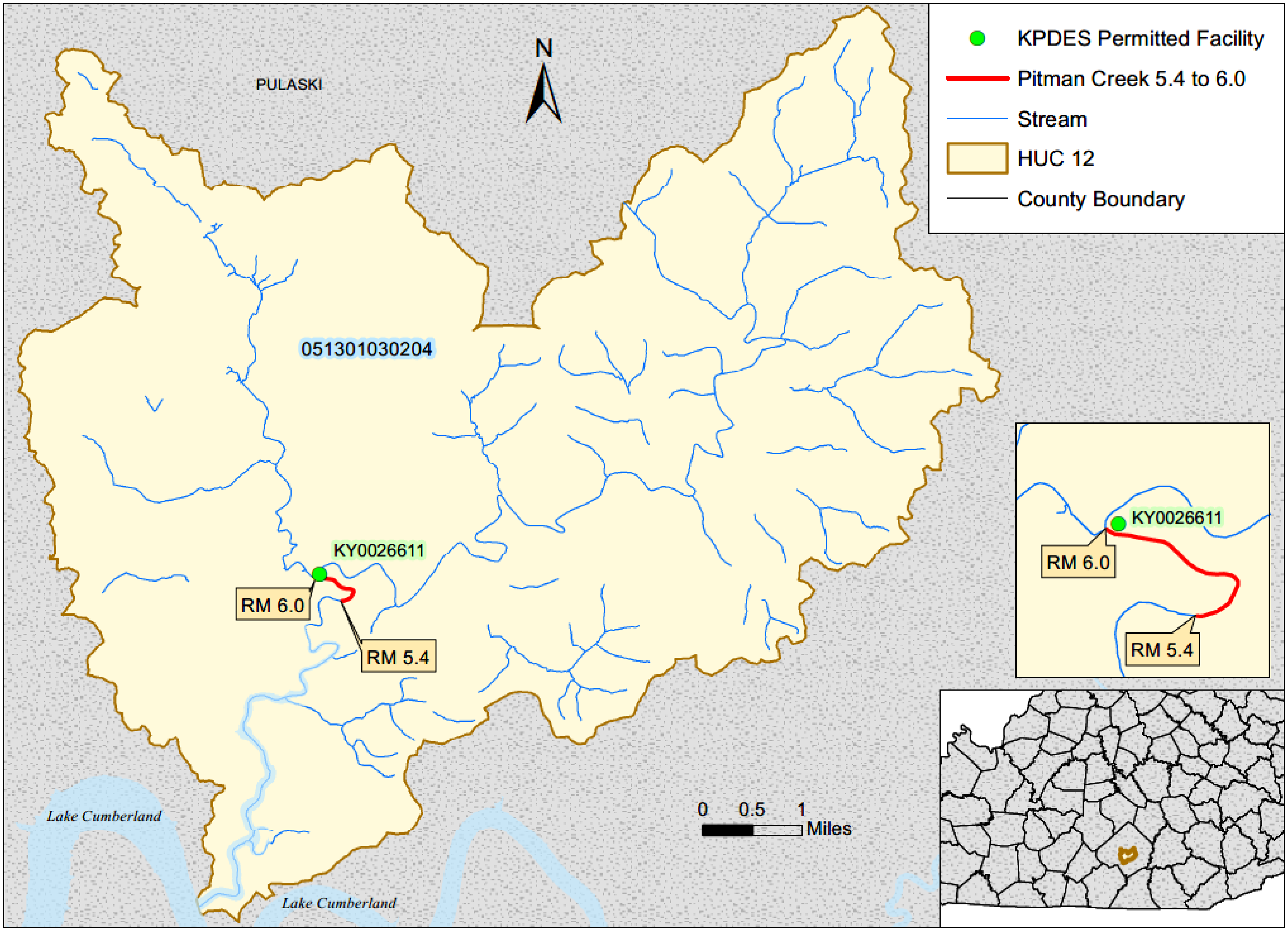


Figure O.6-1 Location of the KPDES-permitted Facility on Pitman Creek 5.4 to 6.0

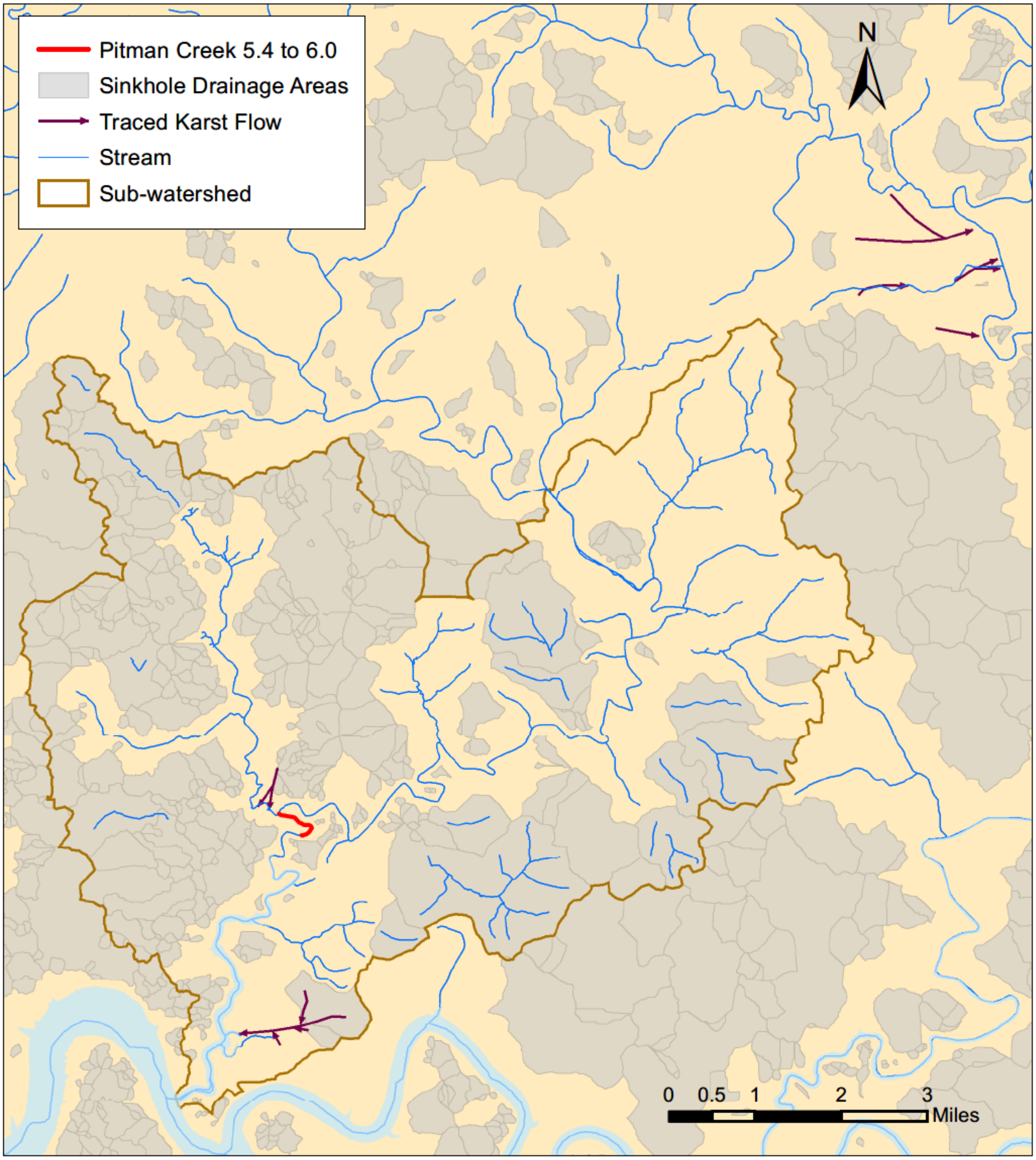


Figure O.6-2. Karst Influence in the Region of Pitman Creek 5.4 to 6.0

Section O.7 Powder Mill Creek 0.0 to 4.95

Waterbody ID: KY-2476

Receiving Water: Sinking Creek

Impaired Uses: PCR

Support Status: partial support

Listed Pollutant/TMDL Pollutant: *E. coli*

HUC 12: 051301020501

County: Laurel

University of Louisville collected samples from station PM, located near river mile 0.4, from 2012 to 2013, as part of a 319(h) nonpoint source project conducted in the Sinking Creek watershed. The station was sampled twelve times during the PCR season. Table O.7-1 summarizes information about this sampling station; Table O.7-2 provides a summary of the data collected from this station.

Table O.7-1 DOW Sample Site Location

Station Name	Latitude	Longitude	Stream Segment	River Mile
PM	37.10337	-84.15473	Powder Mill Creek 0.0 to 4.95	0.4

Table O.7-2 DOW Sample Data Summary(1)

Station Name	Indicator Bacteria(2)	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
PM	*E. coli*	12	74	3,080	726

(1)The full data set for samples collected at PM may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.

(2)The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for Powder Mill Creek 0.0 to 4.95 are presented in Table O.7-3. As of October 2021, there are no KPDES-permitted discharges of bacteria into this segment of Powder Mill Creek. The location within the Sinking Creek watershed is shown in Figure O.7-1.

Table O.7-3 Powder Mill Creek 0.0 to 4.95 *E. coli* TMDL Allocations(1)

TMDL(2)	Allocations for Direct Loads to the Segment	Allocations for Tributary Loads to the Segment(4)	MOS(5)
	LA(3)		
$Q_S \times WQC \times CF$	$\sum(Q_{LA} \times WQC \times CF)$	$\sum(Q_{Tributary} \times WQC \times CF)$	Implicit

(1)All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2)Q_S is the flow (ft^3/s) in the segment.

(3)Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(4)$Q_{Tributary}$ is the flow contribution (ft^3/s) from a tributary to the segment. This load includes both WLA and LA sources on tributaries to the impaired segment.

(5)The following assumptions provide an implicit MOS:

(a)Tributary bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b)There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

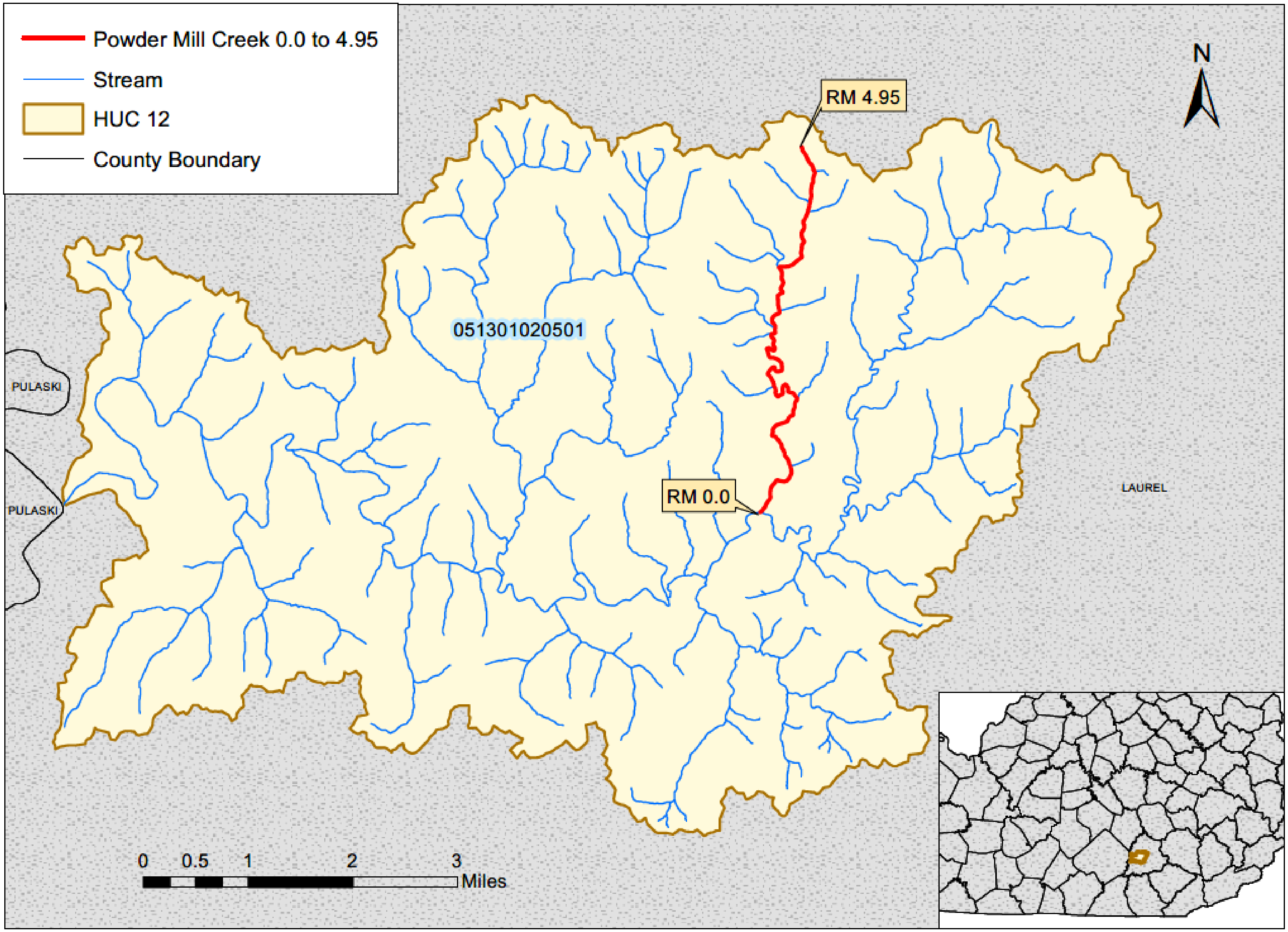


Figure O.7-1 Location of Powder Mill Creek 0.0 to 4.95

Section O.8 Roaring Paunch Creek 15.6 to 15.75

Waterbody ID: KY-2503

Receiving Water: Big South Fork Cumberland River

Impaired Use: PCR

Support Status: nonsupport

Listed Pollutant/TMDL Pollutant: *E. coli*

HUC 12: 051301040507

County: McCreary

Samples were collected from station RP3, located near river mile 15.6, in 2008 as part of a nonpoint source project within the subwatersheds of the Big South Fork Cumberland River watershed. The station was sampled eight times during the PCR season. Table O.8-1 summarizes information about this sampling station; Table O.8-2 summarizes the data collected from this station.

Table O.8-1 Sample Site Location

Station Name	Latitude	Longitude	Stream Segment	River Mile
RP3	36.59852	-84.45884	Roaring Paunch Creek 15.6 to 15.75	15.6

Table O.8-2 Sample Data Summary[1]

Station Name	Indicator Bacteria[2]	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
RP3	*E. coli*	17	50	2,150	547
RP3	fecal coliform	18	50	2,200	636

[1] The full data set for samples collected at RP3 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.

[2] The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for Roaring Paunch Creek 15.6 to 15.75 are presented in Table O.8-3. As of October 2021, there are no KPDES-permitted discharges of bacteria into this segment of Roaring Paunch Creek. The location within the Roaring Paunch Creek watershed is shown in Figure O.8-1.

Table O.8-3 Roaring Paunch Creek 15.6 to 15.75 *E. coli* TMDL Allocations(1)

TMDL(2)	Allocations for Direct Loads to the Segment	Allocations for Upstream Loads to the Segment(4)	MOS(5)
	LA(3)		
$Q_S \times WQC \times CF$	$\sum(Q_{LA} \times WQC \times CF)$	$\sum(Q_{Upstream} \times WQC \times CF)$	Implicit

(1)All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2)Q_S is the flow (ft^3/s) in the segment.

(3)Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(4)$Q_{Upstream}$ is the flow contribution (ft^3/s) from upstream of the segment. This load includes both WLA and LA sources upstream of the impaired segment.

(5)The following assumptions provide an implicit MOS:

(a)Upstream bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b)There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

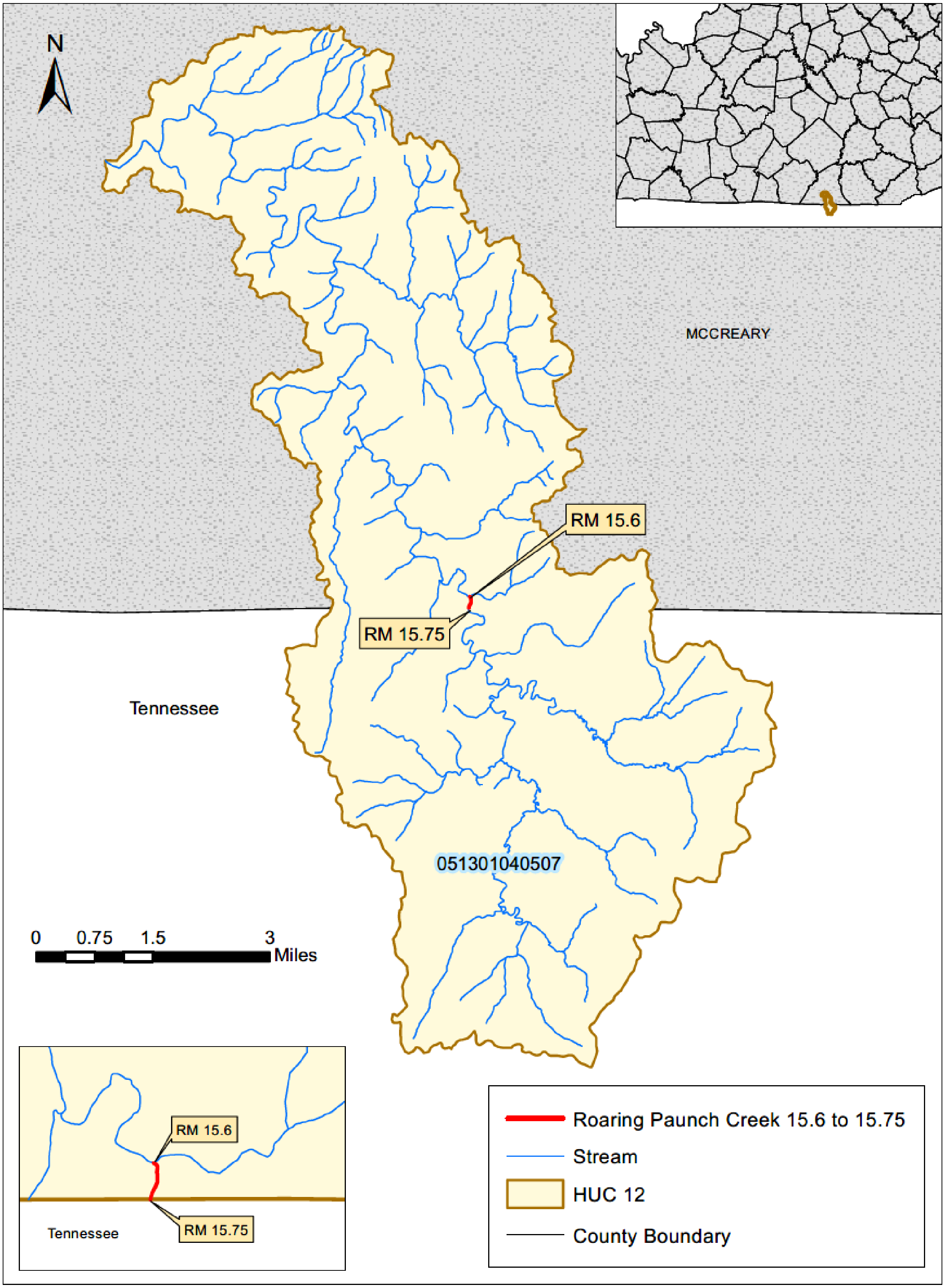


Figure O.8-1 Location of Roaring Paunch Creek 15.6 to 15.75

Section O.9 White Oak Creek 0.0 to 1.0

Waterbody ID: KY-2615

Receiving Water: Sinking Creek

Impaired Use: PCR

Support Status: partial support

Listed Pollutant/TMDL Pollutant: *E. coli*

HUC 12: 051301020501

County: Laurel

University of Louisville collected samples from station WO, located near river mile 0.8, from 2012 to 2013, as part of a 319(h) nonpoint source project conducted in the Sinking Creek watershed. The station was sampled twelve times during the PCR season. Table O.9-1 summarizes information about this sampling station; Table O.9-2 summarizes the data collected from this station.

Table O.9-1 DOW Sample Site Location

Station Name	Latitude	Longitude	Stream Segment	River Mile
WO	37.09972	-84.20008	White Oak Creek 0.0 to 1.0	0.8

Table O.9-2 DOW Sample Data Summary[(1)]

Station Name	Indicator Bacteria[(2)]	Number of Observations	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
WO	*E. coli*	12	82	365	210

[(1)] The full data set for samples collected from WO may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to EEC.KORA@ky.gov.

[(2)] The numeric water quality criteria (WQC) for indicator bacteria can be found in Section 1.3 of this document.

The TMDL allocations for White Oak Creek 0.0 to 1.0 are presented in Table O.9-3. As of October 2021, there are no KPDES-permitted discharges of bacteria into this segment of White Oak Creek. The location within the Sinking Creek watershed is shown in Figure O.9-1.

Table O.9-3 White Oak Creek 0.0 to 1.0 *E. coli* TMDL Allocations(1)

TMDL(2)	Allocations for Direct Loads to the Segment	Allocations for Upstream Loads to the Segment(4)	Allocations for Tributary Loads to the Segment(5)	MOS(6)
	LA(3)			
Q_S×WQC×CF	∑(Q_{LA}×WQC×CF)	∑($Q_{Upstream}$×WQC×CF)	∑($Q_{Tributary}$×WQC×CF)	Implicit

(1)All loads are colonies/day of *E. coli*. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft^3-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft^3/s) into a load (colonies/day). The symbol "∑" indicates that the total allocation is the sum of all the individual allowable loads.

(2)Q_S is the flow (ft^3/s) in the segment.

(3)Q_{LA} is the flow (ft^3/s) in the segment due to a LA source.

(4)$Q_{Upstream}$ is the flow contribution (ft^3/s) from upstream of the segment. This load includes both WLA and LA sources upstream of the impaired segment.

(5)$Q_{Tributary}$ is the flow contribution (ft^3/s) from a tributary to the segment. This load includes both WLA and LA sources on tributaries to the impaired segment.

(6)The following assumptions provide an implicit MOS:

(a)Upstream and tributary bacterial concentrations are at the maximum allowable limit; there is no dilution capacity from these areas.

(b)There is no bacteria die-off; in reality bacteria concentrations diminish downstream from their source. Thus, bacteria loads to the upper portion of a segment will diminish prior to reaching the lower portion of the segment.

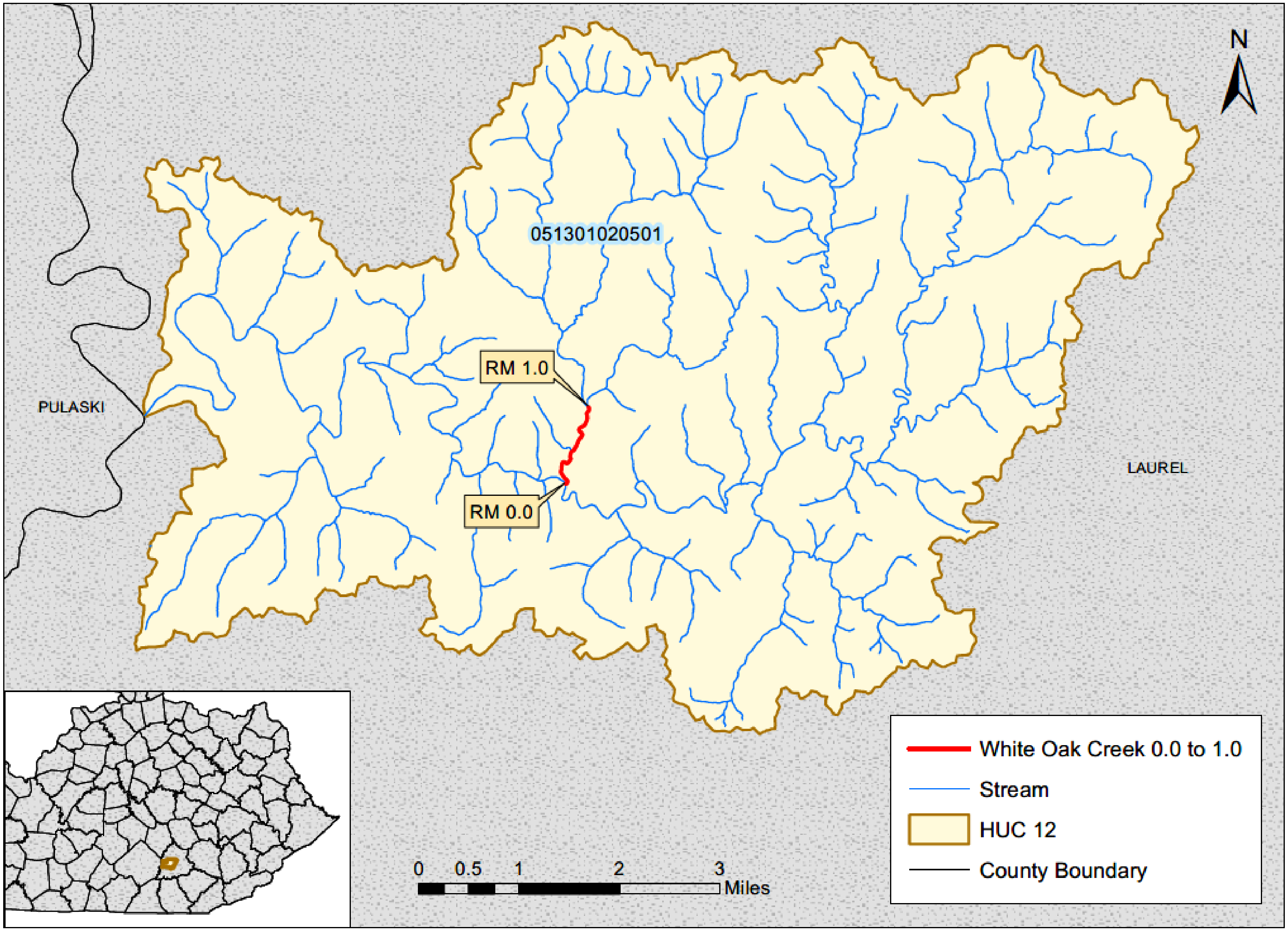


Figure O.9-1 Location of White Oak Creek 0.0 to 1.0