

## Appendix D Green River Basin

**HUC 8:** 05110001, 05110002, 05110003, 05110004, 05110005, 05110006

**Level IV Ecoregions:** Green River-Southern Wabash Lowlands, Wabash-Ohio Bottomlands, Caseyville Hills, Crawford-Mammoth Cave Uplands, Western Pennyroyal Karst Plain, Mitchell Plain, Eastern Highland Rim

**Drainage Area Within Kentucky:** 8,822 square miles

**Counties:** Adair, Allen, Barren, Breckinridge, Butler, Casey, Christian, Daviess, Edmonson, Grayson, Green, Hancock, Hardin, Hart, Henderson, Hopkins, Larue, Lincoln, Logan, Marion, McLean, Metcalfe, Monroe, Muhlenberg, Ohio, Pulaski, Russell, Simpson, Taylor, Todd, Warren, Webster

**Major Cities:** Bowling Green, Elizabethtown, Madisonville, Glasgow, Campbellsville, Franklin, Russellville, Leitchfield, Central City, Columbia, Greenville, Scottsville, Beaver Dam, Hodgenville, Hartford, Tompkinsville, Morgantown, Horse Cave

The Green River basin is located in south-central to western Kentucky.

The Green River originates in Lincoln Co., Ky., near Halls Gap. At a 1:100,000 scale, it quickly becomes a fourth order stream at the confluence with the South Fork of the Green. It flows southwest through Casey Co. (where it becomes fifth order below Knob Lick Creek), then west through Adair. The river briefly passes through Taylor Co., where a dam at mile 308.9 forms Green River Lake, before flowing into Green Co. The river meanders westward into Hart and Edmonson counties, where springs draining the area's sinkhole plain replace surface streams as tributaries. After flowing through Mammoth Cave National Park, its meanders broaden and the Green forms the border between Warren and Butler counties. At Rochester, the Green veers northwest along the Muhlenberg-Ohio Co. border. After passing through McLean Co., the river turns north along the borders of Webster, Henderson and Daviess counties. At its confluence with the Barren River, a major tributary, the Green becomes a seventh order stream. It discharges into the Ohio River at river mile 781 near Henderson, Ky., after flowing for nearly 384 miles.

Table D.1. provides a summary of the stream segments in the Green basin that have been included on the 303(d) list for impairment due to fecal coliform and/or *E. coli*. The locations of the stream segments are shown in Figure D.1.

**Table D.1 Bacteria-impaired Stream Segments in the Green Basin**

Waterbody Name	Waterbody ID	Impaired Use (Support Status)	Pollutant	Suspected Source(s)	Year of TMDL Public Notice
Barren River 0 to 8.4	KY517526_01	PCR (partial support)	<i>E. coli</i>	Non-Point Source	2018

Waterbody Name	Waterbody ID	Impaired Use (Support Status)	Pollutant	Suspected Source(s)	Year of TMDL Public Notice
Barren River 104.8 to 119.3	KY517526_06	PCR (nonsupport), SCR (nonsupport)	Fecal Coliform	Source Unknown	2018
Beaver Creek 8.5 to 15.75	KY486609_01	PCR (nonsupport)	Fecal Coliform	Upstream Source	2018
Big Reedy Branch 0 to 2.4 <sup>1</sup>	KY487230_01	PCR (nonsupport)	Fecal Coliform	Crop Production (Crop Land or Dry Land), Habitat Modification - other than Hydromodification, Source Unknown	See footnote
Buck Creek 0 to 8.0	KY488213_01	PCR (nonsupport)	Fecal Coliform	Loss of Riparian Habitat, Permitted Runoff from Confined Animal Feeding Operations (CAFOs)	2018
Buck Creek 8.0 to 11.0	KY488213_02	PCR (nonsupport)	<i>E. coli</i>	Animal Feeding Operations (NPS), Non-Point Source	2018
Buck Fork Pond River 12.9 to 19.3	KY488223_02	PCR (nonsupport)	Fecal Coliform	Source Unknown	2018
Caney Creek 0 to 6.8	KY488846_01	PCR (nonsupport)	<i>E. coli</i>	Source Unknown	2018
Caney Creek 1.4 to 5.25 <sup>1</sup>	KY488828_01	PCR (nonsupport)	Fecal Coliform	Source Unknown	See footnote
Crooked Creek 0 to 3.0	KY490376_00	PCR (nonsupport)	Fecal Coliform	Source Unknown	2018
Deer Creek 0 to 8.4	KY490771_01	PCR (partial support)	<i>E. coli</i>	Non-Point Source	2018
Deserter Creek 0 to 3.1	KY490828_01	PCR (nonsupport)	Fecal Coliform	Source Unknown	2018
Elk Creek 7.6 to 10.6	KY491656_02	PCR (nonsupport)	Fecal Coliform	Sanitary Sewer Overflows (Collection System Failures)	2018
Elk Pond Creek 0 to 4.9	KY491671_00	PCR (nonsupport)	Fecal Coliform	Source Unknown	2018
Gasper River 7.8 to 14.6	KY492748_01	PCR (partial support)	<i>E. coli</i>	Source Unknown	2018
Goodman Springs (9000-0230) <sup>2</sup>	KY499512-59.65_00	PCR (nonsupport)	<i>E. coli</i>	Source Unknown	See footnote
Goren Mill Spring (9000-0793) <sup>2</sup>	KY493284-226.7_00	PCR (nonsupport)	<i>E. coli</i>	Source Unknown	See footnote
Graham Spring (9000-0051) <sup>2</sup>	KY517526-34.65_00	PCR (partial support)	<i>E. coli</i>	Source Unknown	See footnote
Green River 210.4 to 250.2	KY493284_08	PCR (partial support)	<i>E. coli</i>	Source Unknown	2018
Green River 283.1 to 309.0	KY493284_13	PCR (nonsupport)	Fecal Coliform	Package Plant or Other Permitted Small Flows Discharges	2018
Head of Rough River Spring 154.85 to 155.8 <sup>2</sup>	KY502390_07	PCR (nonsupport)	<i>E. coli</i>	Source Unknown	See footnote
Jarrels Creek 0 to 1.8	KY495175_00	PCR (nonsupport)	Fecal Coliform	Source Unknown	2018
Knoblick Creek 0 to 2.1	KY495848_00	PCR (nonsupport)	Fecal Coliform	Source Unknown	2018

Waterbody Name	Waterbody ID	Impaired Use (Support Status)	Pollutant	Suspected Source(s)	Year of TMDL Public Notice
Long Falls Creek 0 to 7.6	KY497098_01	PCR (nonsupport)	Fecal Coliform	Source Unknown	2018
Long Falls Creek 7.6 to 11.9	KY497098_02	PCR (nonsupport)	Fecal Coliform	Loss of Riparian Habitat	2018
Lost River Rise (9000-0054) <sup>2</sup>	KY495207-3.2_00	PCR (nonsupport)	<i>E. coli</i>	Source Unknown	See footnote
Mahurin Spring (9000-0202) <sup>2</sup>	KY504135-4.35_00	PCR (nonsupport)	<i>E. coli</i>	Source Unknown	See footnote
McCoy Bluehole Spring (9000-0792) <sup>2</sup>	KY493284-212.5_00	PCR (nonsupport)	<i>E. coli</i>	Source Unknown	See footnote
Mill Creek 0 to 4.2	KY498260_00	PCR (nonsupport)	Fecal Coliform	Source Unknown	2018
Mill Spring (9000-1193) <sup>2</sup>	KY499512-38.7_00	PCR (nonsupport)	<i>E. coli</i>	Source Unknown	See footnote
Nolynn Spring (9000-2673) <sup>2</sup>	KY499559-1.3_00	PCR (nonsupport)	<i>E. coli</i>	Source Unknown	See footnote
North Fork of Panther Creek 4.2 to 9.1	KY499562_02	PCR (nonsupport)	Fecal Coliform	Source Unknown	2018
Panther Creek 0.1 to 3.0	KY500157_01	PCR (nonsupport)	<i>E. coli</i>	Agriculture, Unspecified Urban Stormwater	2018
Panther Creek 0.1 to 3.0	KY500157_01	SCR (nonsupport)	Fecal Coliform	Agriculture, Unspecified Urban Stormwater	2018
Panther Creek 3.0 to 5.9	KY500157_02	PCR (nonsupport)	Fecal Coliform	Agriculture	2018
Pond Run 0 to 6.75	KY501057_01	PCR (partial support)	<i>E. coli</i>	Source Unknown	2018
Rough River 0.1 to 10.45	KY502390_01	PCR (partial support) <sup>3</sup>	<i>E. coli</i>	Non-Point Source	See footnote
Rough River 0.1 to 10.45	KY502390_01	SCR (partial support)	Fecal Coliform	Non-Point Source	2018
Rough River 125.2 to 149.4	KY502390_06	PCR (partial support)	Fecal Coliform	Source Unknown	2018
Rough River 55.1 to 64.5	KY502390_04	PCR (nonsupport)	<i>E. coli</i>	Non-Point Source	2018
Rough River 55.1 to 64.5	KY502390_04	SCR (nonsupport)	Fecal Coliform	Non-Point Source	2018
Skaggs Creek 12.7 to 23.55	KY503595_01	PCR (nonsupport)	<i>E. coli</i>	Source Unknown	2018
Skees KW#1 (9000-1398) <sup>2</sup>	KY499512-79.0_00	PCR (nonsupport)	<i>E. coli</i>	Source Unknown	See footnote
South Fork of Panther Creek 14.0 to 18.3	KY503939_04	PCR (nonsupport)	Fecal Coliform	Source Unknown	2018
South Fork of Panther Creek 9.55 to 14.0	KY503939_03	PCR (nonsupport)	Fecal Coliform	Managed Pasture Grazing	2018
Trammel Creek 0 to 24.0	KY505463_01	PCR (partial support) <sup>3</sup>	<i>E. coli</i>	Source Unknown	See footnote
UT of Buck Creek 0 to 1.7	KY488213-8.0_01	PCR (nonsupport)	<i>E. coli</i>	Animal Feeding Operations (NPS)	2018
UT of Elk Creek 0 to 1.0	KY491656-7.1_01	PCR (nonsupport)	Fecal Coliform	Sanitary Sewer Overflows (Collection System Failures)	2018
UT of Flat Creek 3.1 to 4.1	KY492181-2.0_02	PCR (nonsupport)	Fecal Coliform	Sanitary Sewer Overflows (Collection System Failures)	2018

Waterbody Name	Waterbody ID	Impaired Use (Support Status)	Pollutant	Suspected Source(s)	Year of TMDL Public Notice
West Fork of Buck Creek 0 to 3.3	KY506423_01	PCR (nonsupport)	<i>E. coli</i>	Non-Point Source	2018
Wolf Lick Creek 0 to 14.6	KY507017_01	PCR (partial support) <sup>3</sup>	<i>E. coli</i>	Agriculture, Non-Point Source	See footnote

<sup>1</sup>A TMDL is not included for this segment while the rationale for this listing is researched.

<sup>2</sup>TMDLs for impaired springs will be developed separately from this TMDL document.

<sup>3</sup>A TMDL is not included because this segment will be proposed for delisting in 2018. The most recent monitoring data has indicated that the segment fully supports the designated use.

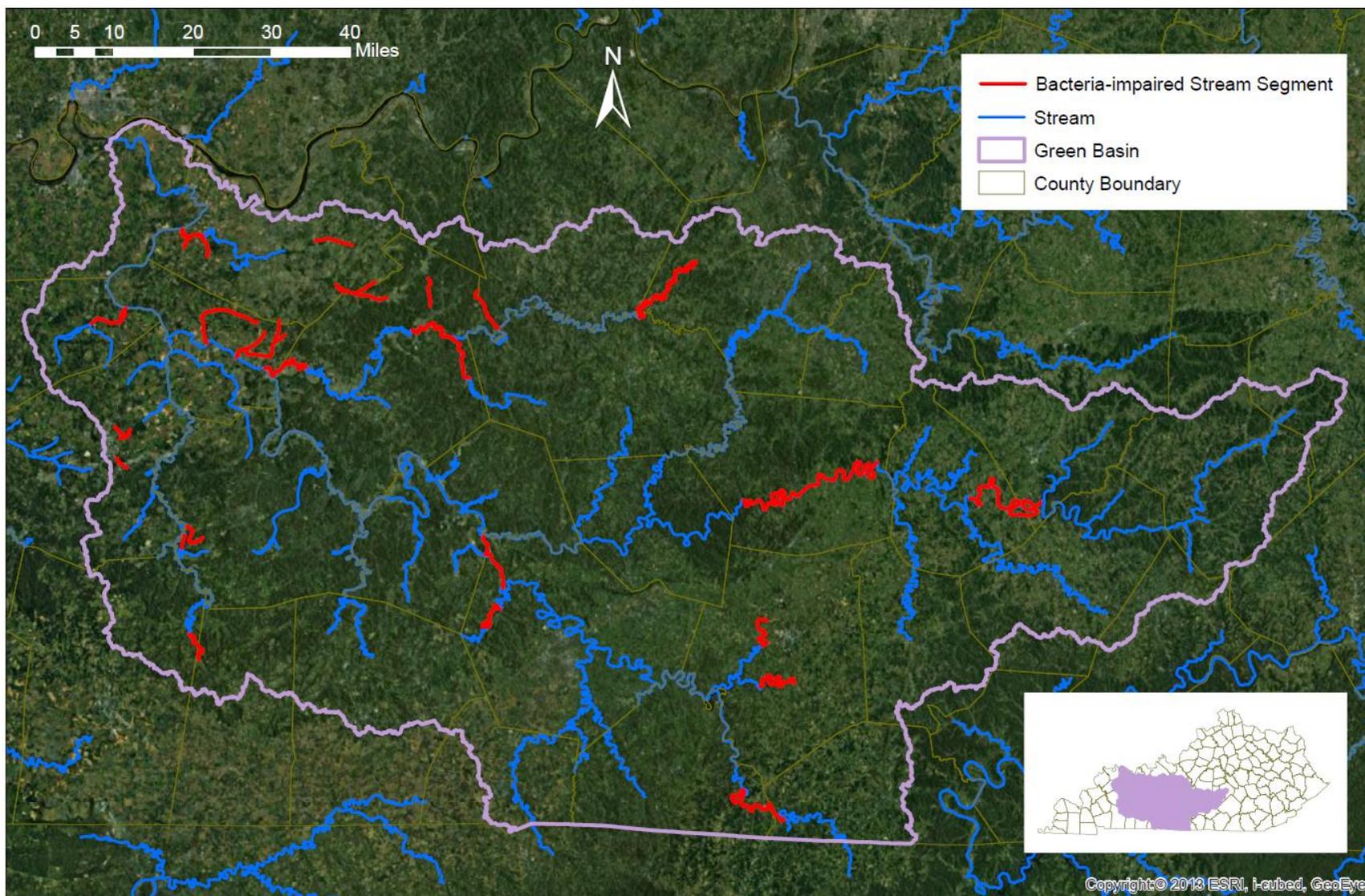


Figure D.1 Location of the Green Basin and Bacteria-impaired Waterbodies (January 2017)

Land cover data is summarized in Table D.2, and its geographic distribution is shown in Figure D.2. Deciduous forest is the predominant class of land cover in the Green basin, accounting for 43 percent. The next three classes by magnitude are pasture/hay, cultivated crops, and open developed. Land cover classes are described in Appendix P.

**Table D.2 Land Cover Classes in the Green Basin (NLCD 2011)**

Land Cover	Percent of Total Area	Square Miles	Acres
Open Water	1.06	93.12	59,596.34
Developed, Open	4.82	425.18	272,117.43
Developed, Low Intensity	0.76	67.20	43,009.18
Developed, Medium Intensity	0.32	28.29	18,106.54
Developed, High Intensity	0.12	10.87	6,959.78
Barren Land (Rock, Sand, Clay)	0.15	13.46	8,615.49
Deciduous Forest	43.32	3,821.72	2,445,899.36
Evergreen Forest	2.20	193.66	123,943.43
Mixed Forest	0.36	31.32	20,044.03
Shrub/Scrub	0.23	20.17	12,907.89
Grassland/Herbaceous	3.30	291.40	186,498.26
Pasture/Hay	27.03	2,384.18	1,525,875.39
Cultivated Crops	15.38	1,356.89	868,412.64
Woody Wetlands	0.55	48.95	31,329.34
Emergent Herbaceous Wetlands	0.40	35.67	22,827.05

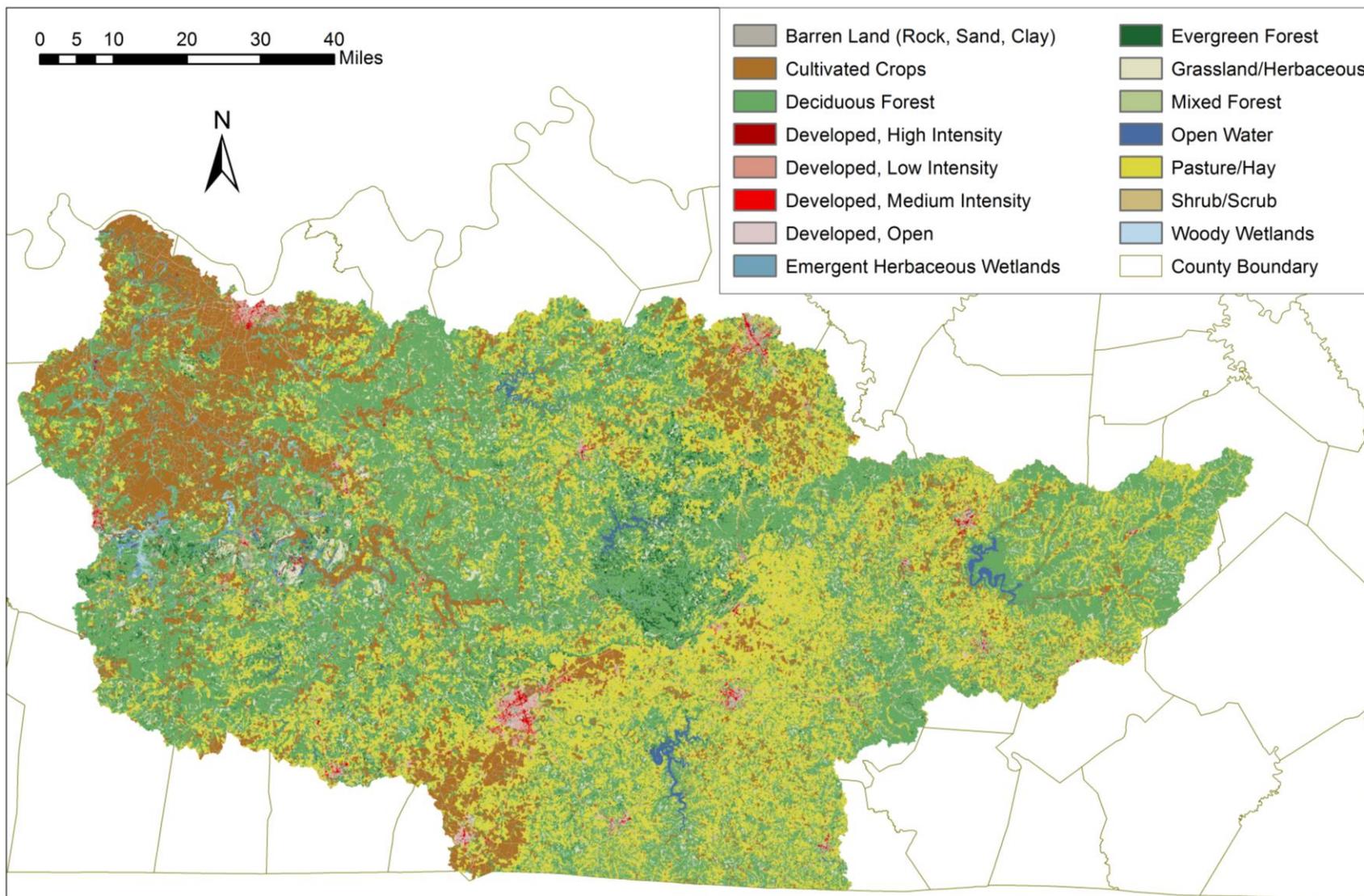


Figure D.2 Land Cover Classes in the Green Basin

**Section D.1 Barren River 0.0 to 8.4****Waterbody ID:** KY517526\_01**Receiving Water:** Green River**Impaired Use:** PCR**Support Status:** partial support**Indicator Bacteria:** *E. coli***HUC 12:** 051100020905**Counties:** Butler, Warren

The Division of Water has collected samples from station PRI 072, located at river mile 0.55, since 1998. The station typically has been sampled three or more times during the PCR season, although it was not sampled in 2004, 2009 or 2010. Table D.1-1 summarizes information about this sampling station; Table D.1-2 provides a summary of the data collected from this station.

**Table D.1-1 Division of Water Sample Site Location**

Station Name	Latitude	Longitude	Stream Segment	River Mile
PRI 072	37.1732777	-86.6231944	Barren River 0 to 8.4	0.55

**Table D.1-2 Division of Water Sample Data Summary<sup>(1)</sup>**

Station Name	Indicator Bacteria	Number of Observations	Percent Exceeding WQC <sup>2</sup>	Minimum (colonies/100 ml)	Maximum (colonies/100 ml)	Average (colonies/100 ml)
PRI 072	fecal coliform	30	16.7	2	3,800	412
PRI 072	<i>E. coli</i>	35	22.9	10	8,664	468

<sup>(1)</sup>The full data set for samples collected at PRI 072 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to [DEP.KORA@ky.gov](mailto:DEP.KORA@ky.gov) or by fax to 502-564-9232. The DEP KORA point of contact may also be reached at 502-564-3999.

<sup>(2)</sup>400 colonies/100 ml for fecal coliform; 240 colonies/100 ml for *E. coli*.

The TMDL allocations for Barren River 0.0 to 8.4 are presented in Table D.1-3. There are no KPDES-permitted discharges of bacteria into this segment of the Barren River. The location of the segment within the Gasper River and Little Muddy Creek-Barren River watersheds is shown in Figure D.1-1.

**Table D.1-3 Barren River 0.0 to 8.4 TMDL Allocations<sup>(1)</sup>**

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

<sup>(1)</sup>All loads are colonies/day of either *E. coli* or fecal coliform. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-mi/ft<sup>3</sup>-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft<sup>3</sup>/s) into a load (colonies/day). The symbol “ $\sum$ ” indicates that the total allocation is the sum of all the individual allowable loads.

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

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

<sup>(6)</sup>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.

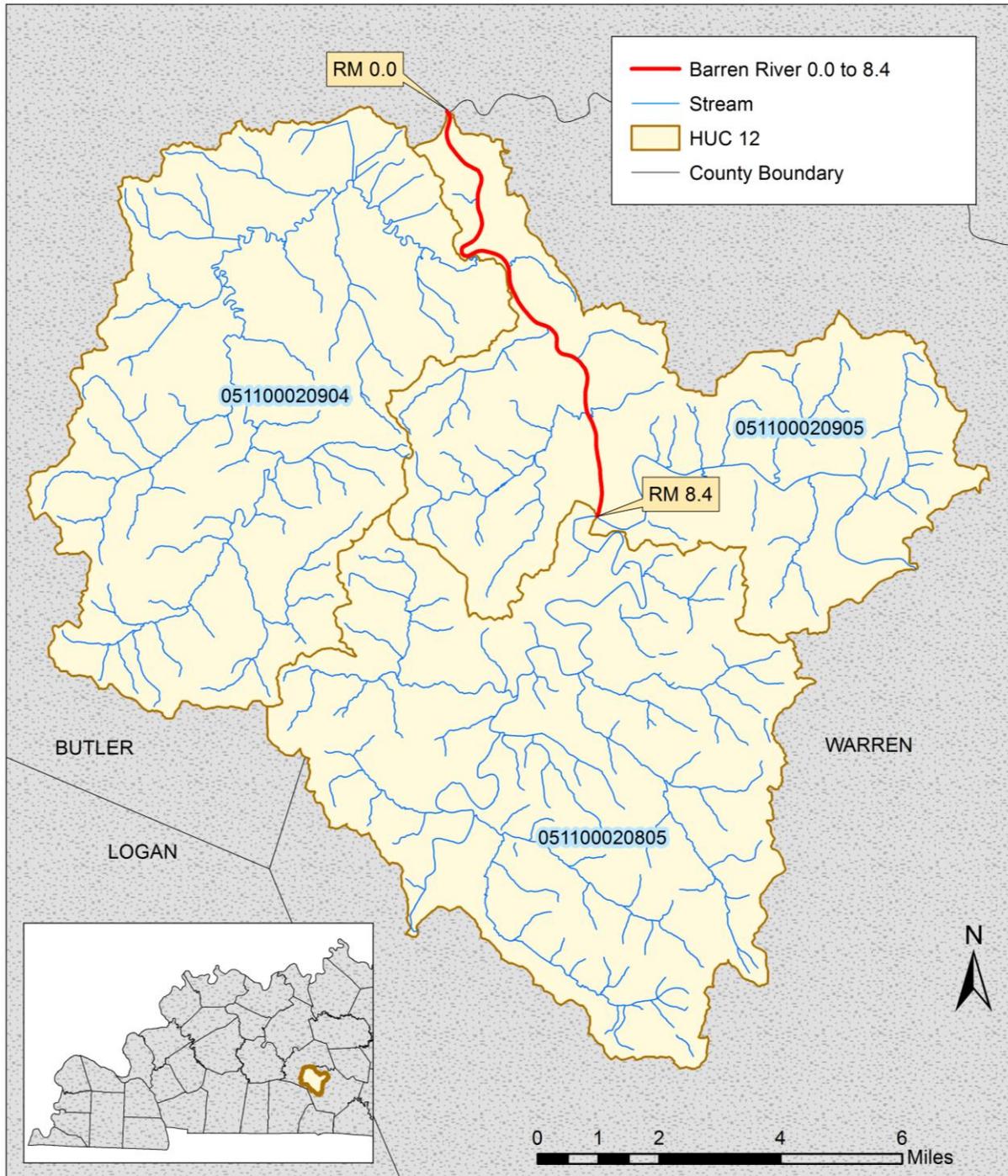


Figure D.1-1 Location of Barren River 0.0 to 8.4

This watershed exists in a karst area with sinkholes and springs. 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. Figure D.1-2 shows

sinkhole occurrence, trends in traced flow through karst areas, and groundwater basins in the region of Barren River 0.0 to 8.4. Dye tracing in the region has shown that a small area of the Beaverdam Creek-Green River watershed (0511000113) in the north contributes karst flow to Poorhouse Spring, which discharges near milepost 32.6 of the Barren River. In the southwest, a small portion of the Red River watershed contributes karst flow to the Barren River watershed. For more detailed information about karst geology, see Section 3.2, Karst.

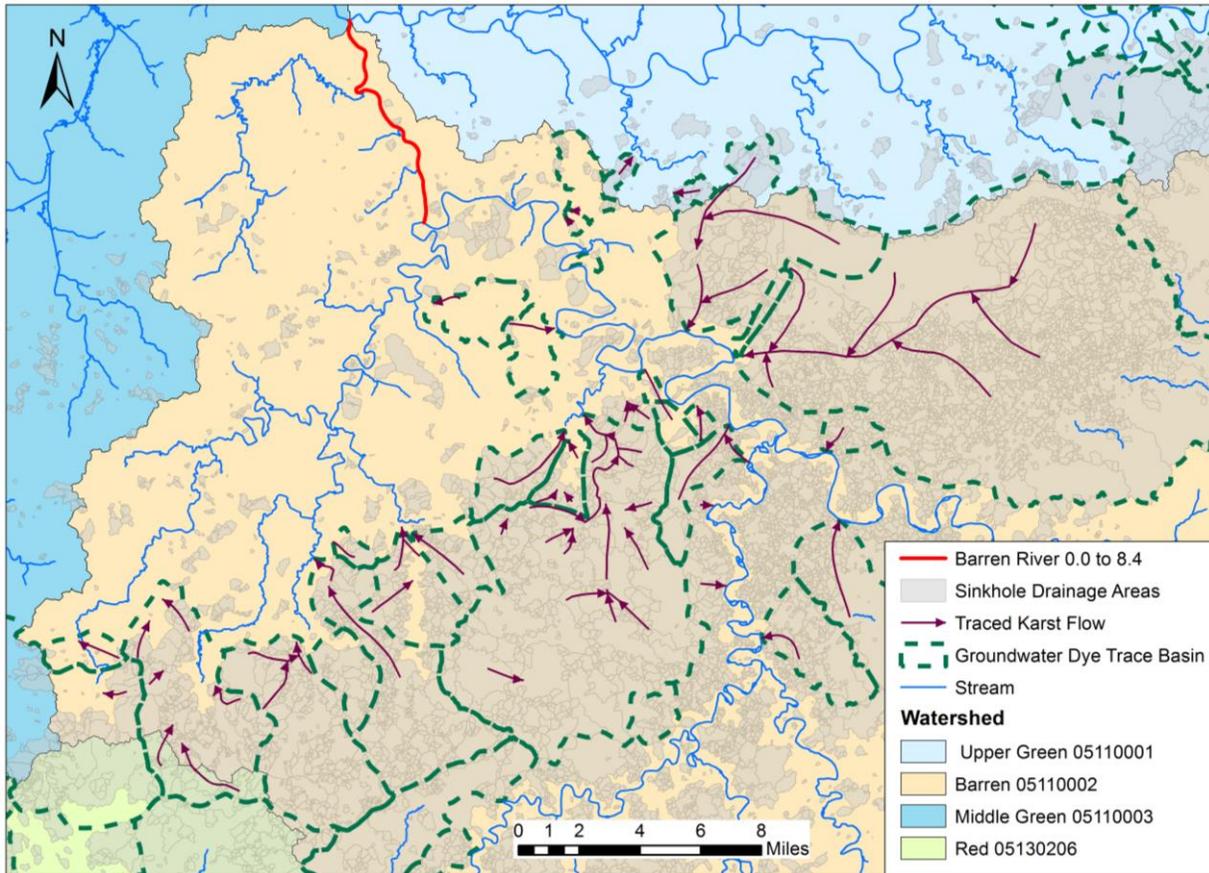


Figure D.1-2 Karst Influence in the Region of Barren River 0.0 to 8.4

**Section D.2 Barren River 104.8 to 119.3****Waterbody ID:** KY517526\_06**Receiving Water:** Green River**Impaired Uses:** PCR, SCR**Support Status:** nonsupport (both uses)**Indicator Bacteria:** fecal coliform**HUC 12:** 051100020109, 051100020203**Counties:** Allen, Barren, Monroe

The Division of Water has collected samples from station PRI 073, located at river mile 108.65, since 1998. The station typically has been sampled three or more times during the PCR season, except in 2007, when it was not sampled. Table D.2-1 summarizes information about this sampling station; Table D.2-2 provides a summary of the data collected from this station.

**Table D.2-1 Division of Water Sample Site Location**

Station Name	Latitude	Longitude	Stream Segment	River Mile
PRI 073	36.6963333	-86.0467222	Barren River 104.8 to 119.3	108.65

**Table D.2-2 Division of Water Sample Data Summary<sup>(1)</sup>**

Station Name	Indicator Bacteria	Number Of Observations	Percent Exceeding WQC <sup>2</sup>	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
PRI 073	fecal coliform	28	57.1	1	30,000	2,711
PRI 073	<i>E. coli</i>	37	75.7	52	2,420	698

<sup>(1)</sup>The full data set for samples collected at PRI 073 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to [DEP.KORA@ky.gov](mailto:DEP.KORA@ky.gov) or by fax to 502-564-9232. The DEP KORA point of contact may also be reached at 502-564-3999.

<sup>(2)</sup>400 colonies/100 ml for fecal coliform; 240 colonies/100 ml for *E. coli*.

The TMDL allocations for Barren River 104.8 to 119.3 are presented in Table D.2-3. There are no KPDES-permitted discharges of bacteria into this segment of the Barren River. The location of the segment within the Kentucky portions of the Barren River watershed is shown in Figure D.2-1.

**Table D.2-3 Barren River 104.8 to 119.3 TMDL Allocations<sup>(1)</sup>**

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

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

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

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

<sup>(6)</sup>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.

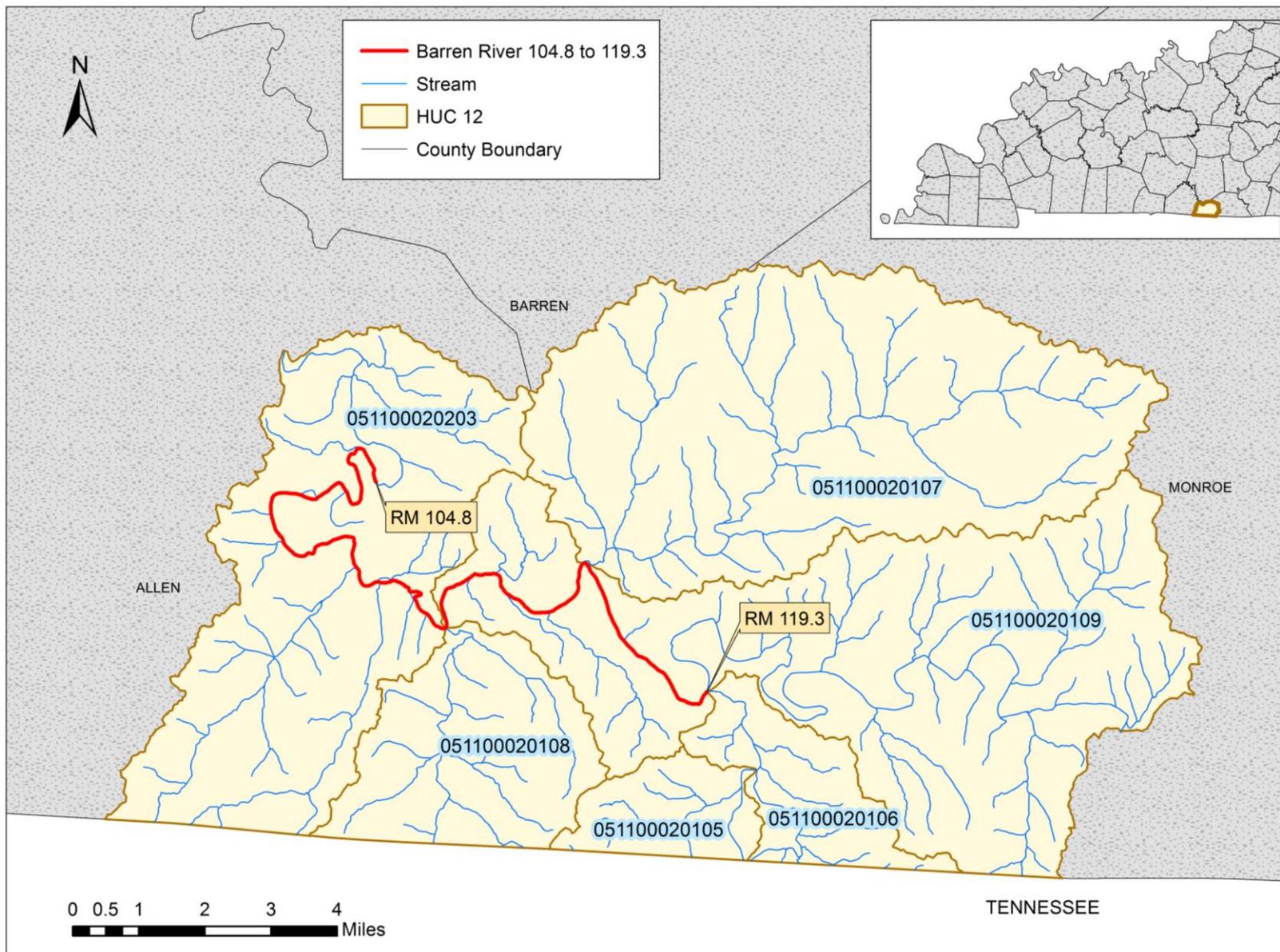


Figure D.2-1 Location of Barren River 104.8 to 119.3

**Section D.3 Beaver Creek 8.5 to 15.75****Waterbody ID:** KY486609\_01**Receiving Water:** Skaggs Creek**Impaired Use:** PCR**Support Status:** nonsupport**Indicator Bacteria:** fecal coliform**HUC 12:** 051100020305, 051100020306**County:** Barren

The Division of Water has collected samples from station GRN 023, located at river mile 8.5, since 2001. The station is sampled five to six times during the PCR season as part of the Division's five-year rotating schedule for basin monitoring (see also Section 7.2.1, Kentucky Watershed Management Framework). Table D.3-1 summarizes information about this sampling station; Table D.3-2 summarizes the data collected from this station.

**Table D.3-1 Division of Water Sample Site Location**

Station Name	Latitude	Longitude	Stream Segment	River Mile
GRN 023	36.98	-85.976	Beaver Creek 8.5 to 15.75	8.5

**Table D.3-2 Division of Water Sample Data Summary<sup>(1)</sup>**

Station Name	Indicator Bacteria	Number of Observations	Percent Exceeding WQC <sup>2</sup>	Minimum (colonies/100 ml)	Maximum (colonies/100 ml)	Average (colonies/100 ml)
GRN 023	fecal coliform	5	40.0	1	564	288
GRN 023	<i>E. coli</i>	17	58.8	75	921	352

<sup>(1)</sup>The full data set for samples collected at GRN 023 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to [DEP.KORA@ky.gov](mailto:DEP.KORA@ky.gov) or by fax to 502-564-9232. The DEP KORA point of contact may also be reached at 502-564-3999.

<sup>(2)</sup>400 colonies/100 ml for fecal coliform; 240 colonies/100 ml for *E. coli*.

The TMDL allocations for Beaver Creek 8.5 to 15.75 are presented in Table D.3-3. There are no KPDES-permitted discharges of bacteria into this segment of Beaver Creek.

**Table D.3-3 Beaver Creek 8.5 to 15.75 TMDL Allocations<sup>(1)</sup>**

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

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

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

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

<sup>(6)</sup>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 location of the segment within the Beaver Creek watershed is shown in Figure D.3-1. The segment occurs in a karst area with sinkholes and springs. 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 area has shown that groundwater to the north of the Beaver Creek watershed flows generally north toward the Green River. Groundwater west of the Beaver Creek watershed flows west toward the Barren River, while groundwater within the Beaver Creek watershed flows within the watershed (see Figure D.3-2). For more detailed information about karst geology, see Section 3.2, Karst.

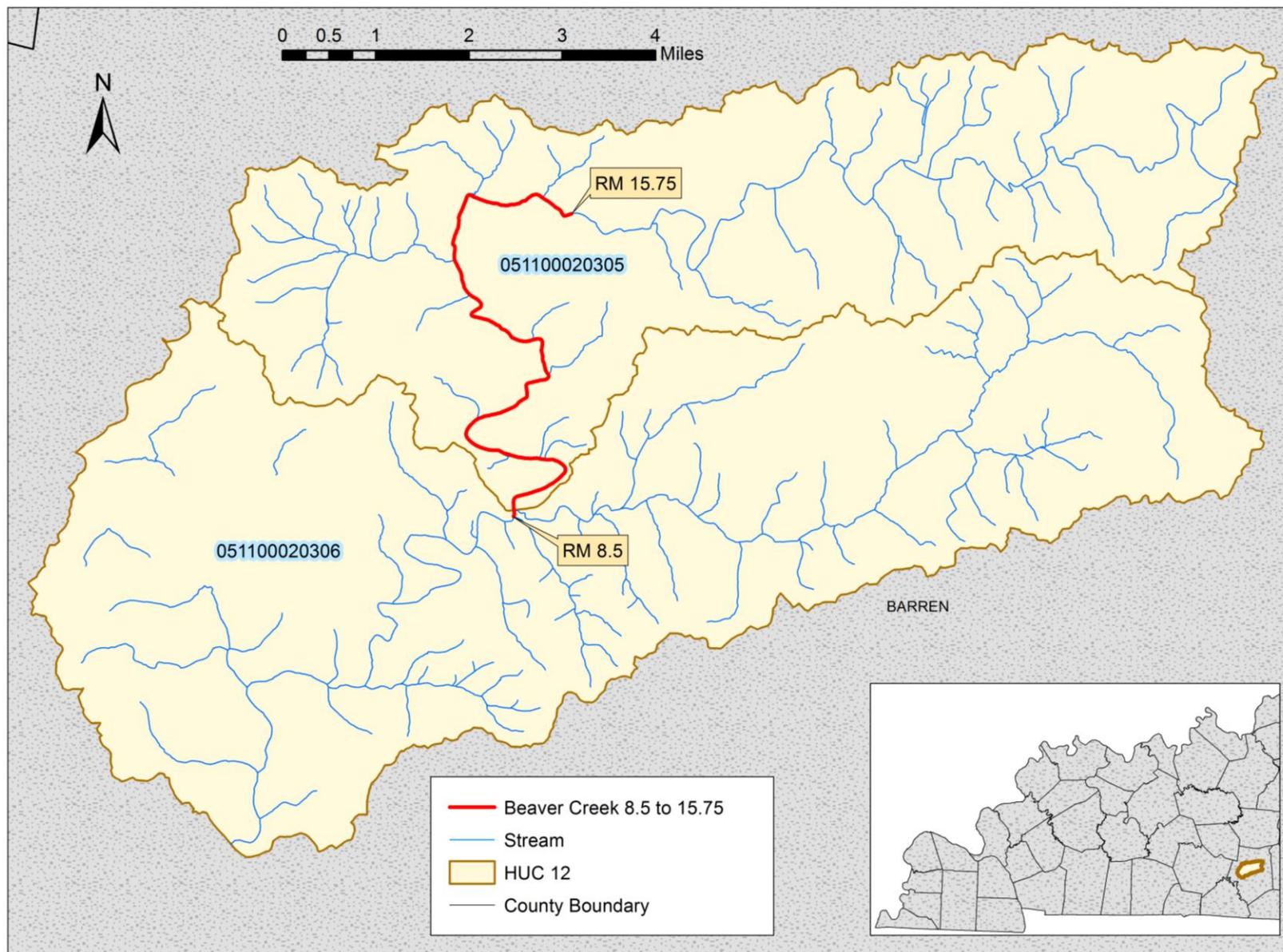


Figure D.3-1 Location of Beaver Creek 8.5 to 15.75

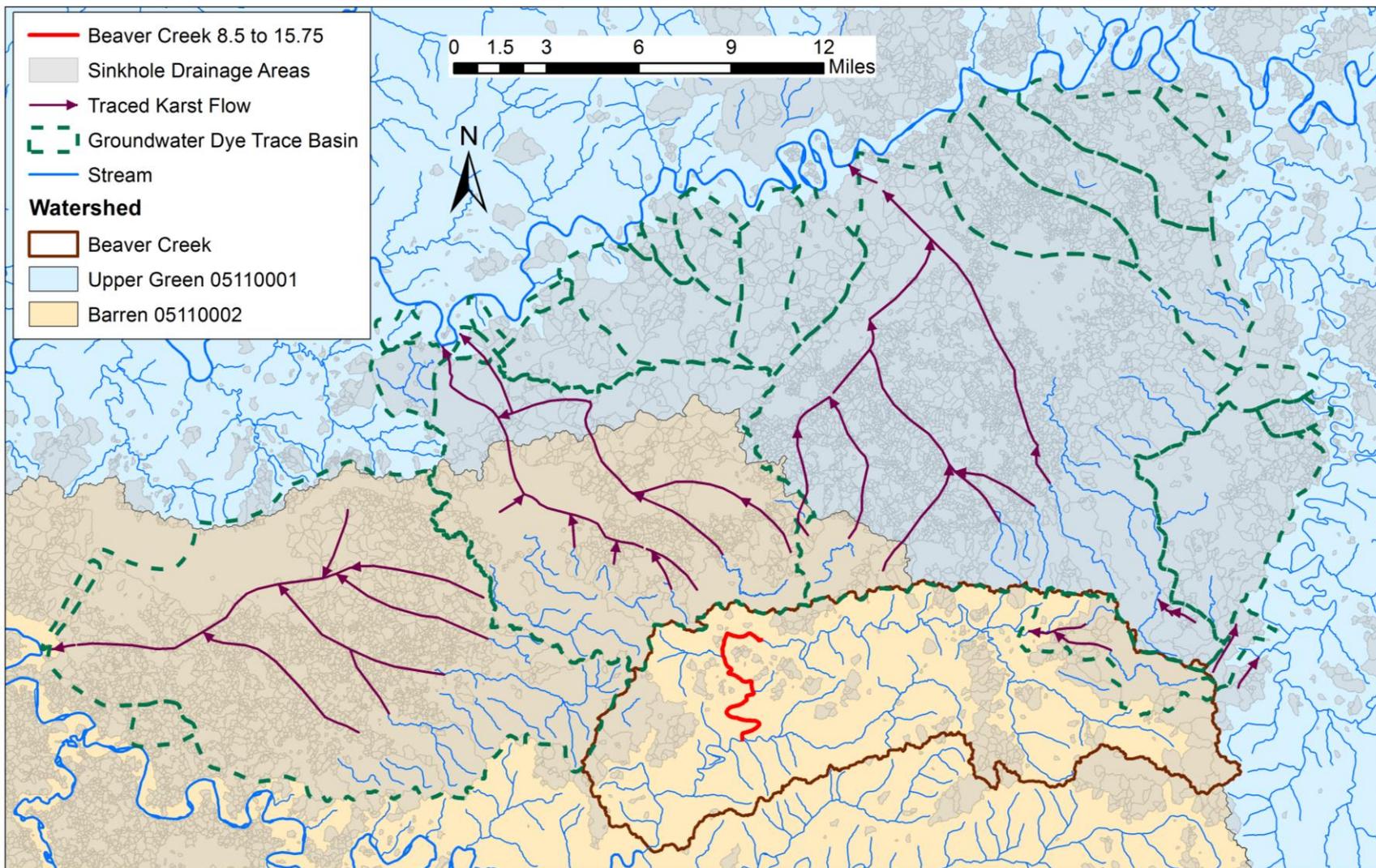


Figure D.3-2 Karst Influence in the Region of Beaver Creek 8.5 to 15.75

**Section D.4 Buck Creek 0 to 8.0****Waterbody ID:** KY488213\_01**Receiving Water:** Green River**Impaired Use:** PCR**Support Status:** nonsupport**Indicator Bacteria:** fecal coliform**HUC 12:** 051100050201**County:** McLean

In 2008 the Division of Water collected samples at three stations along this segment as part of a study of the Buck Creek watershed. Table D.4-1 summarizes information about the stations; Table D.4-2 provides a summary of the data collected from these stations.

**Table D.4-1 Division of Water Sample Site Locations**

Station Name	Latitude	Longitude	Stream Segment	River Mile
DOW03003005	37.50537	-87.19721	Buck Creek 0.0 to 8.0	0.2
DOW03003006	37.51234	-87.17587	Buck Creek 0.0 to 8.0	2.9
DOW03003009	37.50851	-87.14010	Buck Creek 0.0 to 8.0	4.9

**Table D.4-2 Division of Water Sample Data Summary<sup>(1)</sup>**

Station Name	Indicator Bacteria	Number of Observations	Percent Exceeding WQC <sup>2</sup>	Minimum (colonies/100 ml)	Maximum (colonies/100 ml)	Average (colonies/100 ml)
DOW03003005	<i>E. coli</i>	2	50.0	135	1,500	818
DOW03003006	<i>E. coli</i>	7	71.4	105	1,500	643
DOW03003009	<i>E. coli</i>	6	33.3	108	1,500	585

<sup>(1)</sup>The full data set for samples collected from these stations may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to [DEP.KORA@ky.gov](mailto:DEP.KORA@ky.gov) or by fax to 502-564-9232. The DEP KORA point of contact may also be reached at 502-564-3999.

<sup>(2)</sup>400 colonies/100 ml for fecal coliform; 240 colonies/100 ml for *E. coli*.

The TMDL allocations for Buck Creek 0.0 to 8.0 are presented in Table D.4-3. There are no KPDES-permitted discharges of bacteria into this segment of Buck Creek. The location of the segment within the Buck Creek watershed is shown in Figure D.4-1.

**Table D.4-3 Buck Creek 0.0 to 8.0 TMDL Allocations<sup>(1)</sup>**

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

<sup>(1)</sup>All loads are colonies/day of either *E. coli* or fecal coliform. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s·ml/ft<sup>3</sup>-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft<sup>3</sup>/s) into a load (colonies/day). The symbol “ $\sum$ ” indicates that the total allocation is the sum of all the individual allowable loads.

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

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

<sup>(6)</sup>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.

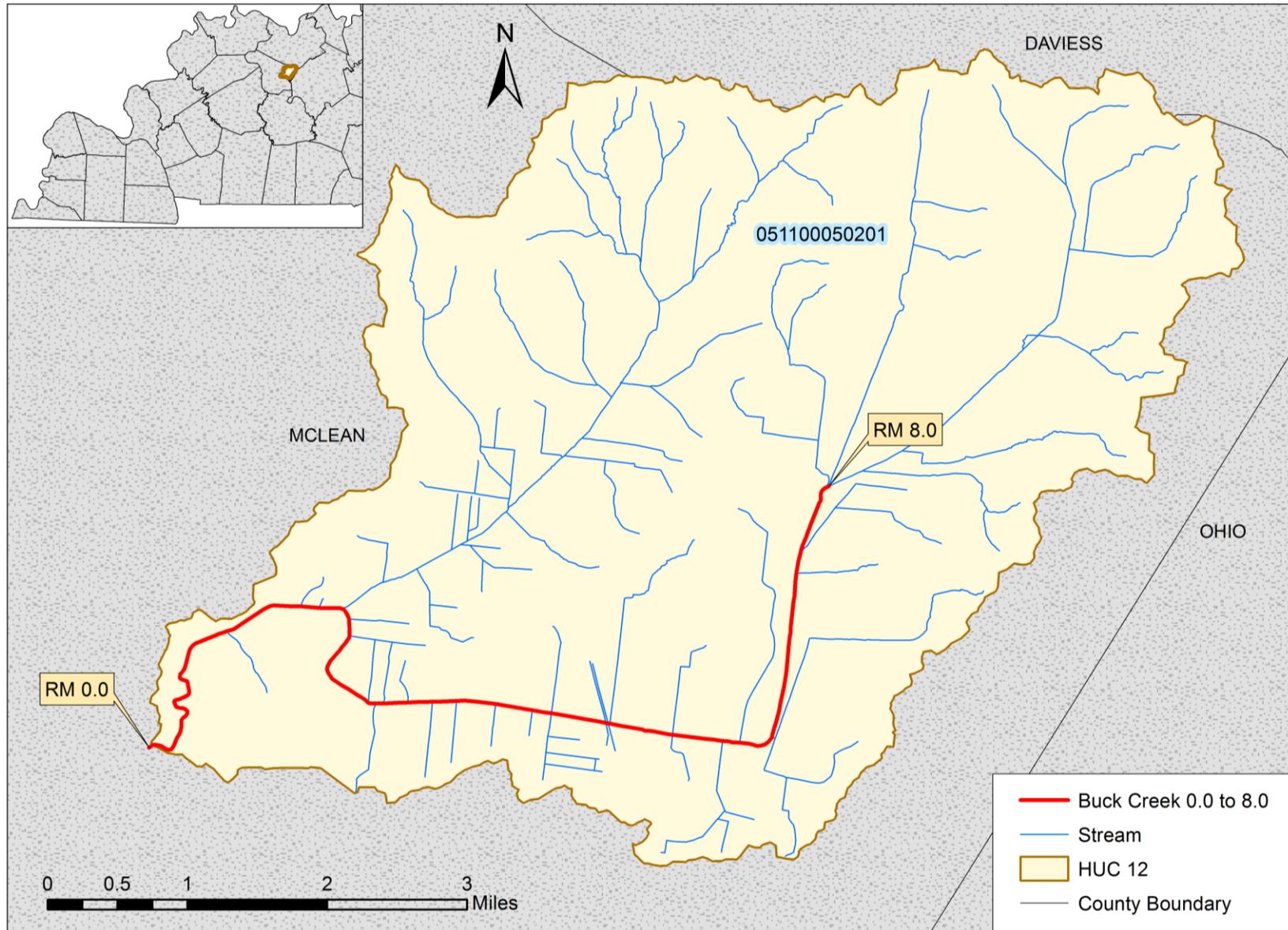


Figure D.4-1 Location of Buck Creek 0.0 to 8.0

**Section D.5 Buck Creek 8.0 to 11.0****Waterbody ID:** KY488213\_02**Receiving Water:** Green River**Impaired Use:** PCR**Support Status:** nonsupport**Indicator Bacteria:** *E. coli***HUC 12:** 051100050201**Counties:** Daviess, McLean

In 2008 the Division of Water collected samples at station DOW03003011 as part of a study of the Buck Creek watershed. Table D.5-1 summarizes information about this sampling station; Table D.5-2 provides a summary of the data collected from this station.

**Table D.5-1 Division of Water Sample Site Location**

Station Name	Latitude	Longitude	Stream Segment	River Mile
DOW03003011	37.54215	-87.10822	Buck Creek 8.0 to 11.0	8.6

**Table D.5-2 Division of Water Sample Data Summary<sup>(1)</sup>**

Station Name	Indicator Bacteria	Number of Observations	Percent Exceeding WQC <sup>2</sup>	Minimum (colonies/100 ml)	Maximum (colonies/100 ml)	Average (colonies/100 ml)
DOW03003011	<i>E. coli</i>	5	60.0	147	1,500	561

<sup>(1)</sup>The full data set for samples collected from DOW03003011 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to [DEP.KORA@ky.gov](mailto:DEP.KORA@ky.gov) or by fax to 502-564-9232. The DEP KORA point of contact may also be reached at 502-564-3999.

<sup>(2)</sup>240 colonies/100 ml for *E. coli*.

The TMDL allocations for Buck Creek 8.0 to 11.0 are presented in Table D.5-3. There are no KPDES-permitted discharges of bacteria into this segment of Buck Creek. The location of the segment within the Buck Creek watershed is shown in Figure D.5-1.

**Table D.5-3 Buck Creek 8.0 to 11.0 TMDL Allocations<sup>(1)</sup>**

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

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

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

<sup>(5)</sup>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.

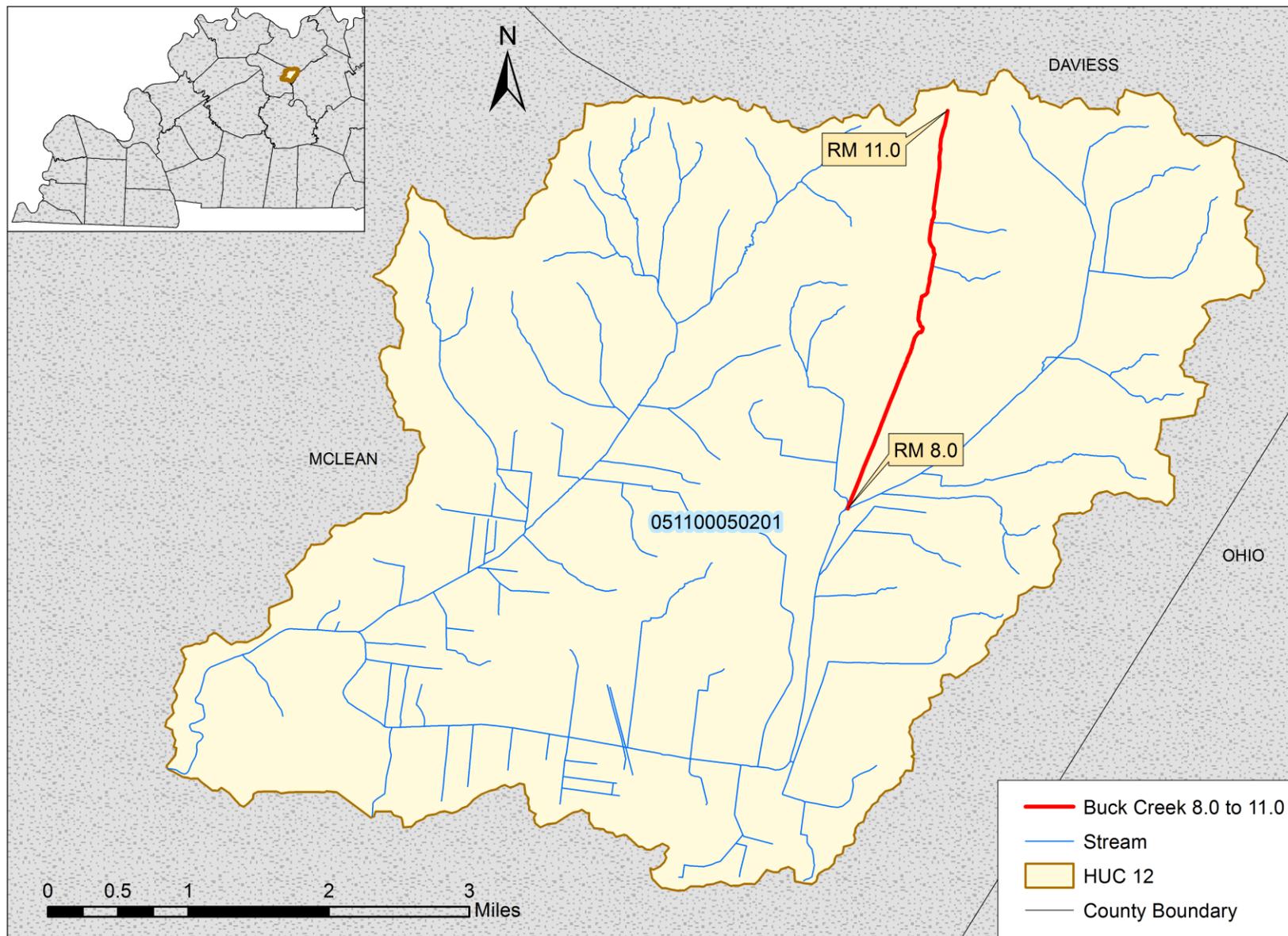


Figure D.5-1 Location of Buck Creek 8.0 to 11.0

**Section D.6 Buck Fork Pond River 12.9 to 19.3****Waterbody ID:** KY488223\_02**Receiving Water:** Pond River**Impaired Use:** PCR**Support Status:** nonsupport**Indicator Bacteria:** fecal coliform**HUC 12:** 051100060201**Counties:** Christian, Todd

In 2001 Western Kentucky University collected five samples at station GRBEX-23. Table D.6-1 summarizes information about this sampling station; Table D.6-2 provides a summary of the data collected from this station.

**Table D.6-1 Western Kentucky University Sample Site Location**

Station Name	Latitude	Longitude	Stream Segment	River Mile
GRBEX-23	36.9925	-87.2986	Buck Fork Pond River 12.9 to 19.3	12.95

**Table D.6-2 Western Kentucky University Sample Data Summary<sup>(1)</sup>**

Station Name	Bacterial Indicator	Number of Observations	Percent Exceeding WQC <sup>2</sup>	Minimum (colonies/100 ml)	Maximum (colonies/100 ml)	Average (colonies/100 ml)
GRBEX-23	fecal coliform	5	40.00	48	1,720	773

<sup>(1)</sup>The full data set for samples collected from GRBEX-23 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to [DEP.KORA@ky.gov](mailto:DEP.KORA@ky.gov) or by fax to 502-564-9232. The DEP KORA point of contact may also be reached at 502-564-3999.

<sup>(2)</sup>400 colonies/100 ml for fecal coliform; 240 colonies/100 ml for *E. coli*.

The TMDL allocations for Buck Fork Pond River 12.9 to 19.3 are presented in Table D.6-3. There are no KPDES-permitted discharges of bacteria into this segment of Buck Fork. The location of the segment within the Upper Buck Fork Pond River watershed is shown in Figure D.6-1.

**Table D.6-3 Buck Fork Pond River 12.9 to 19.3 TMDL Allocations<sup>(1)</sup>**

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

<sup>(1)</sup>All loads are colonies/day of either *E. coli* or fecal coliform. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft<sup>3</sup>-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft<sup>3</sup>/s) into a load (colonies/day). The symbol “ $\Sigma$ ” indicates that the total allocation is the sum of all the individual allowable loads.

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

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

<sup>(6)</sup>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.

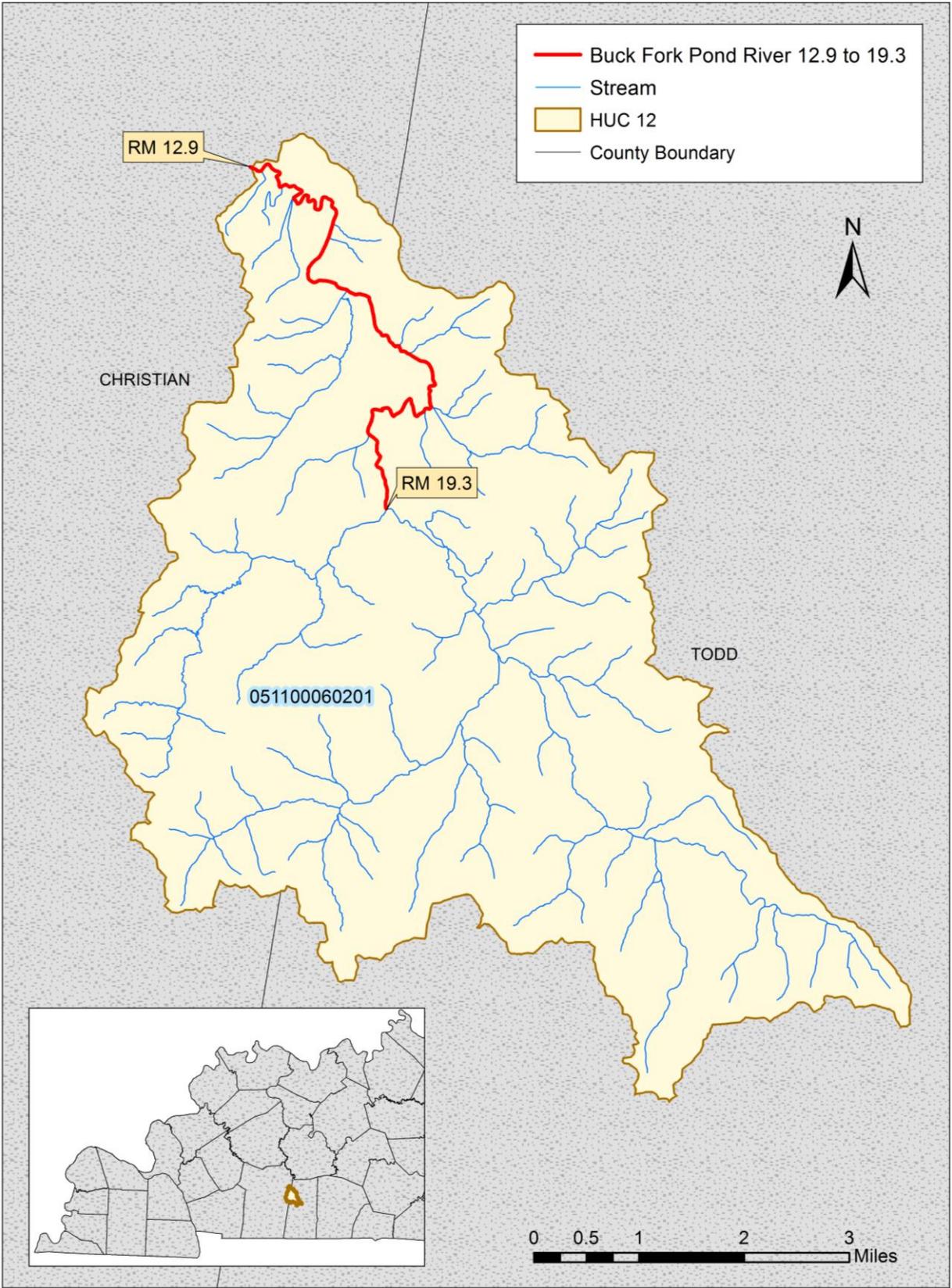


Figure D.6-1 Location of Buck Fork Pond River 12.9 to 19.3

**Section D.7 Caney Creek 0.0 to 6.8****Waterbody ID:** KY488846\_01**Receiving Water:** Rough River**Impaired Use:** PCR**Support Status:** nonsupport**Indicator Bacteria:** *E. coli***HUC 12:** 051100040403**County:** Ohio

The Division of Water has collected samples from station GRN 015, located at river mile 1.85, since 2001. The station has been sampled three to six times during the PCR season as part of the Division's five-year rotating schedule for basin monitoring (see also Section 7.2.1, Kentucky Watershed Management Framework). Table D.7-1 summarizes information about this sampling station; Table D.7-2 provides a summary of the data collected from this station.

**Table D.7-1 Division of Water Sample Site Location**

Station Name	Latitude	Longitude	Stream Segment	River Mile
GRN 015	37.526211	-86.686632	Caney Creek 0 to 6.8	1.85

**Table D.7-2 Division of Water Sample Data Summary<sup>(1)</sup>**

Station Name	Indicator Bacteria	Number of Observations	Percent Exceeding WQC <sup>2</sup>	Minimum (colonies/100 ml)	Maximum (colonies/100 ml)	Average (colonies/100 ml)
GRN 015	fecal coliform	8	12.5	49	2,600	447
GRN 015	<i>E. coli</i>	13	30.8	14	2,420	376

<sup>(1)</sup>The full data set for samples collected from GRN 015 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to [DEP.KORA@ky.gov](mailto:DEP.KORA@ky.gov) or by fax to 502-564-9232. The DEP KORA point of contact may also be reached at 502-564-3999.

<sup>(2)</sup>400 colonies/100 ml for fecal coliform; 240 colonies/100 ml for *E. coli*.

The TMDL allocations for Caney Creek 0.0 to 6.8 are presented in Table D.7-3. There are no KPDES-permitted discharges of bacteria into this segment of Caney Creek. The location of the segment within the Lower Caney Creek watershed is shown in Figure D.7-1.

**Table D.7-3 Caney Creek 0.0 to 6.8 TMDL Allocations<sup>(1)</sup>**

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

<sup>(1)</sup>All loads are colonies/day of either *E. coli* or fecal coliform. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft<sup>3</sup>-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft<sup>3</sup>/s) into a load (colonies/day). The symbol “ $\Sigma$ ” indicates that the total allocation is the sum of all the individual allowable loads.

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

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

<sup>(6)</sup>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.

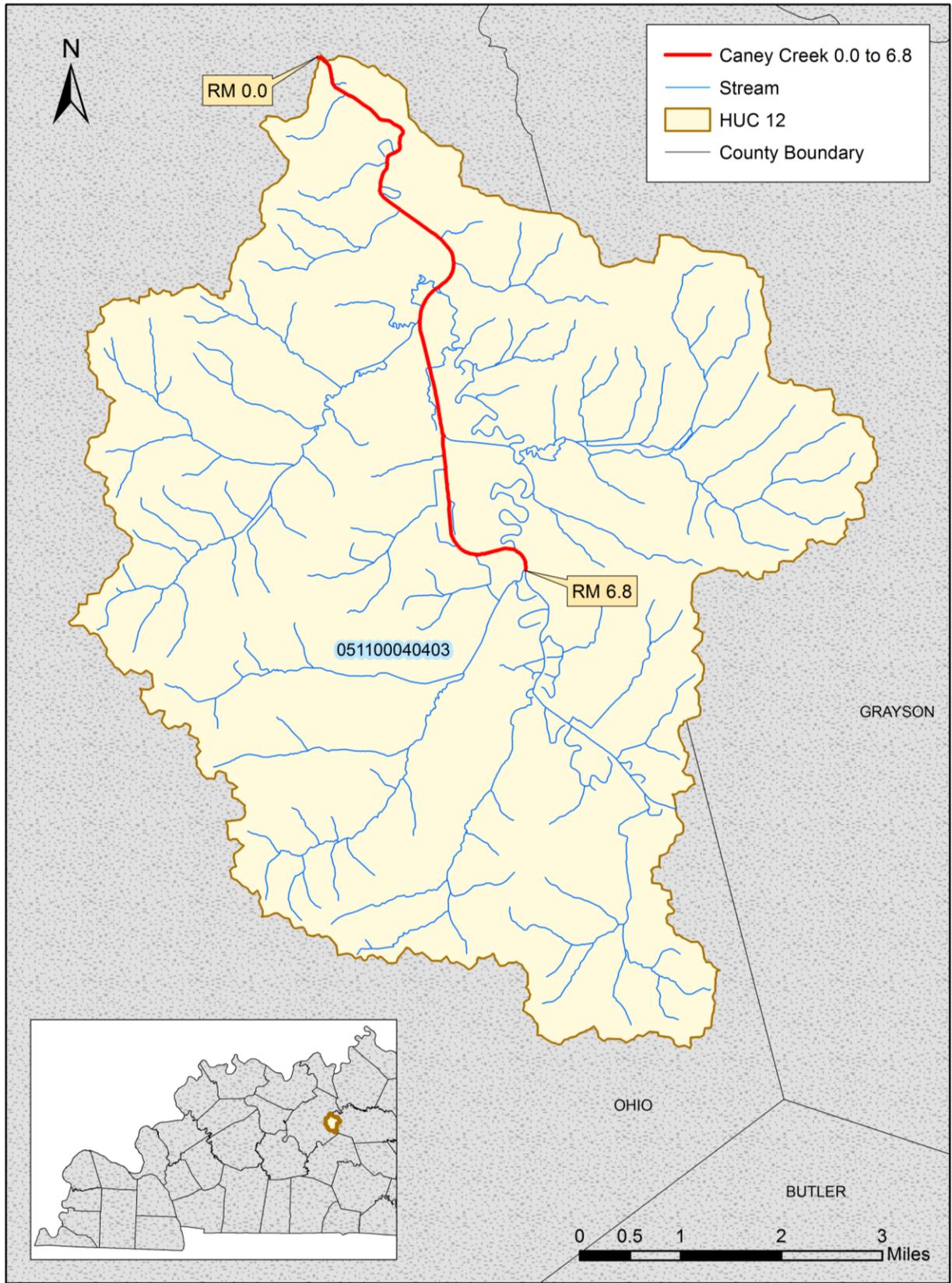


Figure D.7-1 Location of Caney Creek 0.0 to 6.8

**Section D.8 Crooked Creek 0.0 to 3.0****Waterbody ID:** KY490376\_00**Receiving Water:** Panther Creek**Impaired Use:** PCR**Support Status:** nonsupport**Indicator Bacteria:** fecal coliform**HUC 12:** 051100050308**County:** Daviess

Western Kentucky University has collected samples from three stations on this segment. In 2001, five samples were collected from FC-T48. In 2007 and 2008, samples were collected from two stations as part of a study in the Panther Creek watershed. Table D.8-1 summarizes information about these sampling stations; Table D.8-2 provides a summary of the data collected from the stations.

**Table D.8-1 Western Kentucky University Sample Site Locations**

Station Name	Latitude	Longitude	Stream Segment	River Mile
FC-T48	37.7242	-87.2795	Crooked Creek 0.0 to 3.0	0.1
CWRS_ST0001-LP00	37.70867	-87.27047	Crooked Creek 0.0 to 3.0	1.38
CWRS_ST0001-LP01	37.7219	-87.28152	Crooked Creek 0.0 to 3.0	0.27

**Table D.8-2 Western Kentucky University Sample Data Summary<sup>(1)</sup>**

Station Name	Indicator Bacteria	Number of Observations	Percent Exceeding WQC <sup>2</sup>	Minimum (colonies/100 ml)	Maximum (colonies/100 ml)	Average (colonies/100 ml)
FC-T48	fecal coliform	5	60.0	32	5,800	1,587
ST0001-LP00	<i>E. coli</i>	9	88.9	199	2,613	1,094
ST0001-LP01	<i>E. coli</i>	10	90.0	152	2,909	884

<sup>(1)</sup>The full data set for samples collected from these stations may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to [DEP.KORA@ky.gov](mailto:DEP.KORA@ky.gov) or by fax to 502-564-9232. The DEP KORA point of contact may also be reached at 502-564-3999.

<sup>(2)</sup>400 colonies/100 ml for fecal coliform; 240 colonies/100 ml for *E. coli*.

The TMDL allocations for Crooked Creek 0.0 to 3.0 are presented in Table D.8-3. There are no KPDES-permitted discharges of bacteria into this segment of Crooked Creek. The location of the segment within the Panther Creek watershed is shown in Figure D.8-1.

**Table D.8-3 Crooked Creek 0.0 to 3.0 TMDL Allocations<sup>(1)</sup>**

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

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

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

<sup>(5)</sup>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 D.8-1 Location of Crooked Creek 0.0 to 3.0

**Section D.9 Deer Creek 0.0 to 8.4****Waterbody ID:** KY490771\_01**Receiving Water:** Green River**Impaired Use:** PCR**Support Status:** partial support**Indicator Bacteria:** *E. coli***HUC 12:** 051100050105**County:** Webster

The Division of Water has collected samples from station GRN 012, located at river mile 3.1, since 2001. The station has been sampled six or more times during the PCR season as part of the Division's five-year rotating schedule for basin monitoring (see also Section 7.2.1, Kentucky Watershed Management Framework). Western Kentucky University also sampled FC-Station 45 at the same location in 2001. Table D.9-1 summarizes information about this sampling station; Table D.9-2 provides a summary of the data collected from this station.

**Table D.9-1 Sample Site Location**

Station Name	Latitude	Longitude	Stream Segment	River Mile
GRN 012	37.57300	-87.46500	Deer Creek 0 to 8.4	3.1
FC-Station 45	37.5730	-87.4651	Deer Creek 0 to 8.4	3.1

**Table D.9-2 Sample Data Summary<sup>(1)</sup>**

Station Name	Indicator Bacteria	Number of Observations	Percent Exceeding WQC <sup>2</sup>	Minimum (colonies/100 ml)	Maximum (colonies/100 ml)	Average (colonies/100 ml)
FC-Station 45	fecal coliform	5	20.0	8	8,400	1,813
GRN 012	fecal coliform	13	23.1	40	4,700	808
GRN 012	<i>E. coli</i>	12	50.0	11	1,203	359

<sup>(1)</sup>The full data set for samples collected from these stations may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to [DEP.KORA@ky.gov](mailto:DEP.KORA@ky.gov) or by fax to 502-564-9232. The DEP KORA point of contact may also be reached at 502-564-3999.

<sup>(2)</sup>400 colonies/100 ml for fecal coliform; 240 colonies/100 ml for *E. coli*.

The TMDL allocations for Deer Creek 0.0 to 8.4 are presented in Table D.9-3. There are no KPDES-permitted discharges of bacteria into this segment of Deer Creek. The location of the segment within the Deer Creek watershed is shown in Figure D.9-1.

**Table D.9-3 Deer Creek 0.0 to 8.4 TMDL Allocations<sup>(1)</sup>**

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

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

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

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

<sup>(6)</sup>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.

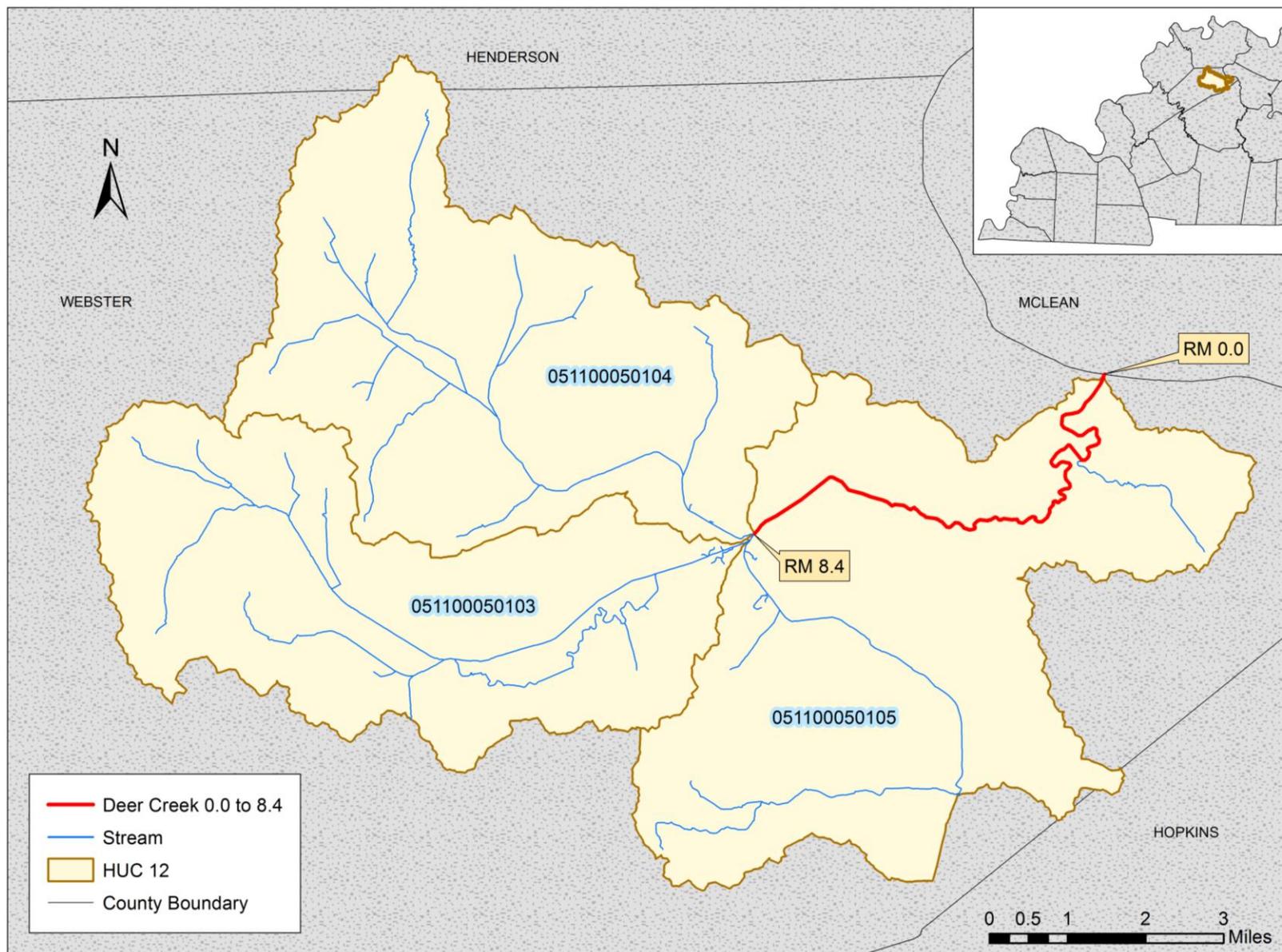


Figure D.9-1 Location of Deer Creek 0.0 to 8.4

**Section D.10 Deserter Creek 0.0 to 3.1****Waterbody ID:** KY490771\_01**Receiving Water:** South Fork Panther Creek**Impaired Use:** PCR**Support Status:** nonsupport**Indicator Bacteria:** fecal coliform**HUC 12:** 051100050302**County:** Daviess, Ohio

Western Kentucky University has collected samples from two locations on this segment. In 2001, samples were collected from GRBEX-20 and FC-T36. In 2007 and 2008, samples were collected from two stations as part of a study in the Panther Creek watershed. Table D.10-1 summarizes information about these sampling locations; Table D.10-2 provides a summary of the data collected from the stations.

**Table D.10-1 Western Kentucky University Sample Site Locations**

Station Name	Latitude	Longitude	Stream Segment	River Mile
GRBEX-20	37.6362	-86.9016	Deserter Creek 0.0 to 3.1	1.6
CWRS_ST0001-LP39	37.63634	-86.9014	Deserter Creek 0.0 to 3.1	1.6
CWRS_ST0001-LP40	37.64528	-86.8832	Deserter Creek 0.0 to 3.1	2.85
FC-T36	37.6465	-86.8835	Deserter Creek 0.0 to 3.1	2.85

**Table D.10-2 Western Kentucky University Sample Data Summary<sup>(1)</sup>**

Station Name	Indicator Bacteria	Number of Observations	Percent Exceeding WQC <sup>2</sup>	Minimum (colonies/100 ml)	Maximum (colonies/100 ml)	Average (colonies/100 ml)
GRBEX-20	fecal coliform	4	50.0	104	12,000	3,196
ST0001-LP39	<i>E. coli</i>	6	16.7	10	767	214
ST0001-LP40	<i>E. coli</i>	7	71.4	41	6,867	1,625
FC-T36	fecal coliform	4	50.0	104	12,000	5,706

<sup>(1)</sup>The full data set for samples collected from these stations may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to [DEP.KORA@ky.gov](mailto:DEP.KORA@ky.gov) or by fax to 502-564-9232. The DEP KORA point of contact may also be reached at 502-564-3999.

<sup>(2)</sup>400 colonies/100 ml for fecal coliform; 240 colonies/100 ml for *E. coli*.

The TMDL allocations for Deserter Creek 0.0 to 3.1 are presented in Table D.10-3. There are no KPDES-permitted discharges of bacteria into this segment of Deserter Creek. The location of the segment within the Panther Creek watershed is shown in Figure D.10-1.

**Table D.10-3 Deserter Creek 0.0 to 3.1 TMDL Allocations<sup>(1)</sup>**

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

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

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

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

<sup>(6)</sup>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.

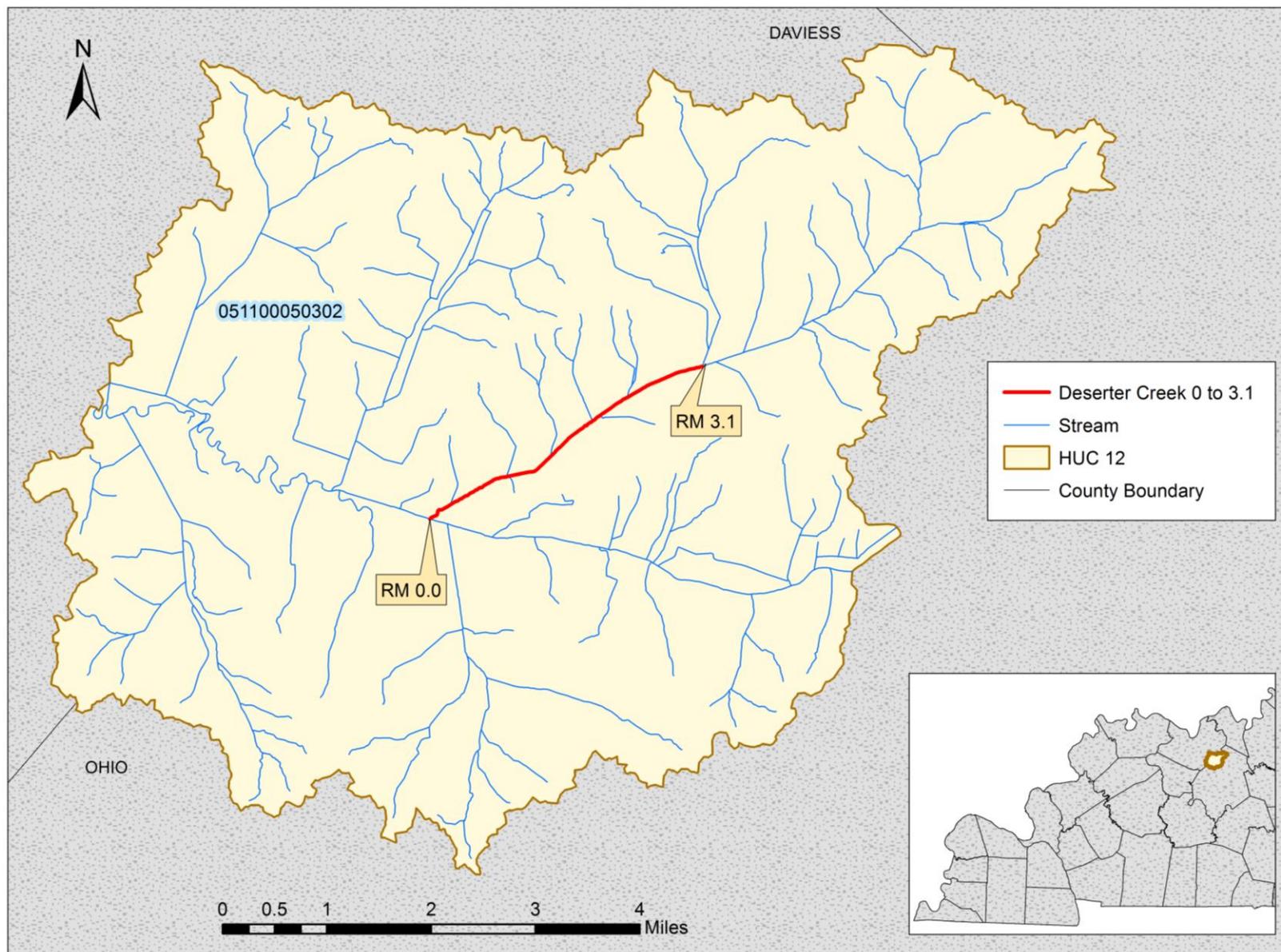


Figure D.10-1 Location of Deserter Creek 0.0 to 3.1

**Section D.11 Elk Creek 7.6 to 10.6****Waterbody ID:** KY491656\_02**Receiving Water:** Pond River**Impaired Use:** PCR**Support Status:** nonsupport**Indicator Bacteria:** fecal coliform**HUC 12:** 051100060504**County:** Hopkins

Sampling data from Elk Creek 7.6 to 10.6 is not available. This segment is located in a sewer area of Madisonville. Beginning in 1994, Division of Water issued Notices of Violation to the City of Madisonville for failure to report the release of untreated wastewater to the waters of the Commonwealth and degradation of the waters of the Commonwealth. These violations were related to a series of sanitary sewer overflows in the Madisonville collection system, and as one of the impacted waters, Elk Creek 7.6 to 10.6 was added to the 303(d) list in 1998. A subsequent Agreed Order outlined the corrective measures required by the city. There are no KPDES-permitted discharges of bacteria into this segment of Elk Creek. The City of Madisonville does have MS4 storm water permit coverage for areas in the watershed, but the discharges occur along tributaries or upstream of the segment.

The TMDL allocations for Elk Creek 7.6 to 10.6 are presented in Table D.11-1. The location of the segment within the Elk Creek watershed is shown in Figure D.11-1.

**Table D.11-1 Elk Creek 7.6 to 10.6 TMDL Allocations<sup>(1)</sup>**

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

<sup>(1)</sup>All loads are colonies/day of either *E. coli* or fecal coliform. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft<sup>3</sup>-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft<sup>3</sup>/s) into a load (colonies/day). The symbol “ $\Sigma$ ” indicates that the total allocation is the sum of all the individual allowable loads.

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

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

<sup>(6)</sup>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.

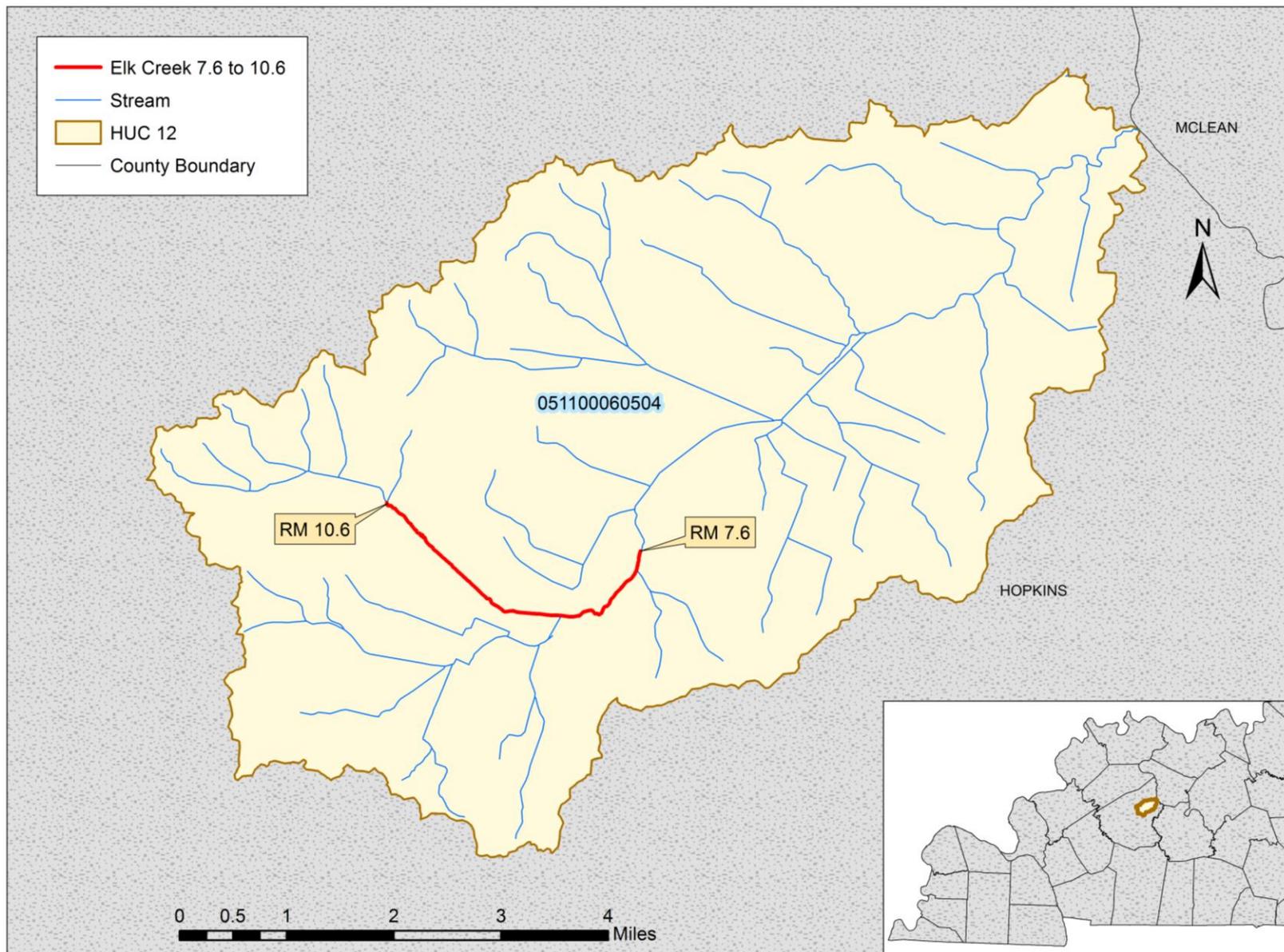


Figure D.11-1 Location of Elk Creek 7.6 to 10.6

**Section D.12 Elk Pond Creek 0.0 to 4.9****Waterbody ID:** KY491671\_00**Receiving Water:** Pond River**Impaired Use:** PCR**Support Status:** nonsupport**Indicator Bacteria:** fecal coliform**HUC 12:** 051100060501**County:** Muhlenberg

In 2001 Western Kentucky University collected five samples at station GRBEX-27. Table D.12-1 summarizes information about this sampling station; Table D.12-2 provides a summary of the data collected from this station.

**Table D.12-1 Western Kentucky University Sample Site Location**

Station Name	Latitude	Longitude	Stream Segment	River Mile
GRBEX-27	37.1618	-87.2885	Elk Pond Creek 0.0 to 4.9	3.7

**Table D.12-2 Western Kentucky University Sample Data Summary<sup>(1)</sup>**

Station Name	Indicator Bacteria	Number Of Observations	Percent Exceeding WQC <sup>2</sup>	Minimum (colonies/100 ml)	Maximum (colonies/100 ml)	Average (colonies/100 ml)
GRBEX-27	fecal coliform	5	60.0	144	12,200	5,005

<sup>(1)</sup>The full data set for samples collected from GRBEX-27 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to [DEP.KORA@ky.gov](mailto:DEP.KORA@ky.gov) or by fax to 502-564-9232. The DEP KORA point of contact may also be reached at 502-564-3999.

<sup>(2)</sup>400 colonies/100 ml for fecal coliform; 240 colonies/100 ml for *E. coli*.

The TMDL allocations for Elk Pond Creek 0.0 to 4.9 are presented in Table D.12-3. There are no KPDES-permitted discharges of bacteria into this segment of Elk Pond Creek. The location of the segment within the Elk Pond Creek-Pond River watershed is shown in Figure D.12-1.

**Table D.12-3 Elk Pond Creek 0.0 to 4.9 TMDL Allocations<sup>(1)</sup>**

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

<sup>(1)</sup>All loads are colonies/day of either *E. coli* or fecal coliform. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-m/ft<sup>3</sup>-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft<sup>3</sup>/s) into a load (colonies/day). The symbol “ $\sum$ ” indicates that the total allocation is the sum of all the individual allowable loads.

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

<sup>(5)</sup>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.

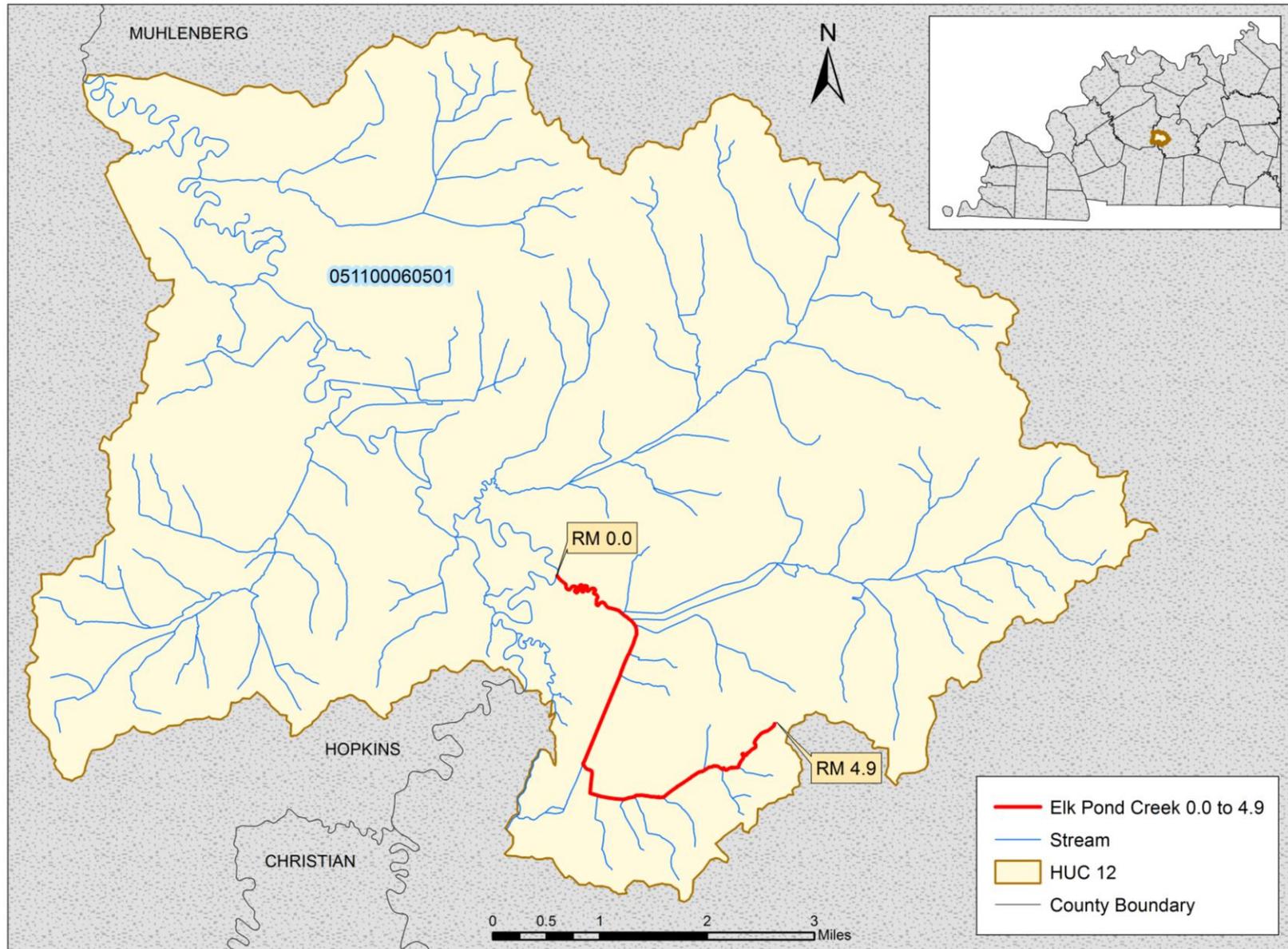


Figure D.12-1 Location of Elk Pond Creek 0.0 to 4.9

**Section D.13 Gasper River 7.8 to 14.6****Waterbody ID:** KY492748\_01**Receiving Water:** Barren River**Impaired Use:** PCR**Support Status:** partial support**Indicator Bacteria:** *E. coli***HUC 12:** 051100020805**County:** Warren

The Division of Water has collected samples from station GRN 020, located at river mile 12.05, since 2001. The station has been sampled four to six times during the PCR season as part of the Division's five-year rotating schedule for basin monitoring (see also Section 7.2.1, Kentucky Watershed Management Framework). Table D.13-1 summarizes information about this sampling station; Table D.13-2 provides a summary of the data collected from this station.

**Table D.13-1 Division of Water Sample Site Location**

Station Name	Latitude	Longitude	Stream Segment	River Mile
GRN 020	37.022069	-86.607015	Gasper River 7.8 to 14.6	12.05

**Table D.13-2 Division of Water Sample Data Summary<sup>(1)</sup>**

Station Name	Indicator Bacteria	Number of Observations	Percent Exceeding WQC <sup>2</sup>	Minimum (colonies/100 ml)	Maximum (colonies/100 ml)	Average (colonies/100 ml)
GRN 020	fecal coliform	4	0.0	1	336	149
GRN 020	<i>E. coli</i>	15	46.7	56	2,420	854

<sup>(1)</sup>The full data set for samples collected from GRN 020 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to [DEP.KORA@ky.gov](mailto:DEP.KORA@ky.gov) or by fax to 502-564-9232. The DEP KORA point of contact may also be reached at 502-564-3999.

<sup>(2)</sup>400 colonies/100 ml for fecal coliform; 240 colonies/100 ml for *E. coli*.

The TMDL allocations for Gasper River 7.8 to 14.6 are presented in Table D.13-3. There are no KPDES-permitted discharges of bacteria into this segment of the Gasper River.

**Table D.13-3 Gasper River 7.8 to 14.6 TMDL Allocations<sup>(1)</sup>**

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

<sup>(1)</sup>All loads are colonies/day of either *E. coli* or fecal coliform. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s·ml/ft<sup>3</sup>-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft<sup>3</sup>/s) into a load (colonies/day). The symbol “ $\Sigma$ ” indicates that the total allocation is the sum of all the individual allowable loads.

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

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

<sup>(6)</sup>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 location of the segment within the Gasper River watershed is shown in Figure D.13-1. This watershed exists in a karst area characterized by many sinkholes, sinking streams, and springs. 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 trace studies in the area indicate that some dye trace basin boundaries in the south and east extend beyond the HUC 12 topographic boundaries of the Gasper River watershed and should be considered additional contributing areas (see Figure D.13-2). For more detailed information about karst geology, see Section 3.2, Karst.

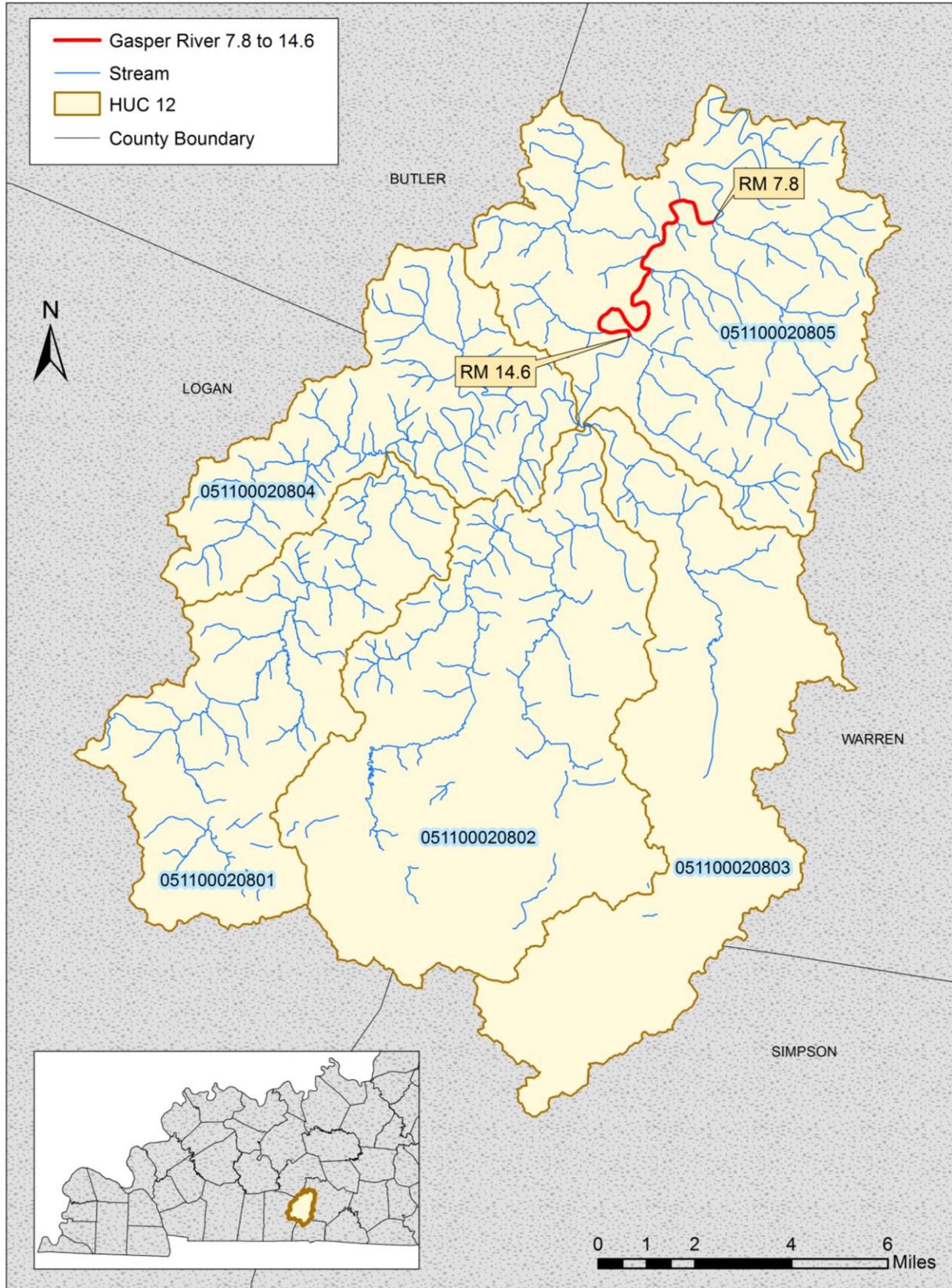


Figure D.13-1 Location of Gasper River 7.8 to 14.6

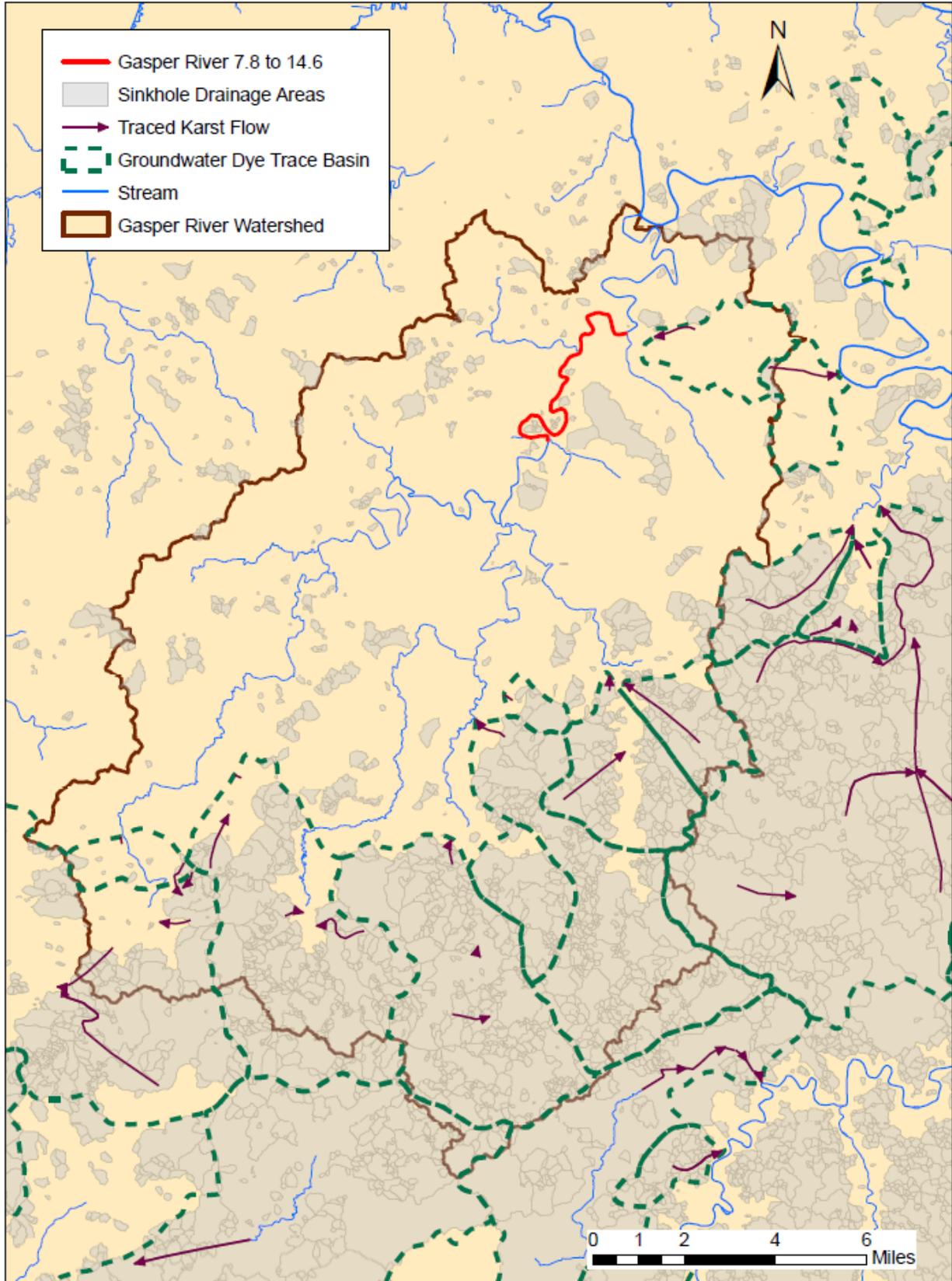


Figure D.13-2 Karst Influence in the Region of Gasper River RM 7.8 to 14.6

**Section D.14 Green River 210.4 to 250.2****Waterbody ID:** KY493284\_08**Receiving Water:** Ohio River**Impaired Use:** PCR**Support Status:** partial support**Indicator Bacteria:** *E. coli***HUC 12s:** 051100010805, 051100010806, 051100010807, 051100010808**County:** Hart

The Division of Water has collected samples from station PRI 018, located at river mile 229.05, since 1980. The station typically has been sampled three or more times during the PCR season, although it was not sampled in 1982. The USGS collected samples from station USGS-03308500 at Munfordville between 1986 and 1994. The National Park Service collected samples from MACA BGR, at Bush Island, from 2002-2005 and 2010-2012. Table D.14-1 summarizes information about these stations; Table D.14-2 provides a summary of the data collected from the stations.

**Table D.14-1 Sample Site Locations**

Station Name	Latitude	Longitude	Stream Segment	River Mile
PRI 018	37.2686666	-85.8852777	Green River 210.4 to 250.2	229.05
MACA_BIGR	37.24779359	-86.02112515	Green River 210.4 to 250.3	210.8
USGS-03308500	37.2694444	-85.8880556	Green River 210.4 to 250.4	227.2

**Table D.14-2 Sample Data Summary<sup>(1)</sup>**

Station Name	Indicator Bacteria	Number of Observations	Percent Exceeding WQC <sup>2</sup>	Minimum (colonies/100 ml)	Maximum (colonies/100 ml)	Average (colonies/100 ml)
PRI 018	fecal coliform	115	30.4	1	16,000	879
PRI 018	<i>E. coli</i>	45	17.8	10.9	2,420	385
MACA-BIGR	fecal coliform	14	28.6	36	5,067	647
MACA-BIGR	<i>E. coli</i>	14	7.1	9.7	649	101
USGS-03308500	fecal coliform	23	47.8	27	8,200	1,078

<sup>(1)</sup>The full data set for samples collected from these stations may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to [DEP.KORA@ky.gov](mailto:DEP.KORA@ky.gov) or by fax to 502-564-9232. The DEP KORA point of contact may also be reached at 502-564-3999.

<sup>(2)</sup>400 colonies/100 ml for fecal coliform; 240 colonies/100 ml for *E. coli*.

The TMDL allocations for Green River 210.4 to 250.2 are presented in Table D.14-3.

**Table D.14-3 Green River 210.4 to 250.2 TMDL Allocations<sup>(1)</sup>**

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

<sup>(1)</sup>All loads are colonies/day of either *E. coli* or fecal coliform. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s·ml/ft<sup>3</sup>-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft<sup>3</sup>/s) into a load (colonies/day). The symbol “ $\Sigma$ ” indicates that the total allocation is the sum of all the individual allowable loads.

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

<sup>(3)</sup> $Q_{SWS}$  is the flow (ft<sup>3</sup>/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 and 240 colonies/100 ml as a maximum weekly average or as a fecal coliform effluent gross limit of 200 colonies/100 ml as a monthly average and 400 colonies/100 ml as a maximum weekly average.

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

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

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

<sup>(7)</sup>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.

Two facilities permitted under the Kentucky Pollutant Discharge Elimination System (KPDES) discharge treated effluent directly into this segment of the Green River. Both of the directly discharging facilities are sanitary wastewater systems (SWSs). There are no MS4 communities or CSOs discharging directly to this segment of the Green River. These facilities are identified in Table D.14-4 and their locations are shown in Figure D.14-1.

**Table D.14-4 Summary of Active KPDES-permitted Sources as of May 2017**

KPDES Permit Number	Facility Name	Design Flow (MGD)	Indicator Bacteria	Outfall Latitude	Outfall Longitude	Permit Expiration Date	WLA <sup>(1)</sup> (colonies/day)
KY0091561	Caveland Environmental Authority	0.48	<i>E. coli</i>	37.2411	-85.9342	10/31/2021	$Q_{SWS} \times WQC \times CF$
KY0031755	Munfordville STP	0.26	<i>E. coli</i>	37.268889	-85.888889	1/31/2021	$Q_{SWS} \times WQC \times CF$

<sup>(1)</sup> All loads are colonies/day of either *E. coli* or fecal coliform.  $Q_{SWS}$  is the flow in the segment due to a SWS entity. The recreational use bacterial WQC are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s·ml/ft<sup>3</sup>-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft<sup>3</sup>/s) into a load (colonies/day).

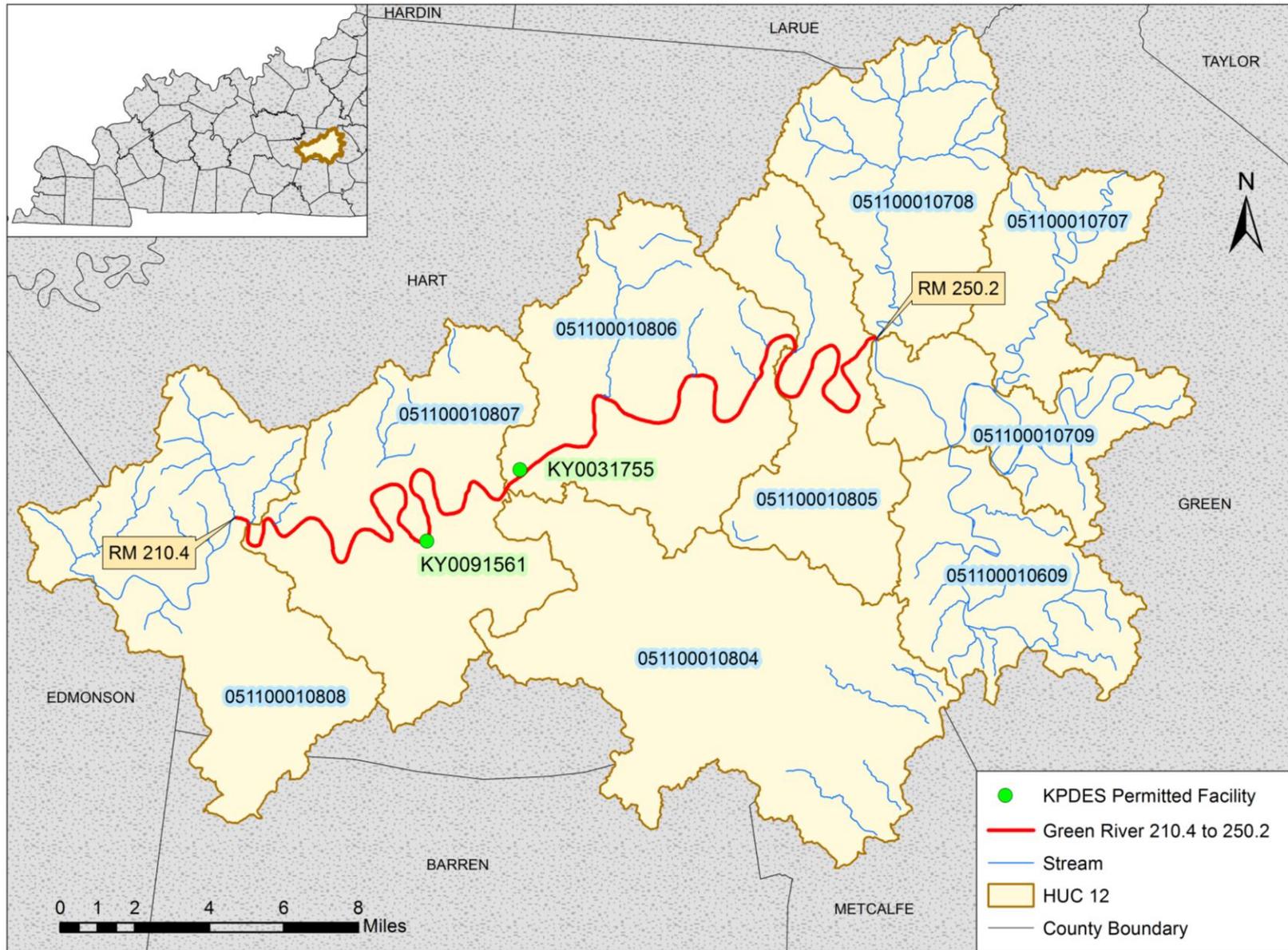


Figure D.14-1 Locations of KPDES-permitted Facilities on Green River 210.4 to 250.2

This watershed exists in a karst area characterized by many sinkholes, sinking streams, and springs. 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. Several springs discharge to this reach of Green River, and the associated dye trace basins are shown in Figure D.18-2. Some of these dye trace basin boundaries extend beyond the HUC 12 topographic boundaries and should be considered additional contributing areas. For more detailed information about karst geology, see Section 3.2.

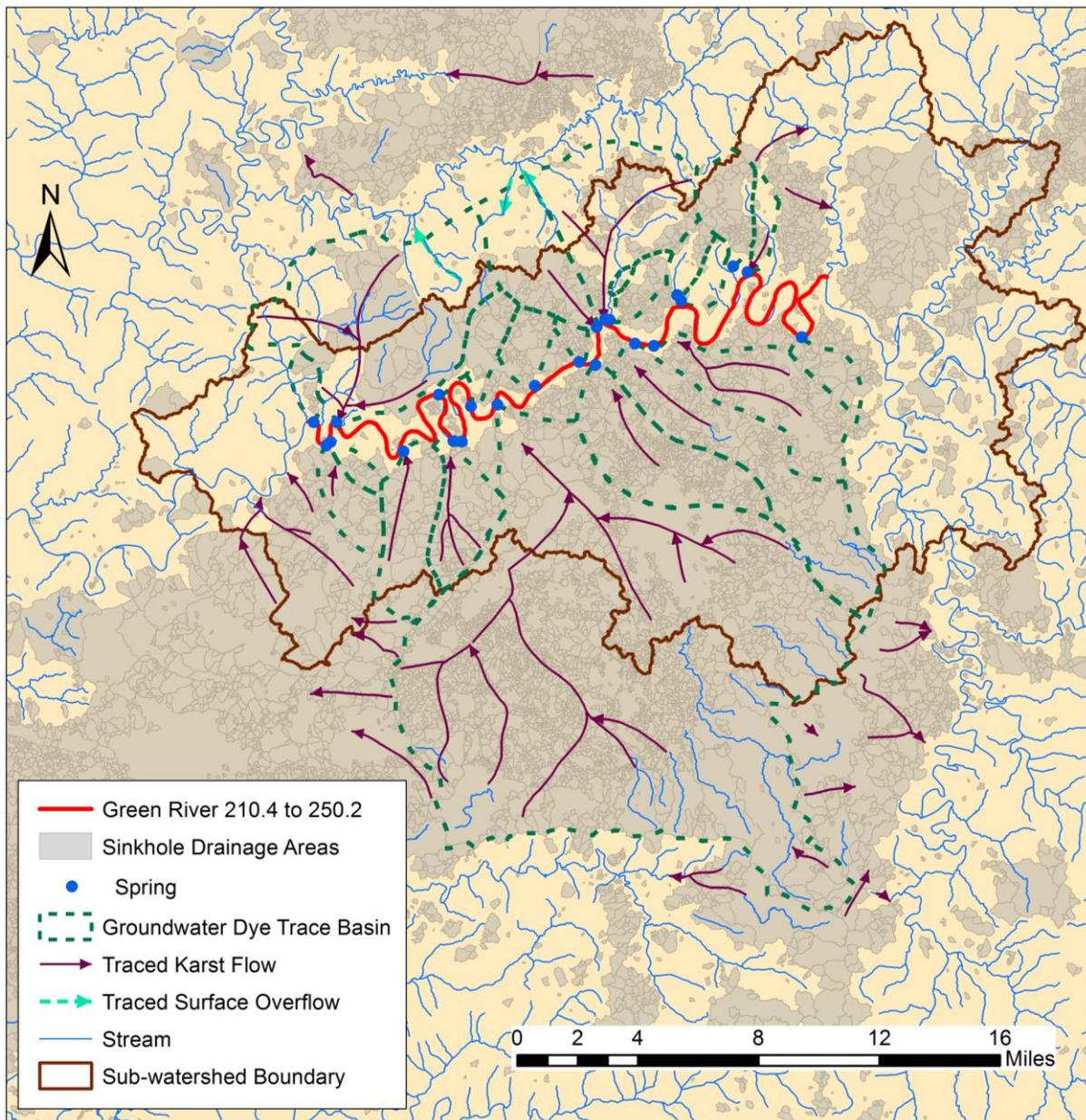


Figure D.14-2 Karst Influence in the Region of Green River 210.4 to 250.2

**Section D.15 Green River 283.1 to 309.0****Waterbody ID:** KY493284\_13**Receiving Water:** Ohio River**Impaired Use:** PCR**Support Status:** nonsupport**Indicator Bacteria:** fecal coliform**HUC 12s:** 051100010308, 051100010701, 051100010703**County:** Green, Taylor

The Division of Water collected samples at PRI 019 year-round between 1980 and 1985, except in 1982, when the station was not sampled. Additionally, Western Kentucky University collected bacteria samples from four stations (GR-8.11 through -8.14) along this segment in 2002 and 2003. Table D.15-1 summarizes information about the five sampling stations; Table D.15-2 provides a summary of the data collected from these stations.

**Table D.15-1 Sample Site Locations**

<b>Station Name</b>	<b>Latitude</b>	<b>Longitude</b>	<b>Stream Segment</b>	<b>River Mile</b>
PRI 019	37.253889	85.503056	Green River 283.1 to 309.0	283.2
GR-8.11	37.2539	-85.5025	Green River 283.1 to 309.0	283.25
GR-8.12	37.2452	-85.4797	Green River 283.1 to 309.0	285.2
GR-8.13	37.235	-85.425	Green River 283.1 to 309.0	294.8
GR-8.14	37.2449	-85.364	Green River 283.1 to 309.0	307.3

**Table D.15-2 Sample Data Summary<sup>(1)</sup>**

Station Name	Indicator Bacteria	Number Of Observations	Percent Exceeding WQC <sup>2</sup>	Minimum (colonies/ 100 ml)	Maximum (colonies/ 100 ml)	Average (colonies/ 100 ml)
PRI 019	fecal coliform	27	25.9	39	10,000	888
GR-8.11	fecal coliform	7	28.6	144	560	423
GR-8.12	fecal coliform	7	57.1	176	1,000	550
GR-8.13	fecal coliform	7	0.0	48	304	220
GR-8.14	fecal coliform	7	14.3	7	672	157

<sup>(1)</sup>The full data set for samples collected from these stations may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to [DEP.KORA@ky.gov](mailto:DEP.KORA@ky.gov) or by fax to 502-564-9232. The DEP KORA point of contact may also be reached at 502-564-3999.

<sup>(2)</sup>400 colonies/100 ml for fecal coliform; 240 colonies/100 ml for *E. coli*.

The TMDL allocations for Green River 283.1 to 309.0 are presented in Table D.15-3. As of May 2017, there are no KPDES-permitted bacteria discharges into this segment of the Green River. The former Indian Ridge Campground (KY0077313) discharged sanitary wastewater into this segment until Feb. 1, 2013, but because these discharges have ceased and the permit has been inactivated, the former facility does not receive a wasteload allocation.

**Table D.15-3 Green River 283.1 to 309.0 TMDL Allocations<sup>(1)</sup>**

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

<sup>(1)</sup>All loads are colonies/day of either *E. coli* or fecal coliform. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-m/ft<sup>3</sup>-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft<sup>3</sup>/s) into a load (colonies/day). The symbol “ $\sum$ ” indicates that the total allocation is the sum of all the individual allowable loads.

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

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

<sup>(6)</sup>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 location of the segment within the Green River watershed is shown in Figure D.15-1. This watershed exists in a karst area with sinkholes and springs. 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 Green River 283.1 to 309.0. For more detailed information about karst geology, see Section 3.2, Karst.

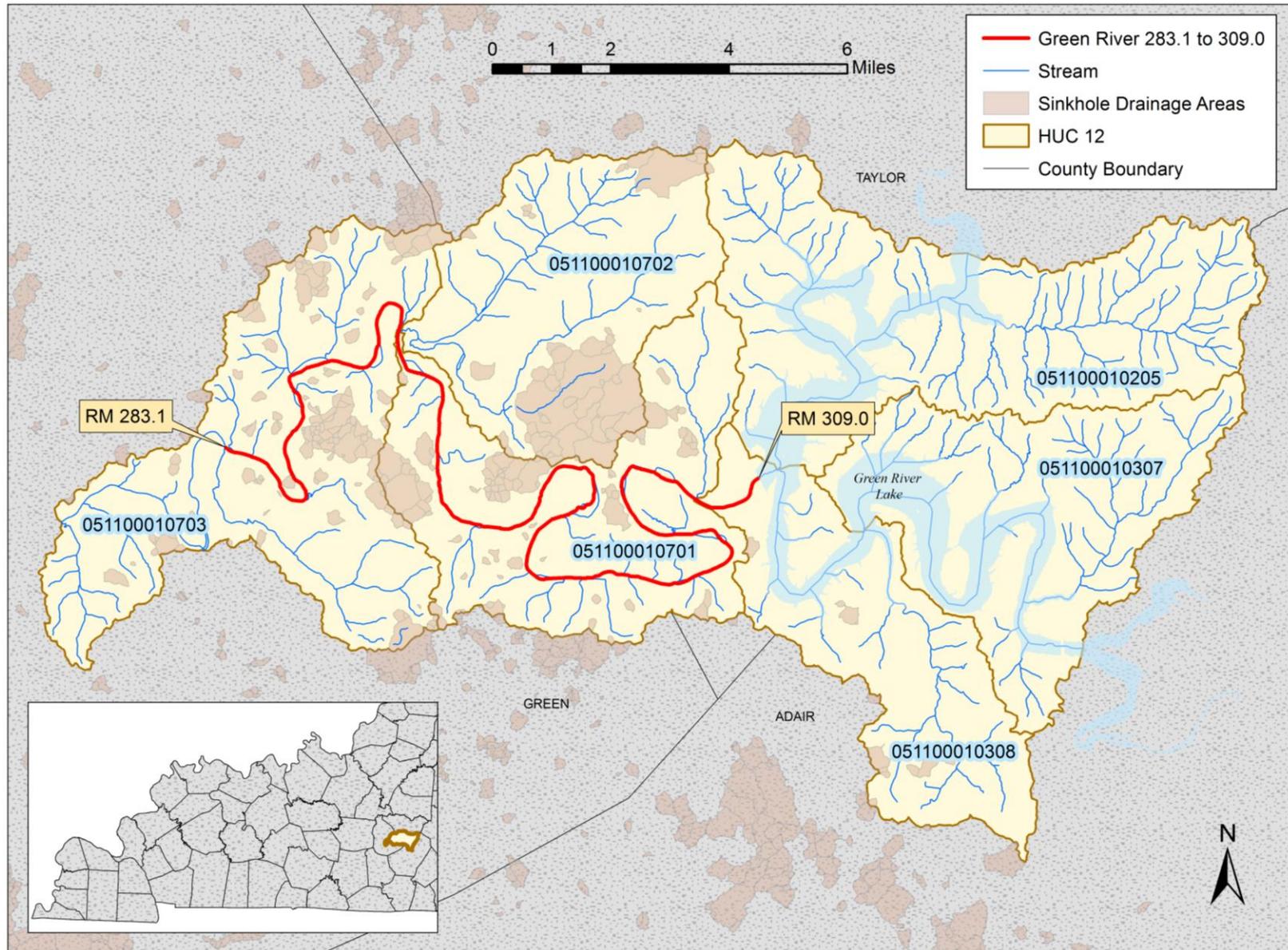


Figure D.15-1 Location of Green River 283.1 to 309.0

**Section D.16 Jarrels Creek 0.0 to 1.8****Waterbody ID:** KY5495175\_00**Receiving Water:** Pond River**Impaired Use:** PCR**Support Status:** nonsupport**Indicator Bacteria:** fecal coliform**HUC 12:** 051100060206**County:** Muhlenberg

In 2001 Western Kentucky University collected five samples at station GRBEX-25. Table D.16-1 summarizes information about this sampling station; Table D.21-2 provides a summary of the data collected from this station.

**Table D.16-1 Western Kentucky University Sample Site Location**

Station Name	Latitude	Longitude	Stream Segment	River Mile
GRBEX-25	37.1573	-87.3171	Jarrels Creek 0.0 to 1.8	1.3

**Table D.16-2 Western Kentucky University Sample Data Summary<sup>(1)</sup>**

Station Name	Indicator Bacteria	Number of Observations	Percent Exceeding WQC <sup>2</sup>	Minimum (colonies/100 ml)	Maximum (colonies/100 ml)	Average (colonies/100 ml)
GRBEX-25	fecal coliform	5	40.0	88	10,000	3,128

<sup>(1)</sup>The full data set for samples collected from GRBEX-25 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to [DEP.KORA@ky.gov](mailto:DEP.KORA@ky.gov) or by fax to 502-564-9232. The DEP KORA point of contact may also be reached at 502-564-3999.

<sup>(2)</sup>400 colonies/100 ml for fecal coliform; 240 colonies/100 ml for *E. coli*.

The TMDL allocations for Jarrels Creek 0.0 to 1.8 are presented in Table D.16-3. There are no KPDES-permitted discharges of bacteria into this segment of Jarrels Creek. The location of the segment within the Jarrels Creek-Pond River watershed is shown in Figure D.16-1.

**Table D.16-3 Jarrels Creek 0.0 to 1.8 TMDL Allocations<sup>(1)</sup>**

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

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

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

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

<sup>(6)</sup>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.

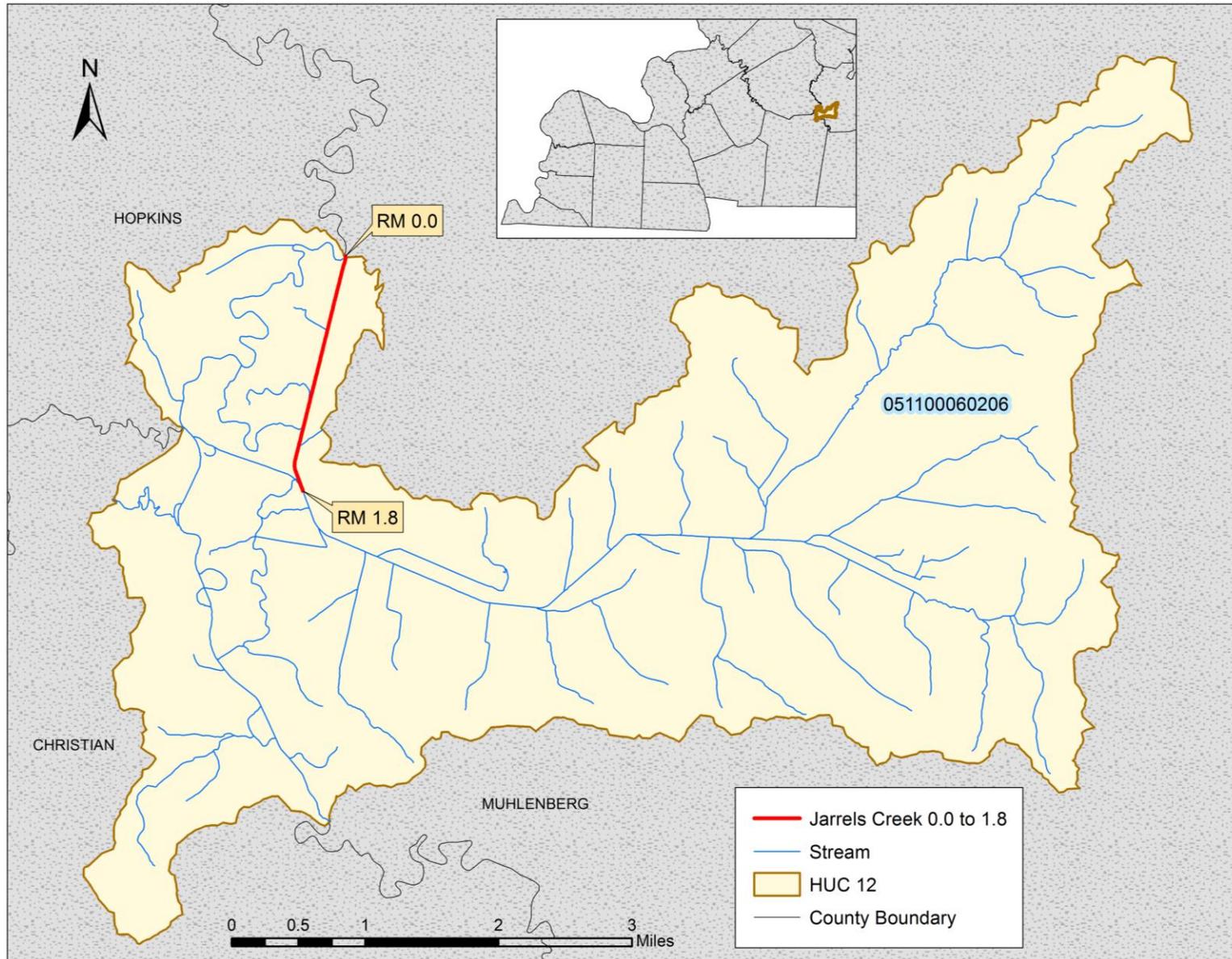


Figure D.16-1 Location of Jarrels Creek 0.0 to 1.8

**Section D.17 Knoblick Creek 0 to 2.1****Waterbody ID:** KY495848\_00**Receiving Water:** Panther Creek**Impaired Use:** PCR**Support Status:** nonsupport**Indicator Bacteria:** fecal coliform**HUC 12:** 051100050308**County:** Daviess

Western Kentucky University has collected samples from two stations on this segment. In 2001, five samples were collected from FC-T47. In 2007 and 2008, samples were collected from a nearby station as part of a study in the Panther Creek watershed. Table D.17-1 summarizes information about these sampling stations; Table D.17-2 provides a summary of the data collected from the stations.

**Table D.17-1 Western Kentucky University Sample Site Locations**

Station Name	Latitude	Longitude	Stream Segment	River Mile
FC-T47	37.7117	-87.3205	Knoblick Creek 0.0 to 2.1	1.45
CWRS_ST0001-LP04	37.71132	-87.32183	Knoblick Creek 0.0 to 2.1	1.53

**Table D.17-2 Western Kentucky University Sample Data Summary<sup>(1)</sup>**

Station Name	Indicator Bacteria	Number of Observations	Percent Exceeding WQC <sup>2</sup>	Minimum (colonies/100 ml)	Maximum (colonies/100 ml)	Average (colonies/100 ml)
FC-T47	fecal coliform	5	80.0	48	12,000	3,042
ST0001-LP04	<i>E. coli</i>	12	58.3	135	1,374	365

<sup>(1)</sup>The full data set for samples collected from these stations may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to [DEP.KORA@ky.gov](mailto:DEP.KORA@ky.gov) or by fax to 502-564-9232. The DEP KORA point of contact may also be reached at 502-564-3999.

<sup>(2)</sup>400 colonies/100 ml for fecal coliform; 240 colonies/100 ml for *E. coli*.

The TMDL allocations for Knoblick Creek 0.0 to 2.1 are presented in Table D.17-3. There are no KPDES-permitted discharges of bacteria into this segment of Knoblick Creek. The location of the segment within the Knoblick-Panther Creek watershed is shown in Figure D.17-1.

**Table D.17-3 Knoblick Creek 0.0 to 2.1 TMDL Allocations<sup>(1)</sup>**

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

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

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

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

<sup>(6)</sup>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.

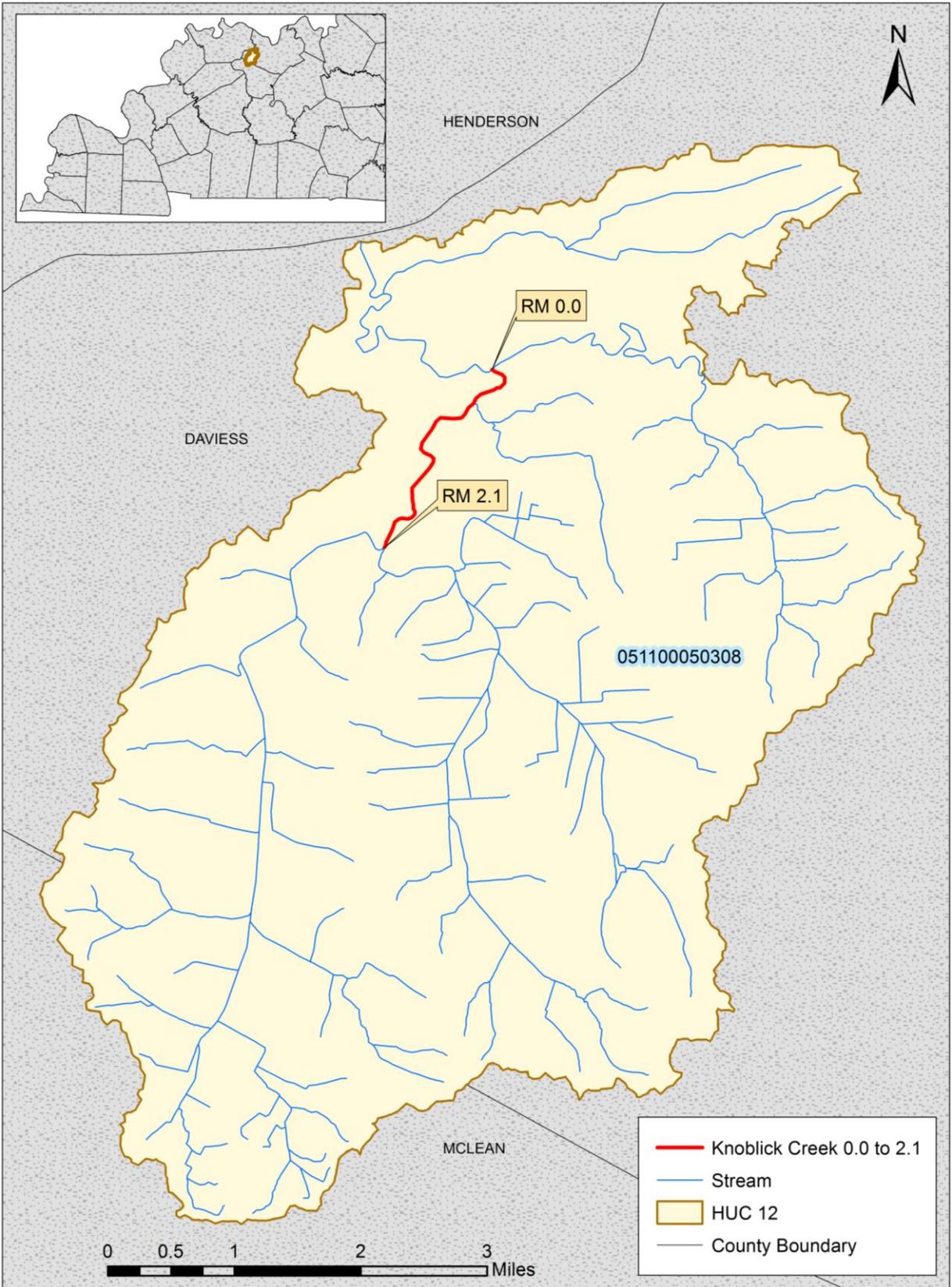


Figure D.17-1 Location of Knoblick Creek 0.0 to 2.1

**Section D.18 Long Falls Creek 0.0 to 7.6****Waterbody ID:** KY 497098\_01**Receiving Water:** Green River**Impaired Use:** PCR**Support Status:** nonsupport**Indicator Bacteria:** fecal coliform**HUC 12:** 051100050203, 051100050204**County:** McLean

In 2007 and 2008, Western Kentucky University collected samples from four stations as part of a study in the Long Falls Creek watershed. Table D.18-1 summarizes information about these sampling locations; Table D.18-2 provides a summary of the data collected from the stations.

**Table D.18-1 Western Kentucky University Sample Site Locations**

Station Name	Latitude	Longitude	Stream Segment	River Mile
CWRS_ST0001-LP06	37.56401	-87.2757	Long Falls Creek 0.0 to 7.6	2.95
CWRS_ST0001-LP07	37.53252	-87.2684	Long Falls Creek 0.0 to 7.6	0.23
CWRS_ST0001-LP08	37.58929	-87.2562	Long Falls Creek 0.0 to 7.6	5.7
CWRS_ST0001-LP54	37.58125	-87.2773	Long Falls Creek 0.0 to 7.6	4.35

**Table D.18-2 Western Kentucky University Sample Data Summary<sup>(1)</sup>**

Station Name	Indicator Bacteria	Number of Observations	Percent Exceeding WQC <sup>2</sup>	Minimum (colonies/100 ml)	Maximum (colonies/100 ml)	Average (colonies/100 ml)
ST0001-LP06	<i>E. coli</i>	11	18.2	41	602	188
ST0001-LP07	<i>E. coli</i>	9	55.6	121	759	337
ST0001-LP08	<i>E. coli</i>	12	58.3	122	495	280
ST0001-LP54	<i>E. coli</i>	11	81.8	218	504	315

<sup>(1)</sup>The full data set for samples collected from these stations may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to [DEP.KORA@ky.gov](mailto:DEP.KORA@ky.gov) or by fax to 502-564-9232. The DEP KORA point of contact may also be reached at 502-564-3999.

<sup>(2)</sup>400 colonies/100 ml for fecal coliform; 240 colonies/100 ml for *E. coli*.

The TMDL allocations for Long Falls Creek 0.0 to 7.6 are presented in Table D.18-3. There are no KPDES-permitted discharges of bacteria into this segment of Long Falls Creek. The location of the segment within the Long Falls Creek-Green River watershed is shown in Figure D.18-1.

**Table D.18-3 Long Falls Creek 0.0 to 7.6 TMDL Allocations<sup>(1)</sup>**

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

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

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

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

<sup>(6)</sup>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.

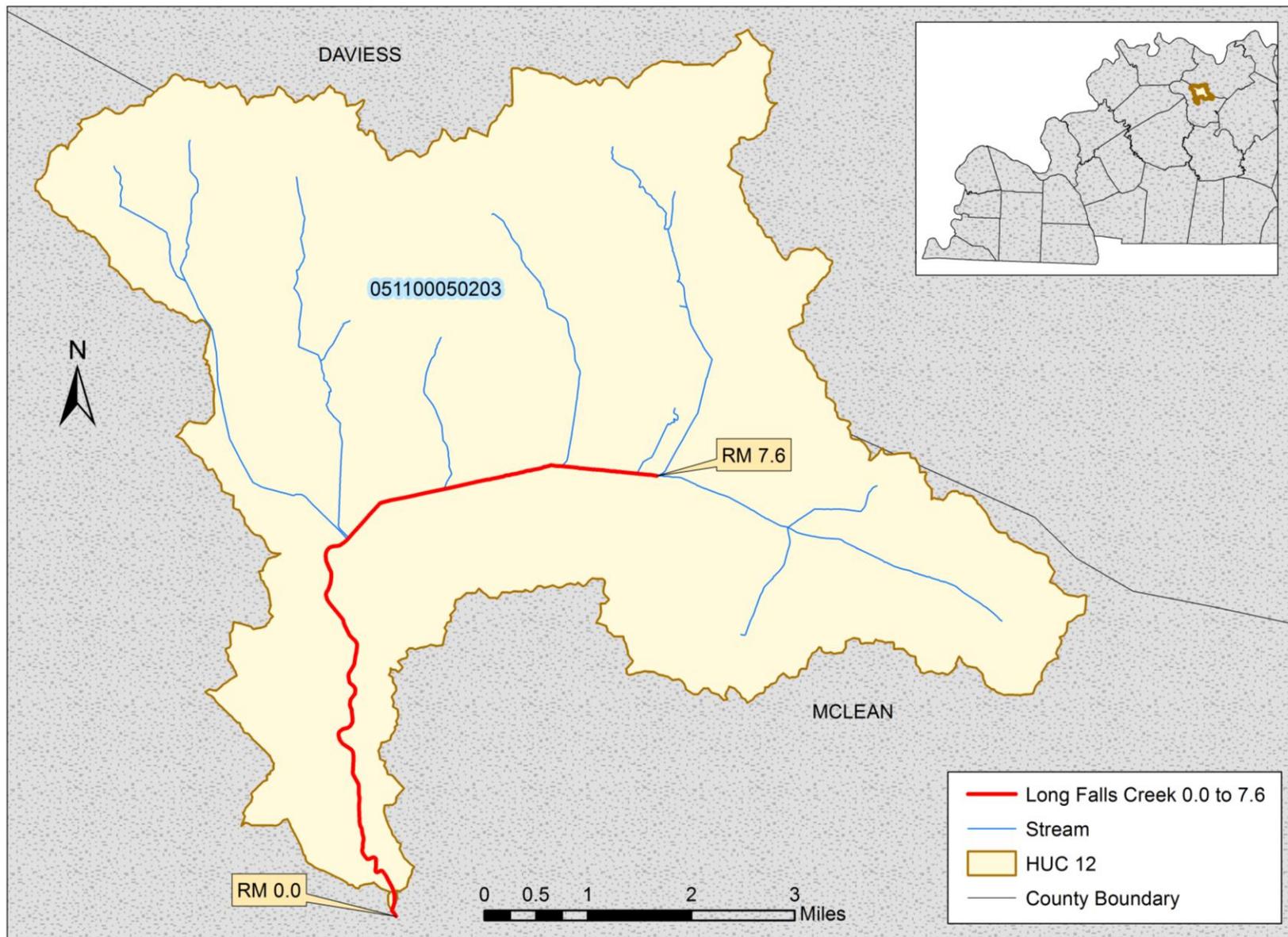


Figure D.18-1 Location of Long Falls Creek 0.0 to 7.6

**Section D.19 Long Falls Creek 7.6 to 11.9****Waterbody ID:** KY 497098\_02**Receiving Water:** Green River**Impaired Use:** PCR**Support Status:** nonsupport**Indicator Bacteria:** fecal coliform**HUC 12:** 051100050203**County:** McLean

In 2007 and 2008, Western Kentucky University collected samples from three stations as part of a study in the Long Falls Creek watershed. Table D.19-1 summarizes information about these sampling locations; Table D.19-2 provides a summary of the data collected from the stations.

**Table D.19-1 Western Kentucky University Sample Site Locations**

Station Name	Latitude	Longitude	Stream Segment	River Mile
CWRS_ST0001-LP12	37.58395	-87.20010	Long Falls Creek 7.6 to 11.9	8.95
CWRS_ST0001-LP13	37.58243	-87.19370	Long Falls Creek 7.6 to 11.9	9.3
CWRS_ST0001-LP14	37.57318	-87.16500	Long Falls Creek 7.6 to 11.9	11.0

**Table D.19-2 Western Kentucky University Sample Data Summary<sup>(1)</sup>**

Station Name	Indicator Bacteria	Number of Observations	Percent Exceeding WQC <sup>2</sup>	Minimum (colonies/100 ml)	Maximum (colonies/100 ml)	Average (colonies/100 ml)
ST0001-LP12	<i>E. coli</i>	8	75.0	20	2,613	583
ST0001-LP13	<i>E. coli</i>	10	90.0	40	2,098	625
ST0001-LP14	<i>E. coli</i>	4	75.0	86	565	286

<sup>(1)</sup>The full data set for samples collected from these stations may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to [DEP.KORA@ky.gov](mailto:DEP.KORA@ky.gov) or by fax to 502-564-9232. The DEP KORA point of contact may also be reached at 502-564-3999.

<sup>(2)</sup>400 colonies/100 ml for fecal coliform; 240 colonies/100 ml for *E. coli*.

The TMDL allocations for Long Falls Creek 7.6 to 11.9 are presented in Table D.19-3. There are no KPDES-permitted discharges of bacteria into this segment of Long Falls Creek. The location of the segment within the Long Falls Creek watershed is shown in Figure D.19-1.

**Table D.19-3 Long Falls Creek 7.6 to 11.9 TMDL Allocations<sup>(1)</sup>**

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

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

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

<sup>(5)</sup>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.

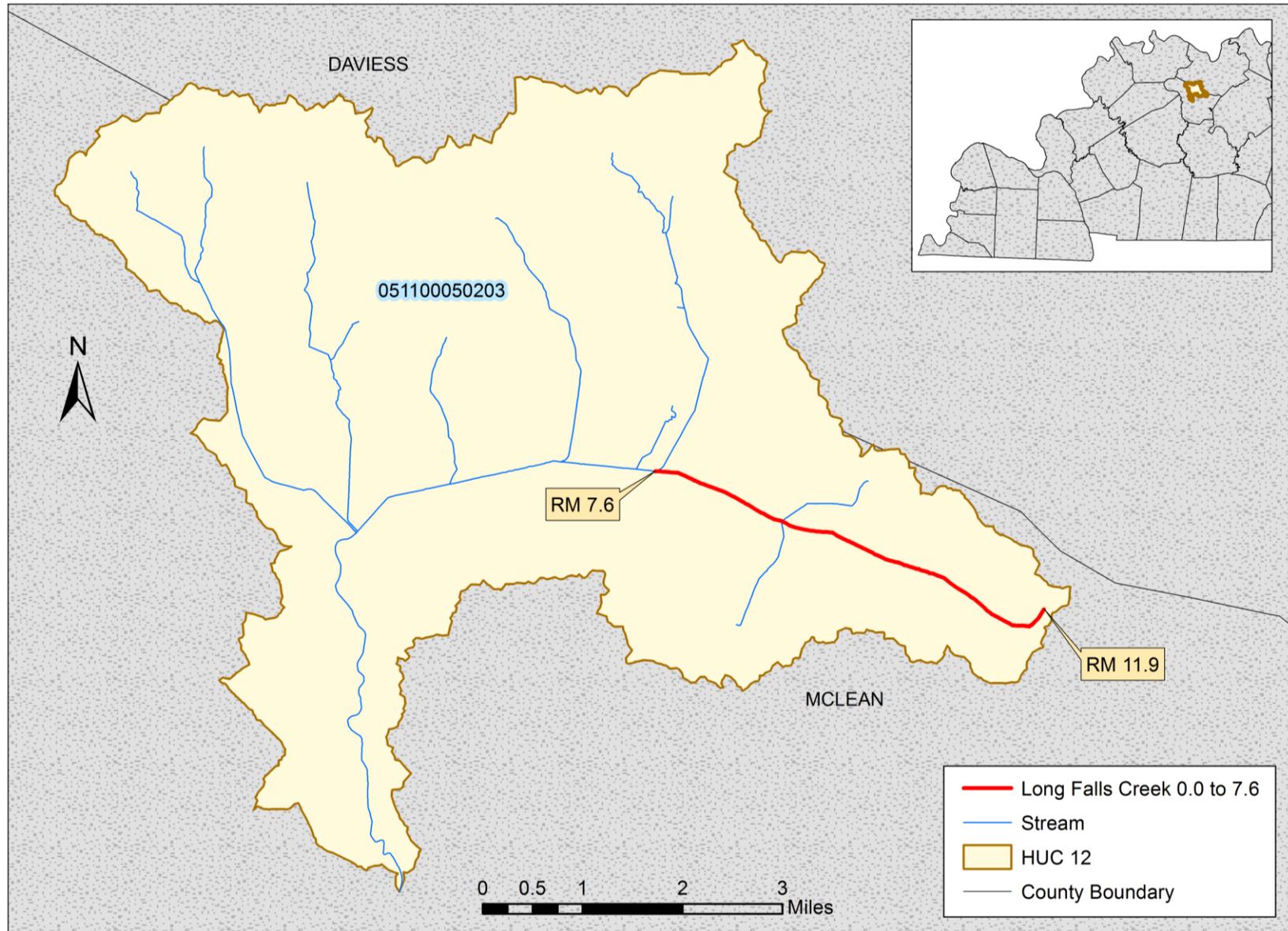


Figure D.19-1 Location of Long Falls Creek 7.6 to 11.9

**Section D.20 Mill Creek 0.0 to 4.2****Waterbody ID:** KY498260\_00**Receiving Water:** Smith Creek (incorrectly identified as Spring Creek in the 2014 303(d) list)**Impaired Use:** PCR**Support Status:** nonsupport**Indicator Bacteria:** fecal coliform**HUC 12:** 051100040404**County:** Ohio

In 2001 Western Kentucky University collected five samples at station FC T-35. Table D.20-1 summarizes information about this sampling station; Table D.20-2 provides a summary of the data collected from this station.

**Table D.20-1 Western Kentucky University Sample Site Location**

Station Name	Latitude	Longitude	Stream Segment	River Mile
FC-T35	37.63640	-86.75660	Mill Creek 0.0 to 4.2	2.5

**Table D.20-2 Western Kentucky University Sample Data Summary<sup>(1)</sup>**

Station Name	Indicator Bacteria	Number of Observations	Percent Exceeding WQC <sup>2</sup>	Minimum (colonies/100 ml)	Maximum (colonies/100 ml)	Average (colonies/100 ml)
FC-T35	fecal coliform	5	40.0	8	2,280	648

<sup>(1)</sup>The full data set for samples collected from FC T-35 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to [DEP.KORA@ky.gov](mailto:DEP.KORA@ky.gov) or by fax to 502-564-9232. The DEP KORA point of contact may also be reached at 502-564-3999.

<sup>(2)</sup>400 colonies/100 ml for fecal coliform; 240 colonies/100 ml for *E. coli*.

The TMDL allocations for Mill Creek 0.0 to 4.2 are presented in Table D.20-3. There are no KPDES-permitted discharges of bacteria into this segment of Mill Creek. The location of the segment within the Adams Fork watershed is shown in Figure D.20-1.

**Table D.20-3 Mill Creek 0.0 to 4.2 TMDL Allocations<sup>(1)</sup>**

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

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

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

<sup>(5)</sup>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.

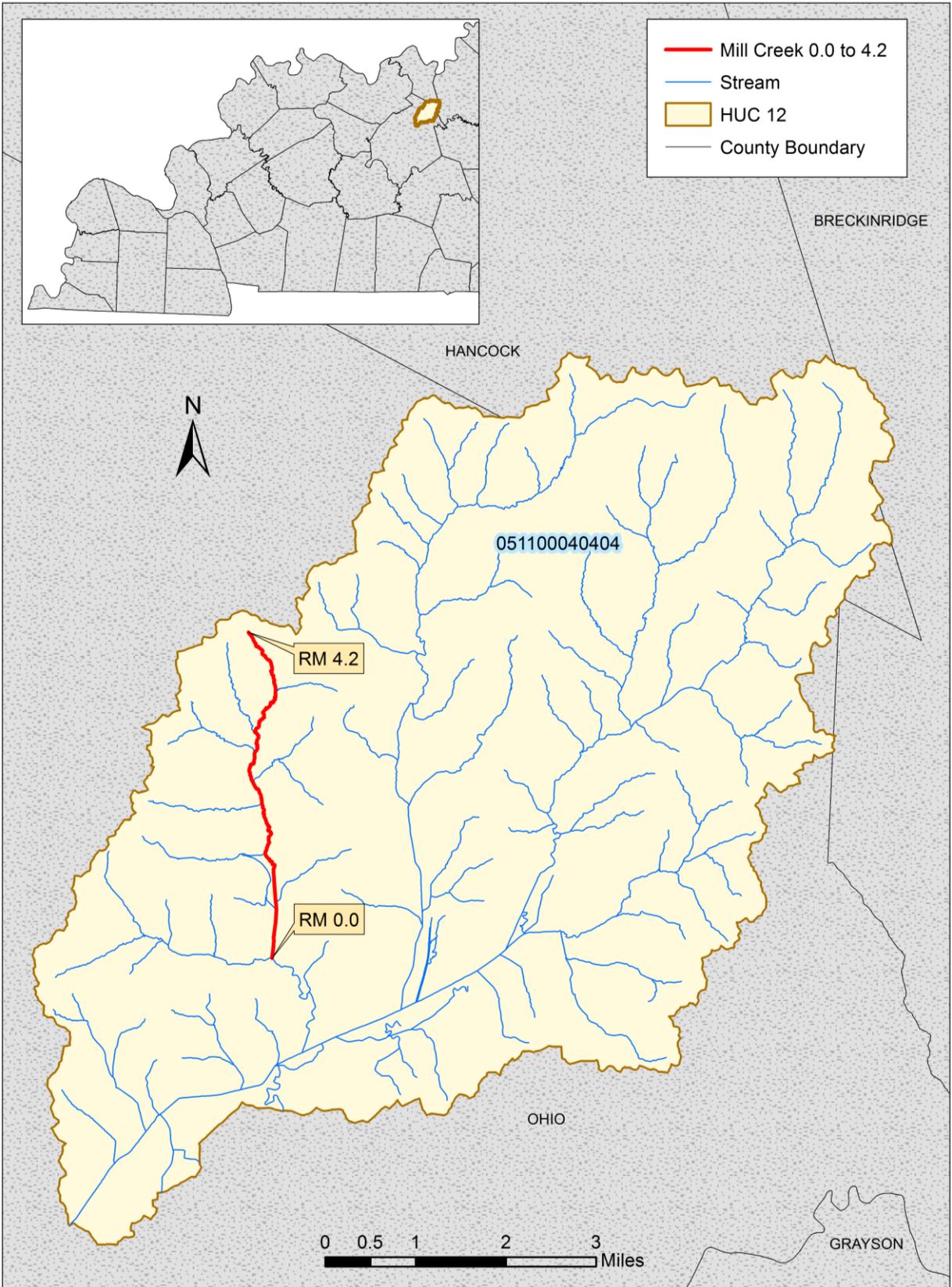


Figure D.20-1 Location of Mill Creek 0.0 to 4.2

**Section D.21 North Fork of Panther Creek 4.2 to 9.1****Waterbody ID:** KY499562\_02**Receiving Water:** Panther Creek**Impaired Use:** PCR**Support Status:** nonsupport**Indicator Bacteria:** fecal coliform**HUC 12:** 051100050305**County:** Daviess

Western Kentucky University has collected samples from three stations on this segment. In 2001, five samples were collected from FC-T41. In 2007 and 2008, samples were collected from two other stations as part of a study in the Panther Creek watershed. Table D.21-1 summarizes information about these sampling stations; Table D.21-2 provides a summary of the data collected from the stations.

**Table D.21-1 Western Kentucky University Sample Site Locations**

Station Name	Latitude	Longitude	Stream Segment	RM
FC T-41	37.72490	-86.99150	North Fork of Panther Creek 4.2 to 9.1	5.85
CWRS_ST0001-LP32	37.72529	-86.99220	North Fork of Panther Creek 4.2 to 9.1	5.74
CWRS_ST0001-LP46	37.72200	-86.97200	North Fork of Panther Creek 4.2 to 9.1	6.9

**Table D.21-2 Western Kentucky University Sample Data Summary<sup>(1)</sup>**

Station Name	Indicator Bacteria	Number of Observations	Percent Exceeding WQC <sup>2</sup>	Minimum (colonies/100 ml)	Maximum (colonies/100 ml)	Average (colonies/100 ml)
FC T-41	fecal coliform	5	60.0	32	12,000	4,928
ST0001-LP32	<i>E. coli</i>	11	45.5	41	2,420	644
ST0001-LP46	<i>E. coli</i>	12	58.3	41	2,382	622

<sup>(1)</sup>The full data set for samples collected from these stations may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to [DEP.KORA@ky.gov](mailto:DEP.KORA@ky.gov) or by fax to 502-564-9232. The DEP KORA point of contact may also be reached at 502-564-3999.

<sup>(2)</sup>400 colonies/100 ml for fecal coliform; 240 colonies/100 ml for *E. coli*.

The TMDL allocations for the North Fork of Panther Creek 4.2 to 9.1 are presented in Table D.21-3. There are no KPDES-permitted discharges of bacteria into this segment of North Fork of Panther Creek. The location of the segment within the North Fork Panther Creek watershed is shown in Figure D.21-1.

**Table D.21-3 North Fork of Panther Creek 4.2 to 9.1 TMDL Allocations<sup>(1)</sup>**

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

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

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

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

<sup>(6)</sup>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.

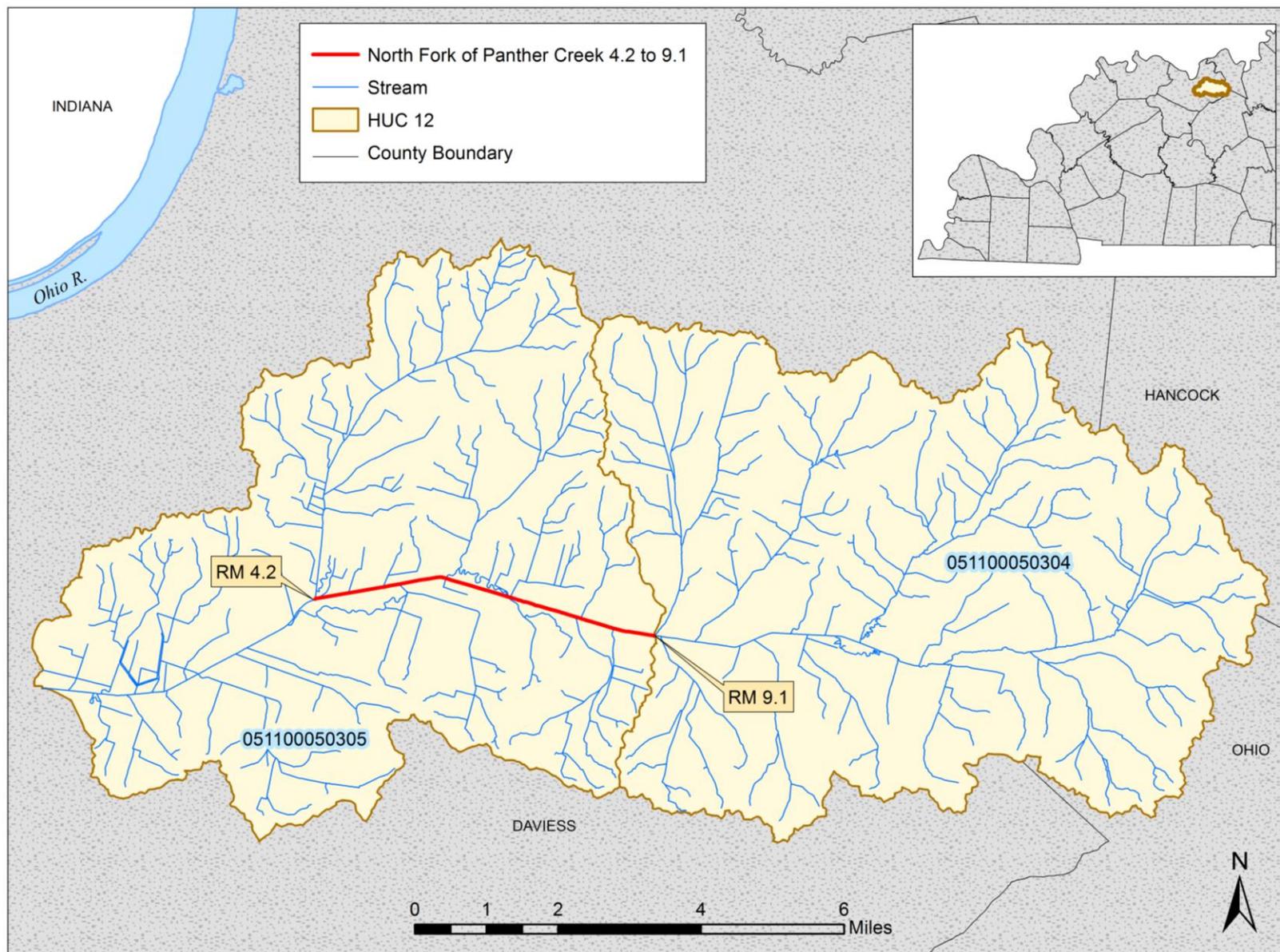


Figure D.21-1 Location of North Fork of Panther Creek 4.2 to 9.1

**Section D.22 Panther Creek 0.1 to 3.0****Waterbody ID:** KY500157\_01**Receiving Water:** Green River**Impaired Use:** PCR, SCR**Support Status:** nonsupport (both uses)**Indicator Bacteria:** *E. coli* (PCR), fecal coliform (SCR)**HUC 12:** 051100050308**County:** Daviess

The Division of Water has collected samples from station PRI 113, located at RM 2.65, since 2005. The station typically has been sampled three or more times during the PCR season. Western Kentucky University also collected samples at a nearby station in 2007 and 2008 as part of a study of the Panther Creek watershed. Table D.22-1 summarizes information about these sampling stations; Table D.22-2 provides a summary of the data collected from the stations.

**Table D.22-1 Sample Site Locations**

Station Name	Latitude	Longitude	Stream Segment	River Mile
PRI113	37.724965	-87.315125	Panther Creek 0.1 to 3.0	2.65
CWRS_ST0001-LP03	37.72486	-87.31525	Panther Creek 0.1 to 3.0	2.42

**Table D.22-2 Sample Data Summary<sup>(1)</sup>**

Station Name	Indicator Bacteria	Number of Observations	Percent Exceeding WQC <sup>2</sup>	Minimum (colonies/100 ml)	Maximum (colonies/100 ml)	Average (colonies/100 ml)
PRI113	fecal coliform	3	33.3	100	24,000	8,070
PRI113	<i>E. coli</i>	40	47.5	3	2,420	478
ST0001-LP03	<i>E. coli</i>	11	54.5	63	2,420	744

<sup>(1)</sup>The full data set for samples collected from these stations may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to [DEP.KORA@ky.gov](mailto:DEP.KORA@ky.gov) or by fax to 502-564-9232. The DEP KORA point of contact may also be reached at 502-564-3999.

<sup>(2)</sup>2,000 colonies/100 ml for fecal coliform; 240 colonies/100 ml for *E. coli*.

The TMDL allocations for Panther Creek 0.1 to 3.0 are presented in Table D.22-3. There are no KPDES-permitted discharges of bacteria into this segment of Panther Creek. The location of the segment within the Knoblick-Panther Creek watershed is shown in Figure D.22-1.

**Table D.22-3 Panther Creek 0.1 to 3.0 TMDL Allocations<sup>(1)</sup>**

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

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

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

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

<sup>(6)</sup>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.

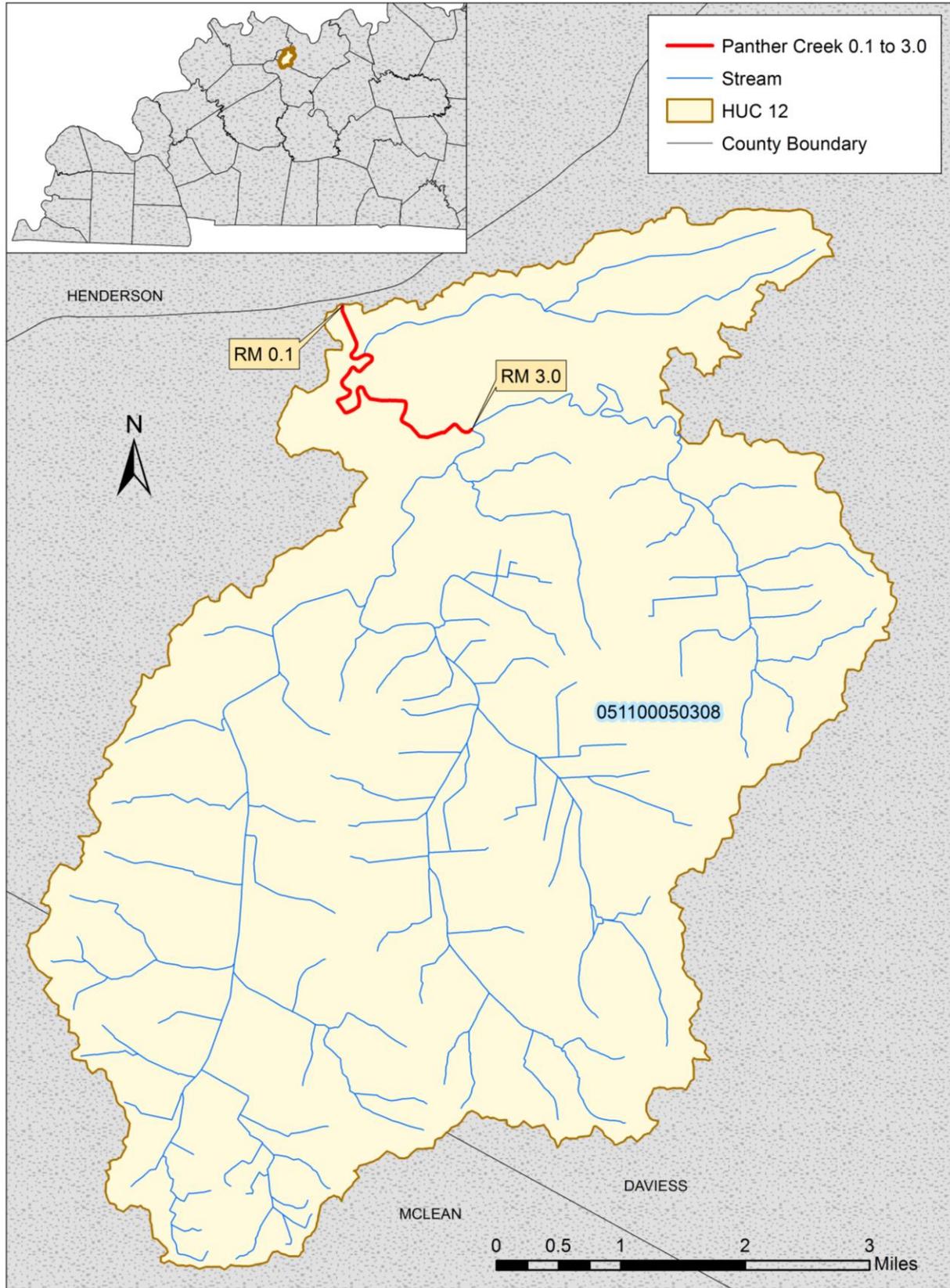


Figure D.22-1 Location of Panther Creek 0.1 to 3.0

**Section D.23 Panther Creek 3.0 to 5.9****Waterbody ID:** KY500157\_02**Receiving Water:** Green River**Impaired Use:** PCR**Support Status:** nonsupport**Indicator Bacteria:** fecal coliform**HUC 12:** 051100050308**County:** Daviess

The Division of Water collected samples from station PRI 070, located at river mile 5.75, between 1998 and 2005. The station typically was sampled three or more times during the PCR season, although no samples were collected in 2004. Western Kentucky University also collected samples at a nearby station in 2007 and 2008 as part of a study of the Panther Creek watershed. Table D.23-1 summarizes information about these sampling stations; Table D.23-2 provides a summary of the data collected from the stations.

**Table D.23-1 Sample Site Locations**

Station Name	Latitude	Longitude	Stream Segment	River Mile
PRI070	37.7273055	-87.2806944	Panther Creek 3.0 to 5.9	5.75
CWRS_ST0001-LP05	37.72737	-87.28172	Panther Creek 3.0 to 5.9	5.7

**Table D.23-2 Sample Data Summary<sup>(1)</sup>**

Station Name	Indicator Bacteria	Number of Observations	Percent Exceeding WQC <sup>2</sup>	Minimum (colonies/100 ml)	Maximum (colonies/100 ml)	Average (colonies/100 ml)
PRI070	fecal coliform	34	38.2	10	7,400	707
ST0001-LP05	<i>E. coli</i>	10	40.0	52	1,785	463

<sup>(1)</sup>The full data set for samples collected from these stations may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to [DEP.KORA@ky.gov](mailto:DEP.KORA@ky.gov) or by fax to 502-564-9232. The DEP KORA point of contact may also be reached at 502-564-3999.

<sup>(2)</sup>400 colonies/100 ml for fecal coliform; 240 colonies/100 ml for *E. coli*.

The TMDL allocations for Panther Creek 3.0 to 5.9 are presented in Table D.23-3. There are no KPDES-permitted discharges of bacteria into this segment of Panther Creek. The location of the segment within the Knoblick-Panther Creek watershed is shown in Figure D.23-1.

**Table D.23-3 Panther Creek 3.0 to 5.9 TMDL Allocations<sup>(1)</sup>**

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

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

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

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

<sup>(6)</sup>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.

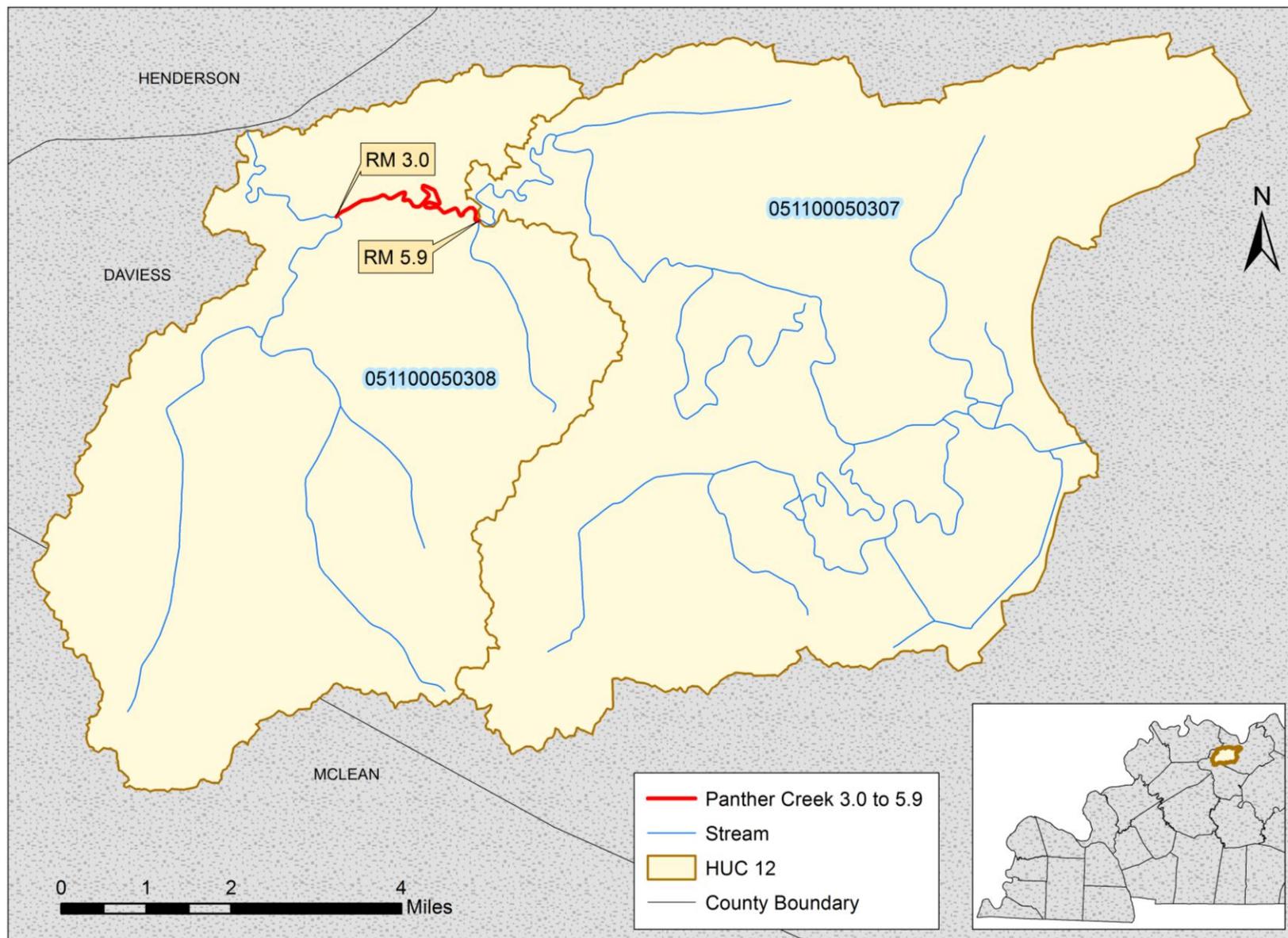


Figure D.23-1 Location of Panther Creek 3.0 to 5.9

**Section D.24 Pond Run 0.0 to 6.75****Waterbody ID:** KY501057\_01**Receiving Water:** Rough River**Impaired Use:** PCR**Support Status:** partial support**Indicator Bacteria:** *E. coli***HUC 12:** 051100040306**County:** Breckinridge

The Division of Water collected several samples from station DOW03007008 at river mile 2.55 during the 2006 PCR season, and additional samples from station GRN 032 at river mile 2.65 during the 2011 PCR season. Table D.24-1 summarizes information about these sampling stations; Table D.24-2 provides a summary of the data collected from the stations.

**Table D.24-1 Division of Water Sample Site Locations**

Station Name	Latitude	Longitude	Stream Segment	River Mile
DOW03007008	37.585391	-86.619369	Pond Run 0 to 6.75	2.55
GRN 032	37.58713	-86.6201	Pond Run 0 to 6.75	2.65

**Table D.24-2 Division of Water Sample Data Summary<sup>(1)</sup>**

Station Name	Indicator Bacteria	Number of Observations	Percent Exceeding WQC <sup>2</sup>	Minimum (colonies/100 ml)	Maximum (colonies/100 ml)	Average (colonies/100 ml)
DOW03007008	fecal coliform	3	33.3	100	1,500	590
DOW03007008	<i>E. coli</i>	1	0.0	129	129	129
GRN 032	<i>E. coli</i>	5	40.0	22	365	163

<sup>(1)</sup>The full data set for samples collected from these stations may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to [DEP.KORA@ky.gov](mailto:DEP.KORA@ky.gov) or by fax to 502-564-9232. The DEP KORA point of contact may also be reached at 502-564-3999.

<sup>(2)</sup>400 colonies/100 ml for fecal coliform; 240 colonies/100 ml for *E. coli*.

The TMDL allocations for Pond Run 0.0 to 6.75 are presented in Table D.24-3. There are no KPDES-permitted discharges of bacteria into this segment of Pond Run. The location of the segment within the Pipe Run-Rough River watershed is shown in Figure D.24-1.

**Table D.24-3 Pond Run 0.0 to 6.75 TMDL Allocations<sup>(1)</sup>**

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

<sup>(1)</sup>All loads are colonies/day of either *E. coli* or fecal coliform. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft<sup>3</sup>-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft<sup>3</sup>/s) into a load (colonies/day). The symbol “ $\Sigma$ ” indicates that the total allocation is the sum of all the individual allowable loads.

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

<sup>(5)</sup>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.

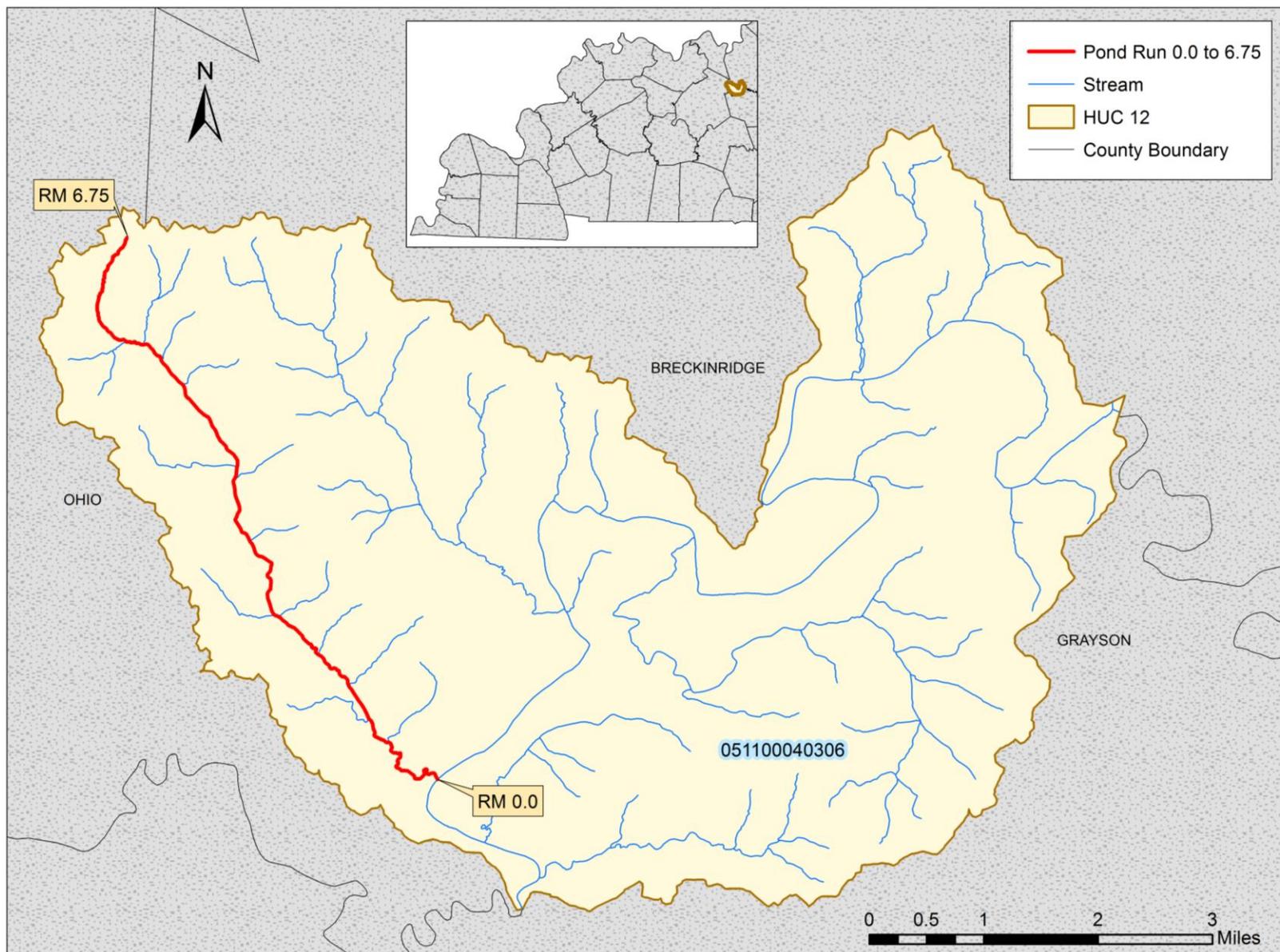


Figure D.24-1 Location of Pond Run 0.0 to 6.75

**Section D.25 Rough River 0.1 to 10.45****Waterbody ID:** KY502390\_01**Receiving Water:** Green River**Impaired Use:** SCR**Support Status:** partial support**Indicator Bacteria:** fecal coliform**HUC 12:** 051100040507**County:** Ohio

The Division of Water has collected samples from station PRI 054 since 1998. The station was located at river mile 1.0 in 1998 and was moved to river mile 7.15 afterward. The station typically has been sampled two or more times each year, although it was not sampled in 2004 and only once in 2002. Table D.34-1 summarizes information about this sampling station; Table D.25-2 provides a summary of the data collected from this station.

**Table D.25-1 Division of Water Sample Site Locations**

Station Name	Latitude	Longitude	Stream Segment	River Mile
PRI 054	37.484194	-87.118778	Rough River 0.1 to 10.45	1.0
PRI 054	37.499	-87.0656	Rough River 0.1 to 10.45	7.15

**Table D.25-2 Division of Water Sample Data Summary<sup>(1)</sup>**

Station Name	Indicator Bacteria	Number of Observations	Percent Exceeding WQC <sup>2</sup>	Minimum (colonies/100 ml)	Maximum (colonies/100 ml)	Average (colonies/100 ml)
PRI 054 (RM 1.0)	fecal coliform	4	0.0	46	230	114
PRI 054 (RM 7.15)	fecal coliform	28	10.7	10	33,000	1,518

<sup>(1)</sup>The full data set for samples collected from PRI 054 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to [DEP.KORA@ky.gov](mailto:DEP.KORA@ky.gov) or by fax to 502-564-9232. The DEP KORA point of contact may also be reached at 502-564-3999.

<sup>(2)</sup>2,000 colonies/100 ml for fecal coliform.

The TMDL allocations for Rough River 0.1 to 10.45 are presented in Table D.25-3. There are no KPDES-permitted discharges of bacteria into this segment of Rough River. The segment's location within the Muddy Creek-Rough River watershed is shown in Figure D.25-1.

**Table D.25-3 Rough River 0.1 to 10.45 TMDL Allocations<sup>(1)</sup>**

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

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

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

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

<sup>(6)</sup>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.

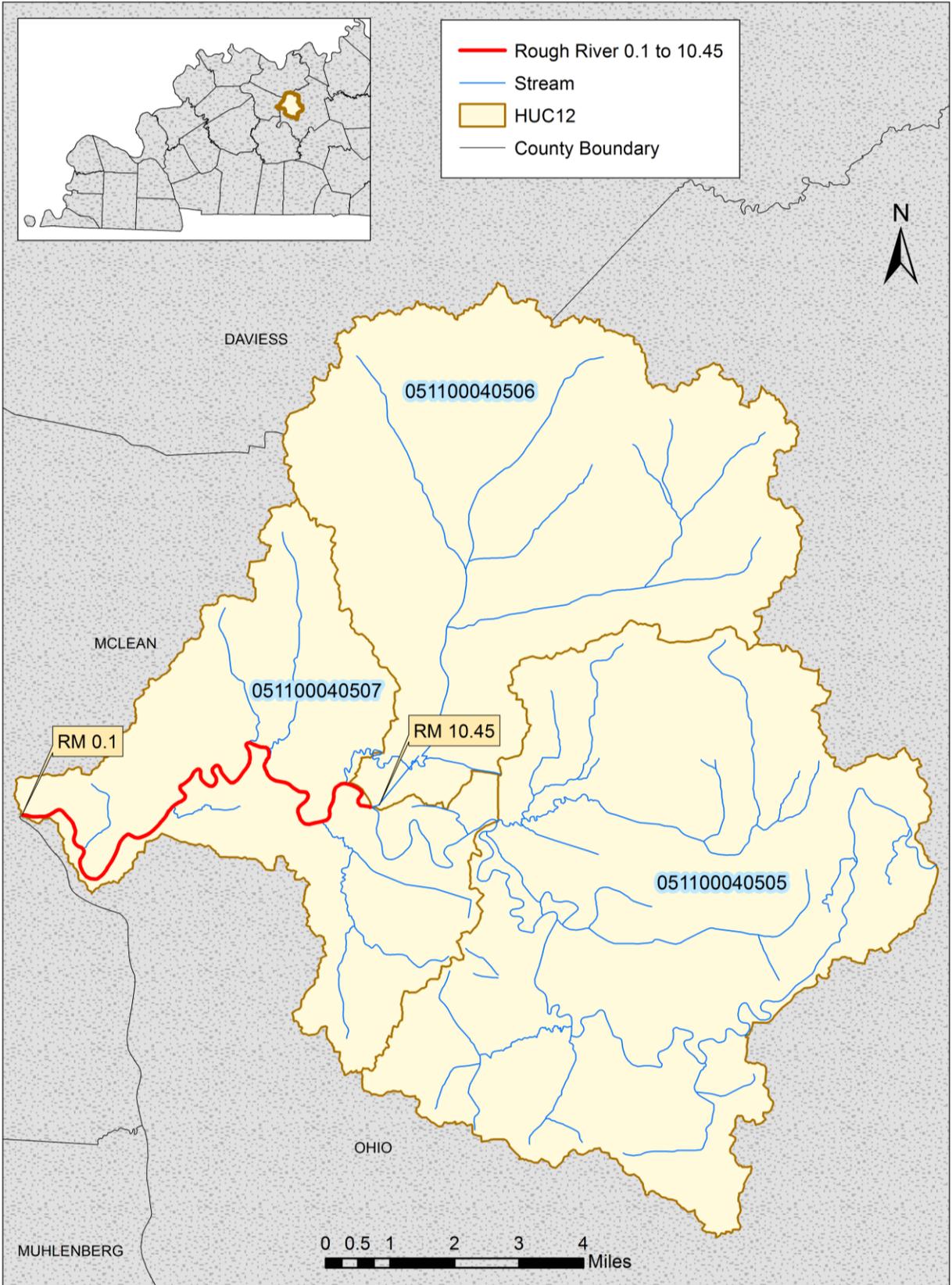


Figure D.25-1 Location of Rough River 0.1 to 10.45

**Section D.26 Rough River 125.2 to 149.4****Waterbody ID:** KY502390\_06**Receiving Water:** Green River**Impaired Use:** PCR**Support Status:** partial support**Indicator Bacteria:** fecal coliform**HUC 12:** 051100040106**County:** Hardin

The Division of Water has collected samples from station GRN 016, located at river mile 129.95, since 2001. The station has been sampled five or more times during the PCR season as part of the Division's five-year rotating schedule for basin monitoring (see also Section 7.2.1, Kentucky Watershed Management Framework). Table D.26-1 summarizes information about this sampling station; Table D.26-2 provides a summary of the data collected from this station.

**Table D.26-1 Division of Water Sample Site Location**

Station Name	Latitude	Longitude	Stream Segment	River Mile
GRN 016	37.6098	-86.2588	Rough River 125.2 to 149.4	129.95

**Table D.26-2 Division of Water Sample Data Summary<sup>(1)</sup>**

Station Name	Indicator Bacteria	Number of Observations	Percent Exceeding WQC <sup>2</sup>	Minimum (colonies/100 ml)	Maximum (colonies/100 ml)	Average (colonies/100 ml)
GRN 016	fecal coliform	5	0.0	1	382	211
GRN 016	<i>E. coli</i>	16	43.8	60.2	1,046	320

<sup>(1)</sup>The full data set for samples collected from GRN 016 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to [DEP.KORA@ky.gov](mailto:DEP.KORA@ky.gov) or by fax to 502-564-9232. The DEP KORA point of contact may also be reached at 502-564-3999.

<sup>(2)</sup>400 colonies/100 ml for fecal coliform; 240 colonies/100 ml for *E. coli*.

The TMDL allocations for Rough River 125.2 to 149.4 are presented in Table D.26-3. There are no KPDES-permitted discharges of bacteria into this segment of Rough River. The segment's location within the Clifty Creek-Rough River watershed is shown in Figure D.26-1.

**Table D.26-3 Rough River 125.2 to 149.4 TMDL Allocations<sup>(1)</sup>**

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

<sup>(1)</sup>All loads are colonies/day of either *E. coli* or fecal coliform. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s·ml/ft<sup>3</sup>-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft<sup>3</sup>/s) into a load (colonies/day). The symbol “ $\Sigma$ ” indicates that the total allocation is the sum of all the individual allowable loads.

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

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

<sup>(6)</sup>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.

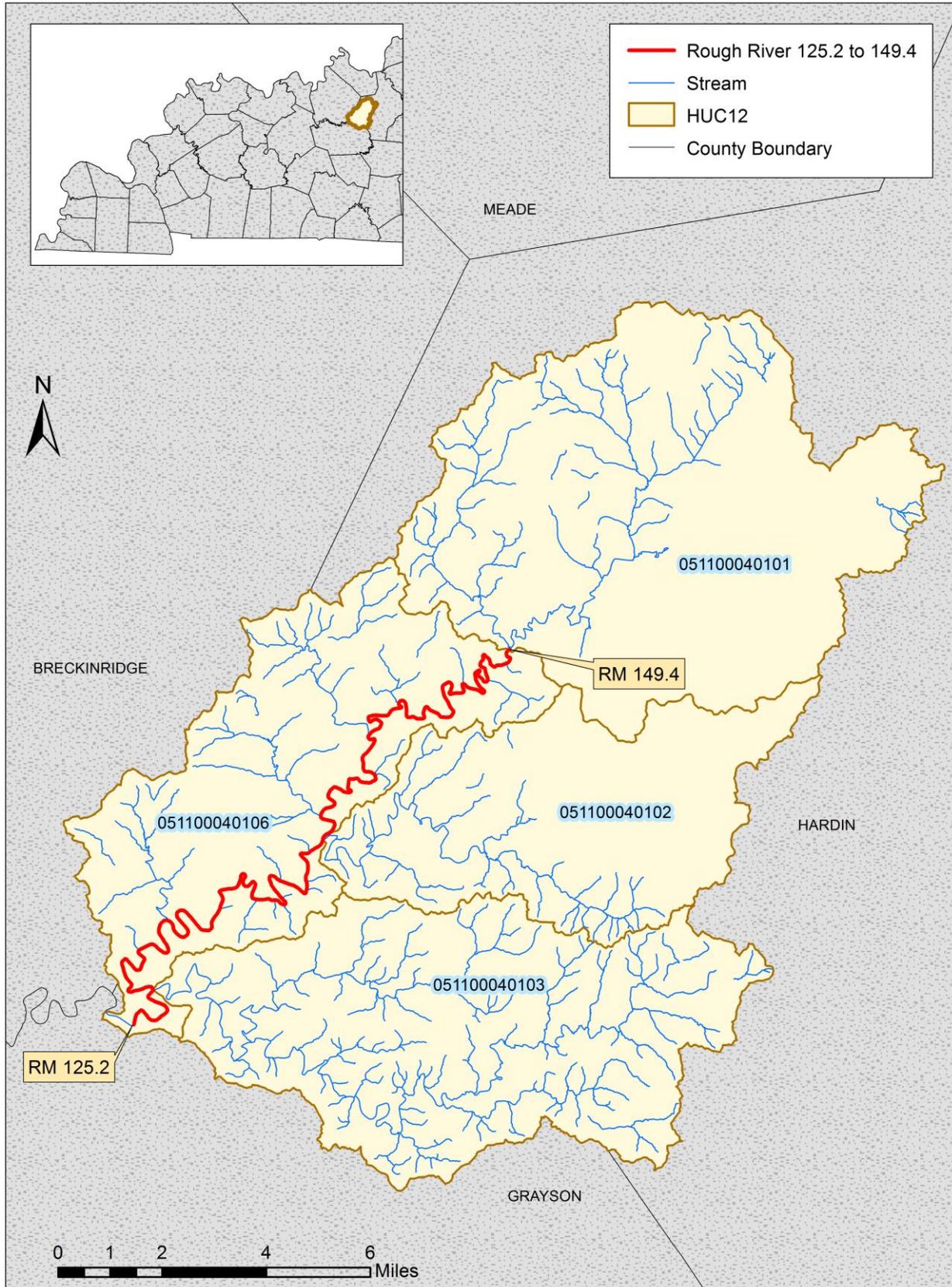


Figure D.26-1 Location of Rough River 125.2 to 149.4

The segment is located in an area where karst features such as sinkholes, sinking streams and springs exist. Groundwater dye traces in the area indicate that groundwater flow paths do not always follow the topographic boundaries of the watershed (see Figure D.26-2). This segment of Rough River may receive surface runoff via karst conduits from areas north and east, respectively, of the 051100040101 and -02 HUC boundaries. For more information about karst, see Section 3.2, Karst.

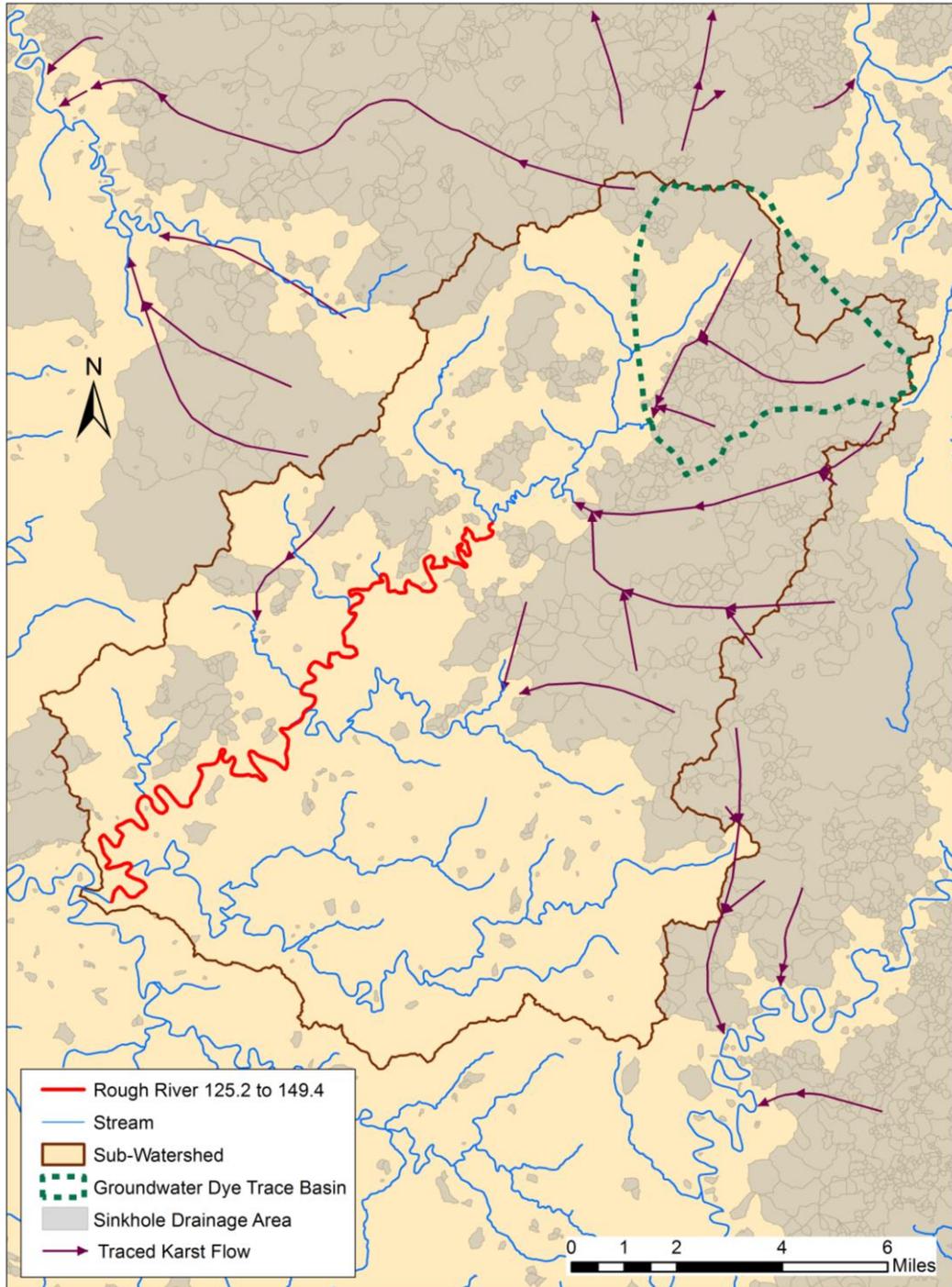


Figure D.26-2 Karst Influence in the Region of Rough River 125.2 to 149.4

**Section D.27 Rough River 55.1 to 64.5****Waterbody ID:** KY502390\_04**Receiving Water:** Green River**Impaired Use:** PCR, SCR**Support Status:** nonsupport (both uses)**Indicator Bacteria:** *E. coli* (PCR), fecal coliform (SCR)**HUC 12:** 051100040405**County:** Ohio

The Division of Water has collected samples from station PRI 014, located at river mile 62.9, since 1980. The station was sampled year-round until 1995. Beginning in 1996, the sampling routine changed to multiple visits each year during the PCR season, although the station was not sampled in 2004. Samples were analyzed for fecal coliform through October, 2006; samples were analyzed for *E. coli* beginning in July, 2006. Table D.27-1 summarizes information about this sampling station; Table D.27-2 provides a summary of the data collected from this station.

**Table D.27-1 Division of Water Sample Site Location**

Station Name	Latitude	Longitude	Stream Segment	River Mile
PRI 014	37.547201	-86.721393	Rough River 55.1 to 64.5	62.9

**Table D.27-2 Division of Water Sample Data Summary<sup>(1)</sup>**

Station Name	Indicator Bacteria	Number of Observations	Percent Exceeding WQC <sup>2</sup>	Minimum (colonies/100 ml)	Maximum (colonies/100 ml)	Average (colonies/100 ml)
PRI 014	fecal coliform	213	3.8	1	60,000	558
PRI 014	<i>E. coli</i>	36	30.6	6	2,420	522

<sup>(1)</sup>The full data set for samples collected from PRI 014 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to [DEP.KORA@ky.gov](mailto:DEP.KORA@ky.gov) or by fax to 502-564-9232. The DEP KORA point of contact may also be reached at 502-564-3999.

<sup>(2)</sup>2,000 colonies/100 ml for fecal coliform; 240 colonies/100 ml for *E. coli*. Among fecal coliform samples collected during the PCR season through 2006, 16.8 percent exceeded the WQC of 400 colonies/100 ml.

The TMDL allocations for Rough River 55.1 to 64.5 are presented in Table D.27-3. There are no KPDES-permitted discharges of bacteria into this segment of Rough River. The location of the segment within the Mistaken Creek-Rough River watershed is shown in Figure D.27-1.

**Table D.27-3 Rough River 55.1 to 64.5 TMDL Allocations<sup>(1)</sup>**

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

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

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

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

<sup>(6)</sup>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.

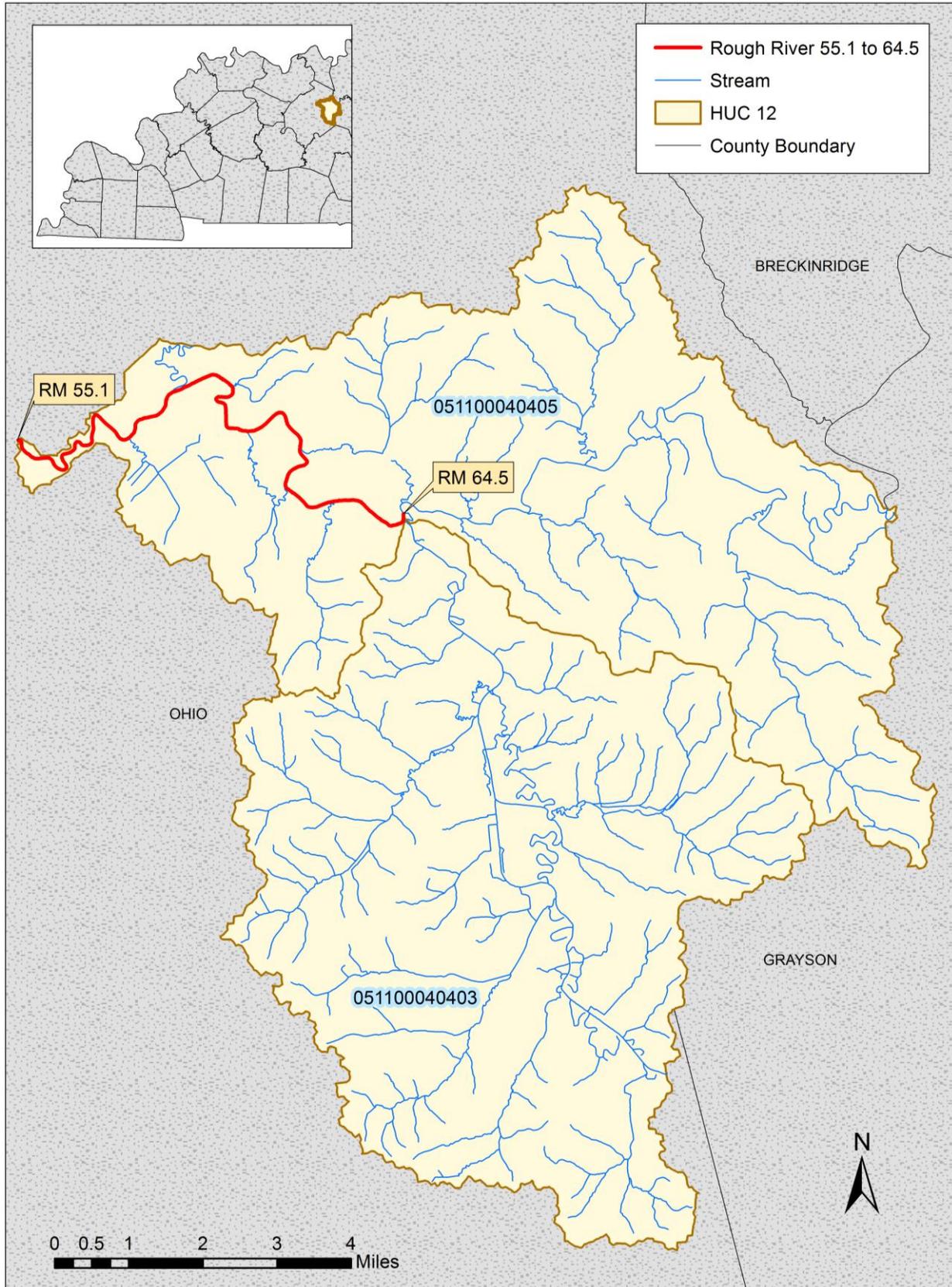


Figure D.27-1 Location of Rough River 55.1 to 64.5

**Section D.28 Skaggs Creek 12.7 to 23.55****Waterbody ID:** KY503595\_01**Receiving Water:** Barren River**Impaired Use:** PCR**Support Status:** nonsupport**Bacteria Indicator:** *E. coli***HUC 12:** 051100020307**County:** Barren

The Division of Water has collected samples from station GRN 024, located at RM 20.4, since 2001. The station has been sampled five to six times during the PCR season as part of the Division's five-year rotating schedule for basin monitoring (see also Section 7.2.1, Kentucky Watershed Management Framework). Table D.28-1 summarizes information about this sampling station; Table D.28-2 provides a summary of the data collected from this station.

**Table D.28-1 Division of Water Sample Site Location**

Station Name	Latitude	Longitude	Stream Segment	River Mile
GRN 024	36.9073	-85.939	Skaggs Creek 12.7 to 23.55	20.4

**Table D.28-2 Division of Water Sample Data Summary<sup>(1)</sup>**

Station Name	Indicator Bacteria	Number of Observations	Percent Exceeding WQC <sup>2</sup>	Minimum (colonies/100 ml)	Maximum (colonies/100 ml)	Average (colonies/100 ml)
GRN 024	fecal coliform	5	40.0	1	2,000	684
GRN 024	<i>E. coli</i>	17	41.2	41	2,420	688

<sup>(1)</sup>The full data set for samples collected from GRN 024 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to [DEP.KORA@ky.gov](mailto:DEP.KORA@ky.gov) or by fax to 502-564-9232. The DEP KORA point of contact may also be reached at 502-564-3999.

<sup>(2)</sup>400 colonies/100 ml for fecal coliform; 240 colonies/100 ml for *E. coli*.

The TMDL allocations for Skaggs Creek 12.7 to 23.55 are presented in Table D.28-3. There are no KPDES-permitted discharges into this segment of Skaggs Creek.

**Table D.28-3 Skaggs Creek 12.7 to 23.55 TMDL Allocations<sup>(1)</sup>**

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

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

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

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

<sup>(6)</sup>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 location of the segment within the Boyds Creek-Skaggs Creek watershed is shown in Figure D.28-1. Some karst features such as sinkholes and sinking springs 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 Boyds Creek-Skaggs Creek watershed. For more detailed information about karst geology, see Section 3.2, Karst.

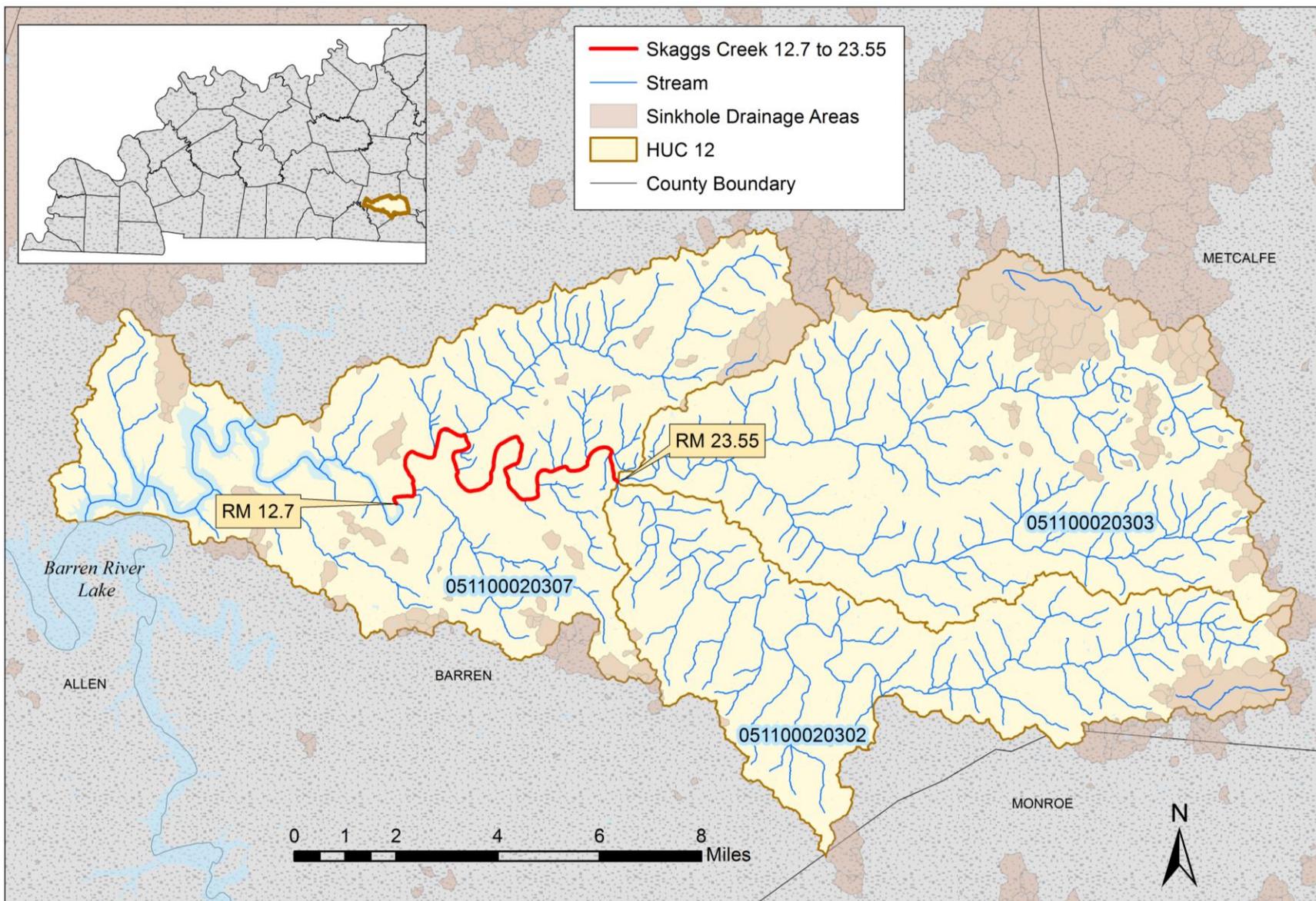


Figure D.28-1 Location of Skaggs Creek 12.7 to 23.55

**Section D.29 South Fork of Panther Creek 14.0 to 18.3****Waterbody ID:** KY503939\_04**Receiving Water:** Panther Creek**Impaired Use:** PCR**Support Status:** nonsupport**Indicator Bacteria:** fecal coliform**HUC 12:** 051100050302**County:** Ohio

Western Kentucky University collected samples at two stations on this reach in 2007 and 2008 as part of a study of the Panther Creek watershed. Table D.29-1 summarizes information about these sampling stations; Table D.29-2 provides a summary of the data collected from the stations.

**Table D.29-1 Western Kentucky University Sample Site Locations**

Station Name	Latitude	Longitude	Stream Segment	River Mile
CWRS_ST0001-LP41	37.61898	-86.8874	South Fork of Panther Creek 14.0 to 18.3	16.15
CWRS_ST0001-LP52	37.624	-86.923	South Fork of Panther Creek 14.0 to 18.3	14.15

**Table D.29-2 Western Kentucky University Sample Data Summary<sup>(1)</sup>**

Station Name	Indicator Bacteria	Number of Observations	Percent Exceeding WQC <sup>2</sup>	Minimum (colonies/100 ml)	Maximum (colonies/100 ml)	Average (colonies/100 ml)
ST0001-LP41	<i>E. coli</i>	9	55.6	41	697	295
ST0001-LP52	<i>E. coli</i>	6	50.0	10	4,352	1,266

<sup>(1)</sup>The full data set for samples collected from these stations may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to [DEP.KORA@ky.gov](mailto:DEP.KORA@ky.gov) or by fax to 502-564-9232. The DEP KORA point of contact may also be reached at 502-564-3999.

<sup>(2)</sup>400 colonies/100 ml for fecal coliform; 240 colonies/100 ml for *E. coli*.

The TMDL allocations for South Fork of Panther Creek 14.0 to 18.3 are presented in Table D.29-3. There are no KPDES-permitted discharges into this segment of the South Fork of Panther Creek. The location of the segment within the South Fork of Panther Creek watershed is shown in Figure D.29-1.

**Table D.29-3 South Fork of Panther Creek 14.0 to 18.3 TMDL Allocations<sup>(1)</sup>**

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

<sup>(1)</sup>All loads are colonies/day of either *E. coli* or fecal coliform. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-m/ft<sup>3</sup>-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft<sup>3</sup>/s) into a load (colonies/day). The symbol “ $\sum$ ” indicates that the total allocation is the sum of all the individual allowable loads.

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

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

<sup>(6)</sup>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.

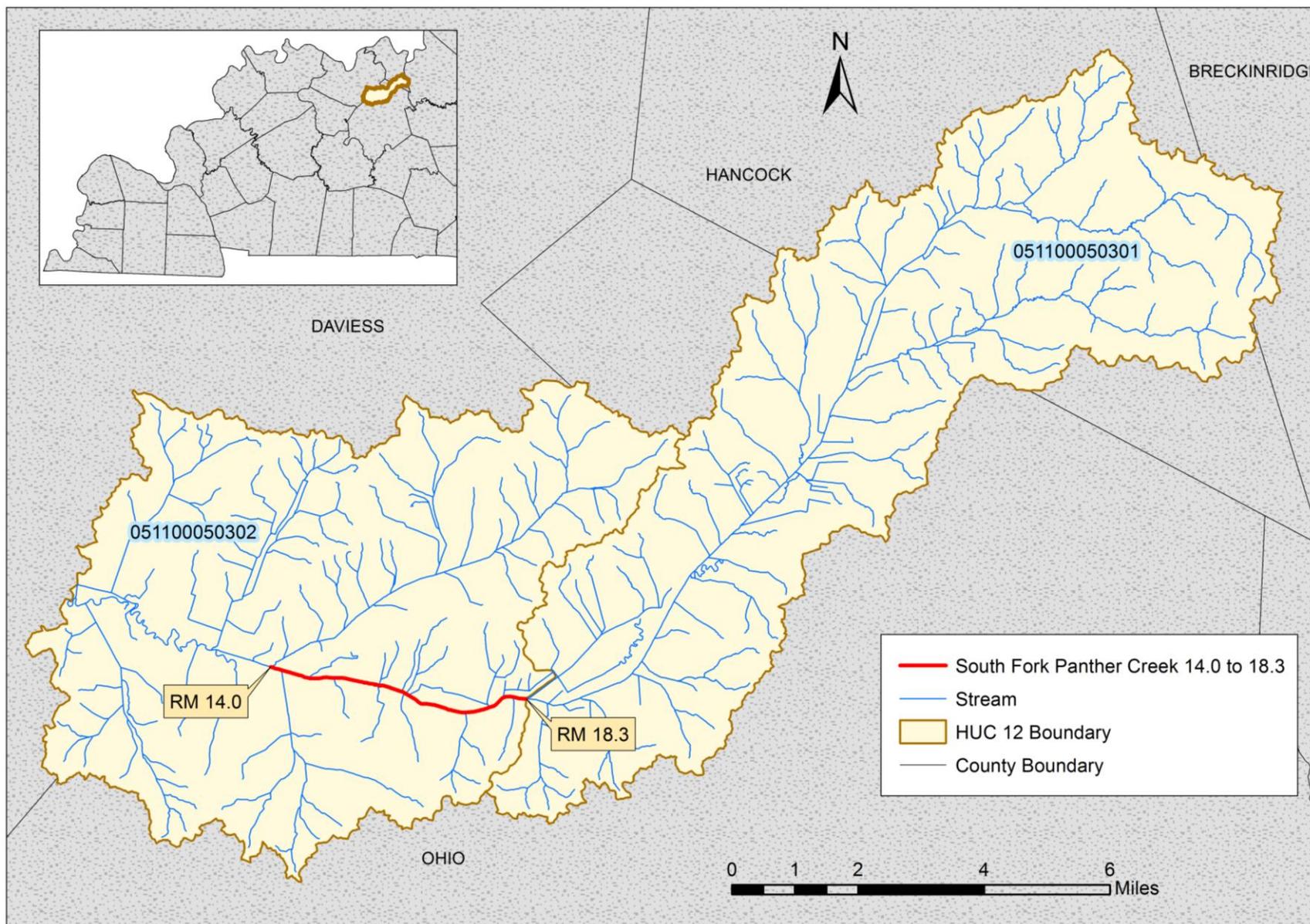


Figure D.29-1 Location of South Fork of Panther Creek 14.0 to 18.3

**Section D.30 South Fork of Panther Creek 9.55 to 14.0****Waterbody ID:** KY503939\_03**Receiving Water:** Panther Creek**Impaired Use:** PCR**Support Status:** nonsupport**Indicator Bacteria:** fecal coliform**HUC 12:** 051100050302**County:** Ohio

Western Kentucky University collected samples at two stations on this reach in 2007 and 2008 as part of a study of the Panther Creek watershed. Table D.30-1 summarizes information about these sampling stations; Table D.30-2 provides a summary of the data collected from the stations.

**Table D.30-1 Western Kentucky University Sample Site Locations**

Station Name	Latitude	Longitude	Stream Segment	River Mile
CWRS_ST0001-LP37	37.63875	-86.9653	South Fork of Panther Creek 9.55 to 14.0	10.0
CWRS_ST0001-LP38	37.62819	-86.9435	South Fork of Panther Creek 9.55 to 14.0	13.0

**Table D.30-2 Western Kentucky University Sample Data Summary<sup>(1)</sup>**

Station Name	Indicator Bacteria	Number of Observations	Percent Exceeding WQC <sup>2</sup>	Minimum (colonies/100 ml)	Maximum (colonies/100 ml)	Average (colonies/100 ml)
ST0001-LP37	<i>E. coli</i>	10	20.0	10	1,918	288
ST0001-LP38	<i>E. coli</i>	8	25.0	10	6,867	930

<sup>(1)</sup>The full data set for samples collected from these stations may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to [DEP.KORA@ky.gov](mailto:DEP.KORA@ky.gov) or by fax to 502-564-9232. The DEP KORA point of contact may also be reached at 502-564-3999.

<sup>(2)</sup>400 colonies/100 ml for fecal coliform; 240 colonies/100 ml for *E. coli*.

The TMDL allocations for South Fork of Panther Creek 9.55 to 14.0 are presented in Table D.30-3. There are no KPDES-permitted discharges into this segment of the South Fork of Panther Creek. The location of the segment within the South Fork of Panther Creek watershed is shown in Figure D.30-1.

**Table D.30-3 South Fork of Panther Creek 9.55 to 14.0 TMDL Allocations<sup>(1)</sup>**

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

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

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

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

<sup>(6)</sup>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.

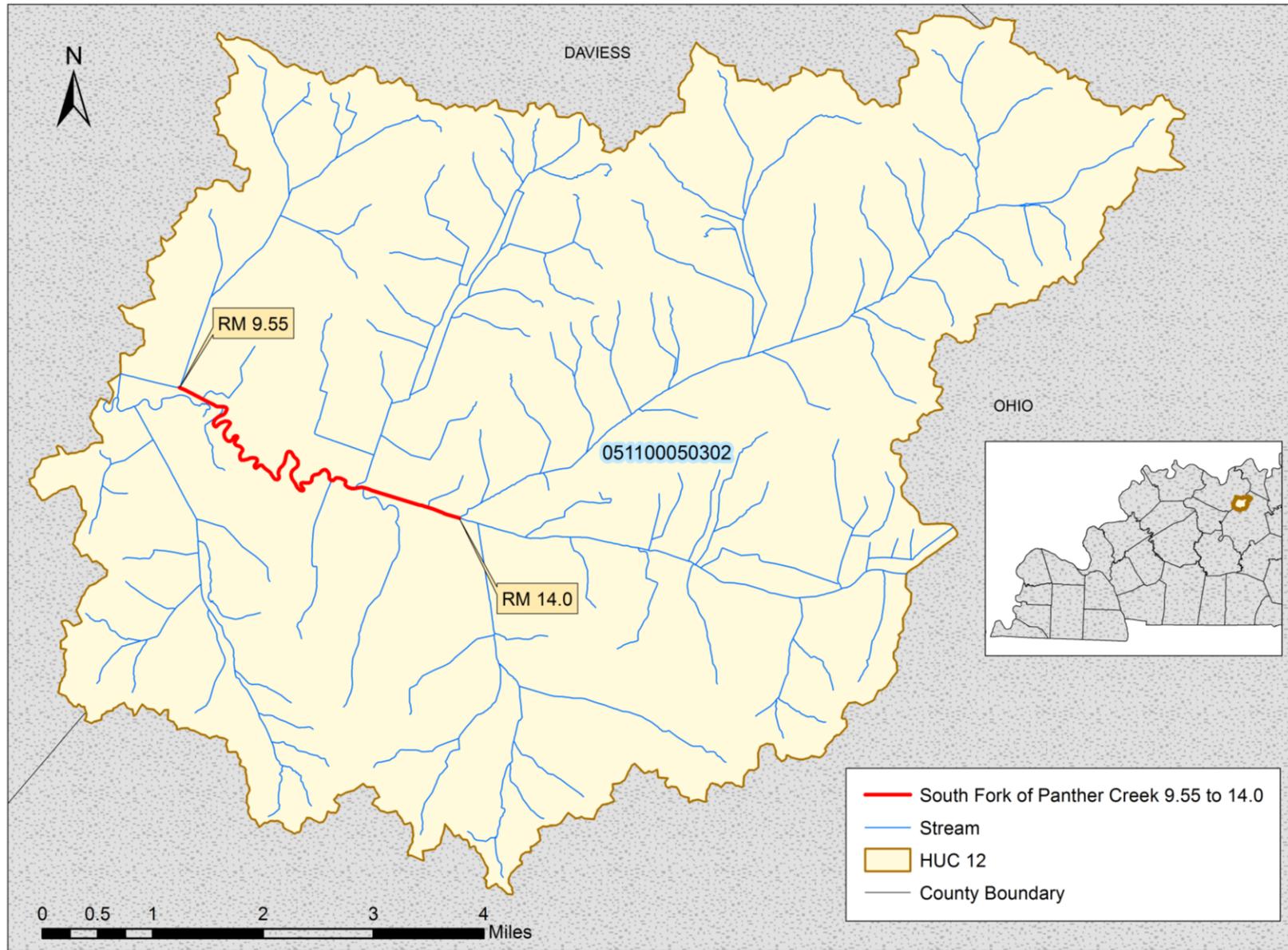


Figure D.30-1 Location of South Fork of Panther Creek 9.55 to 14.0

**Section D.31 UT of Buck Creek 0.0 to 1.7****Waterbody ID:** KY488213-8.0\_01**Receiving Water:** Buck Creek**Impaired Use:** PCR**Support Status:** nonsupport**Indicator Bacteria:** *E. coli***HUC 12:** 051100050201**County:** McLean

In 2008 the Division of Water collected samples at station DOW03003010 as part of a study of the Buck Creek watershed. Table D.31-1 summarizes information about this sampling station; Table D.31-2 provides a summary of the data collected from this station.

**Table D.31-1 Division of Water Sample Site Location**

Station Name	Latitude	Longitude	Stream Segment	River Mile
DOW03003010	37.53493	-87.10857	UT of Buck Creek 0.0 to 1.7	0.21

**Table D.31-2 Division of Water Sample Data Summary<sup>(1)</sup>**

Station Name	Indicator Bacteria	Number of Observations	Percent Exceeding WQC <sup>2</sup>	Minimum (colonies/100 ml)	Maximum (colonies/100 ml)	Average (colonies/100 ml)
DOW03003010	<i>E. coli</i>	6	100.00	520	1,500	1,085

<sup>(1)</sup>The full data set for samples collected from DOW03003010 may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to [DEP.KORA@ky.gov](mailto:DEP.KORA@ky.gov) or by fax to 502-564-9232. The DEP KORA point of contact may also be reached at 502-564-3999.

<sup>(2)</sup>240 colonies/100 ml for *E. coli*.

The TMDL allocations for UT of Buck Creek 0.0 to 1.7 are presented in Table D.31-3. There are no KPDES-permitted discharges into this segment of UT of Buck Creek. The location of the segment within the Buck Creek watershed is shown in Figure D.31-1.

**Table D.31-3 UT of Buck Creek 0.0 to 1.7 TMDL Allocations<sup>(1)</sup>**

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

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

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

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

<sup>(6)</sup>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.

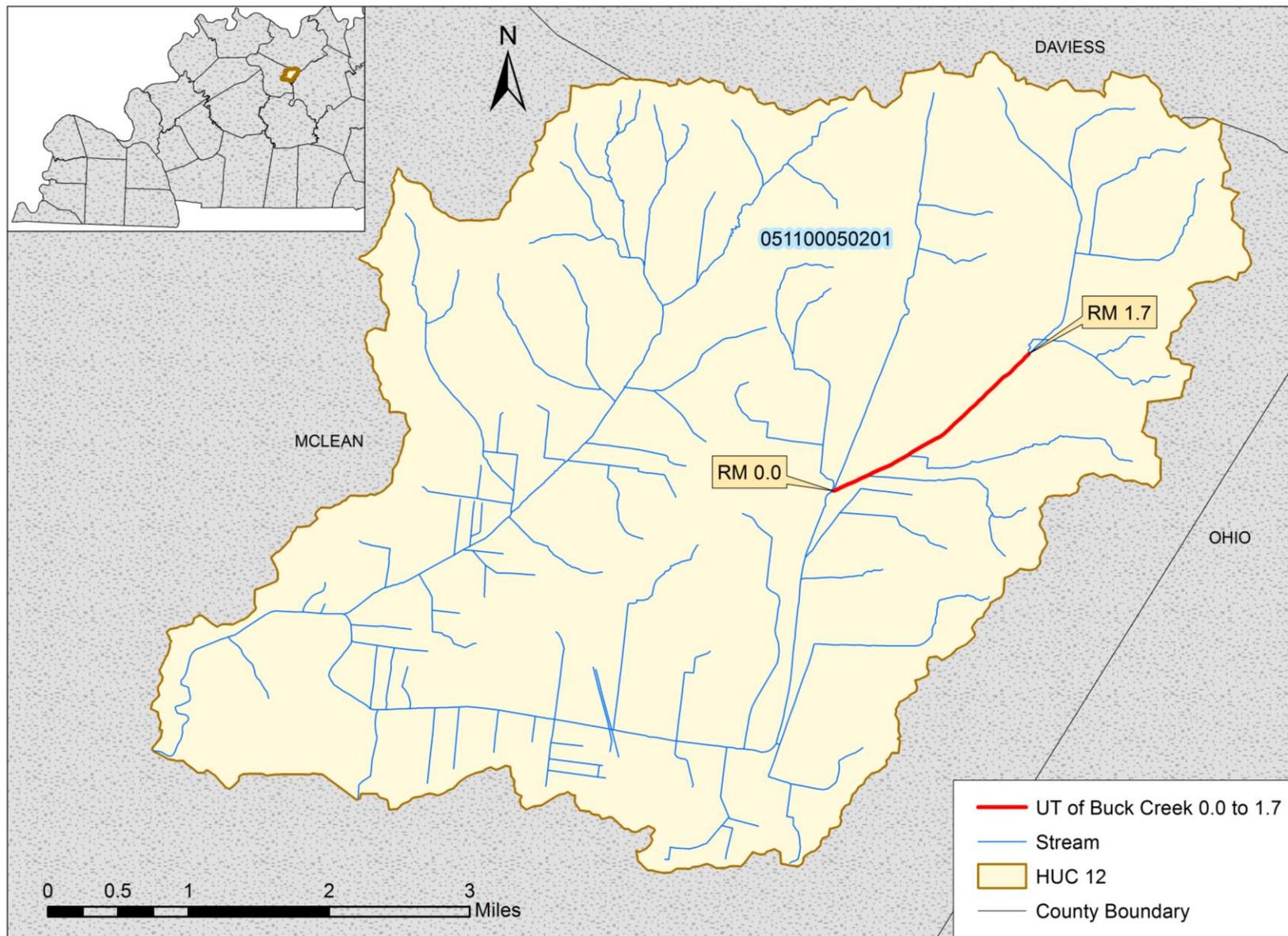


Figure D.31-1 Location of UT of Buck Creek 0.0 to 1.7

**Section D.32 UT of Elk Creek 0.0 to 1.0****Waterbody ID:** KY491656-7.1\_01**Receiving Water:** Elk Creek**Impaired Use:** PCR**Support Status:** nonsupport**Indicator Bacteria:** fecal coliform**HUC 12:** 051100060504**County:** Hopkins

Sampling data from UT of Elk Creek 0.0 to 1.0 is not available. This segment is located in a sewered area of Madisonville. Beginning in 1994, the Division of Water issued Notices of Violation to the City of Madisonville for failure to report the release of untreated wastewater to the waters of the Commonwealth and degradation of the waters of the Commonwealth. These violations were related to a series of sanitary sewer overflows in the Madisonville collection system, and as one of the impacted waters, UT of Elk Creek 0.0 to 1.0 was added to the 303(d) list in 1998. A subsequent Agreed Order outlined the corrective measures required by the city. There are no KPDES-permitted discharges into this segment of UT of Elk Creek. The City of Madisonville does have MS4 storm water permit coverage for areas in the watershed, but the discharges occur upstream of the segment.

The TMDL allocations for UT of Elk Creek 0.0 to 1.0 are presented in Table D.32-1. The location of the segment within the Elk Creek watershed is shown in Figure D.32-1.

**Table D.32-1 UT of Elk Creek 0.0 to 1.0 TMDL Allocations<sup>(1)</sup>**

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

<sup>(1)</sup>All loads are colonies/day of either *E. coli* or fecal coliform. The recreational use bacterial WQCs are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s-ml/ft<sup>3</sup>-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft<sup>3</sup>/s) into a load (colonies/day). The symbol “ $\Sigma$ ” indicates that the total allocation is the sum of all the individual allowable loads.

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

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

<sup>(6)</sup>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.

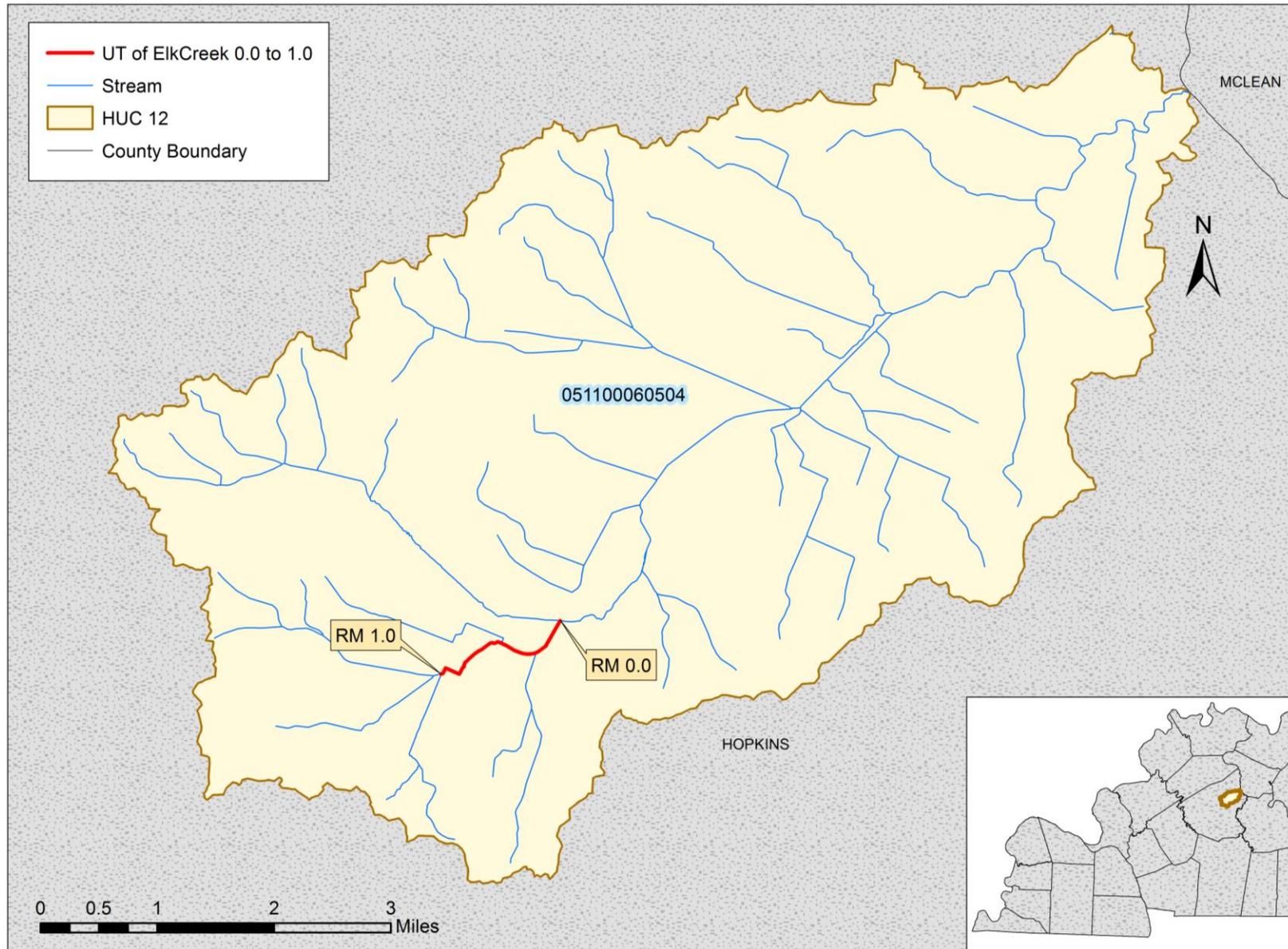


Figure D.32-1 Location of UT of Elk Creek RM 0.0 to 1.0

**Section D.33 UT of Flat Creek 3.1 to 4.1****Waterbody ID:** KY492181-2.0\_02**Receiving Water:** Flat Creek**Impaired Use:** PCR**Support Status:** nonsupport**Indicator Bacteria:** fecal coliform**HUC 12:** 051100060502**County:** Hopkins

Sampling data from UT of Flat Creek 3.1 to 4.1 is not available. This segment is located in a sewered area of Madisonville. Beginning in 1994, the Division of Water issued Notices of Violation to the City of Madisonville for failure to report the release of untreated wastewater to the waters of the Commonwealth and degradation of the waters of the Commonwealth. These violations were related to a series of sanitary sewer overflows in the Madisonville collection system, and as one of the impacted waters, UT of Flat Creek 3.1 to 4.1 was added to the 303(d) list in 1998. A subsequent Agreed Order outlined the corrective measures required by the city.

The TMDL allocations for UT of Flat Creek 3.1 to 4.1 are presented in Table D.33-1.

**Table D.33-1 UT of Flat Creek 3.1 to 4.1 TMDL Allocations<sup>(1)</sup>**

TMDL <sup>(2)</sup>	Allocations for Direct Loads to the Segment		Allocations for Upstream Loads to the Segment <sup>(5)</sup>	Allocations for Tributary Loads to the Segment <sup>(6)</sup>	MOS <sup>(7)</sup>
	MS4-WLA <sup>(3)</sup>	LA <sup>(4)</sup>			
$Q_S \times WQC \times CF$	$\sum(Q_{MS4} \times WQC \times CF)$	$\sum(Q_{LA} \times WQC \times CF)$	$\sum(Q_{Upstream} \times WQC \times CF)$	$\sum(Q_{Tributary} \times WQC \times CF)$	Implicit

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

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

<sup>(3)</sup> $Q_{MS4}$  is the flow (ft<sup>3</sup>/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.

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

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

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

<sup>(7)</sup>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 Madisonville and Kentucky Department of Transportation have MS4 storm water permit coverage for areas along UT of Flat Creek 3.1 to 4.1. Information about the MS4 permits is summarized in Table D.33-2. There are no other KPDES-permitted discharges of bacteria into the segment. Although the Madisonville WWTP once discharged to this segment, it ceased discharges before 1999. The location of the segment within the Flat Creek watershed is shown in Figure D.33-1.

**Table D.33-2 Summary of Active KPDES-permitted Sources as of September 2018**

KPDES Permit Number	Facility Name	Indicator Bacteria	Permit Expiration Date	WLA <sup>(1)</sup> (colonies/day)
KYG200022	City of Madisonville	Fecal Coliform	4/30/2023	$Q_{MS4} \times WQC \times CF$
KYS000003	Kentucky Department of Transportation	Fecal Coliform	9/30/2017	$Q_{MS4} \times WQC \times CF$

<sup>(1)</sup>All loads are colonies/day of either *E. coli* or fecal coliform.  $Q_{MS4}$  is the flow in the segment due to a MS4 entity. The recreational use bacterial WQC are found in 401 KAR 10:031. CF is the conversion factor (24,465,758.4 s·ml/ft<sup>3</sup>-day) to change the product of bacterial concentration (colonies/100 ml) and flow (ft<sup>3</sup>/s) into a load (colonies/day).

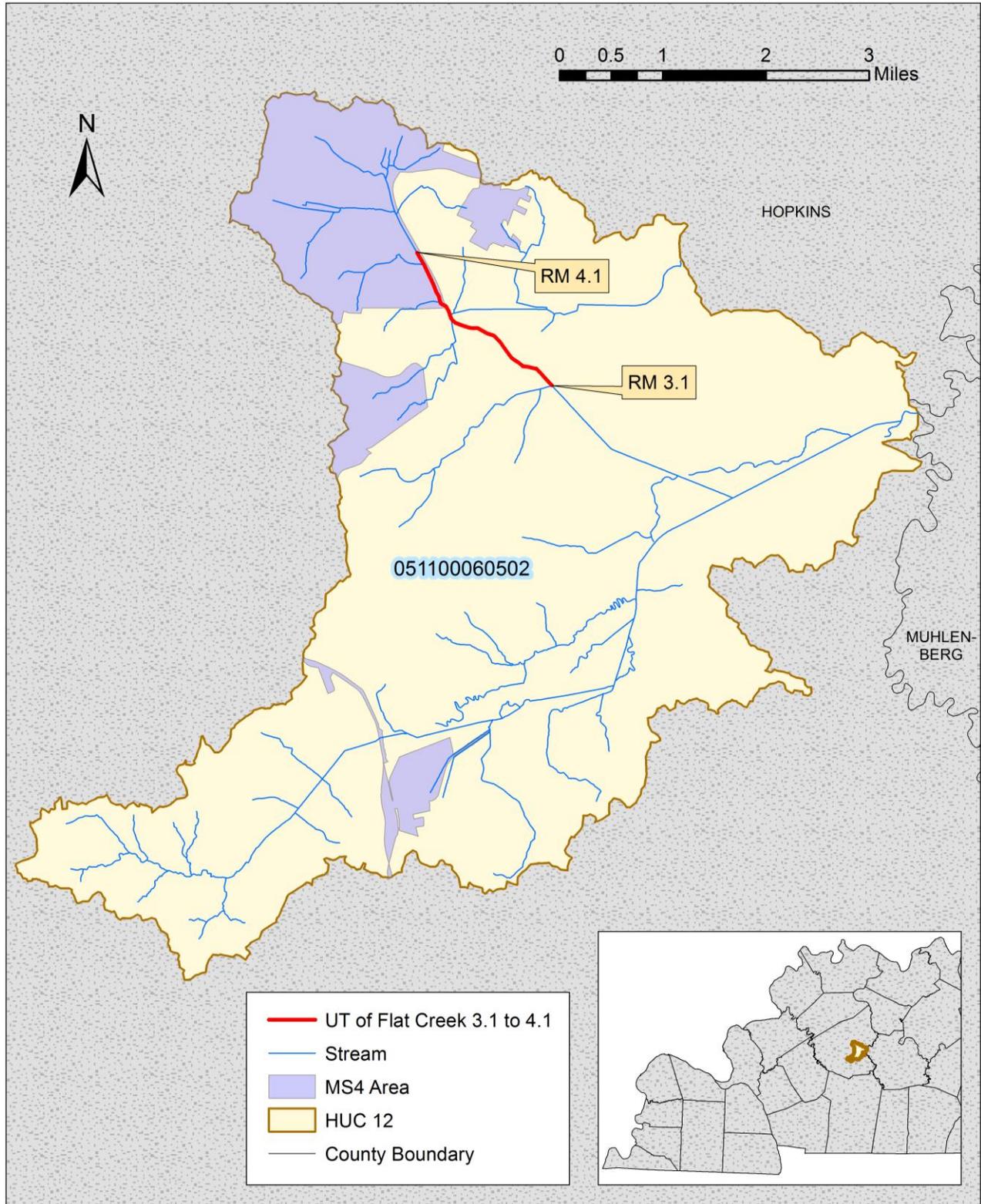


Figure D.33-1 Location of UT of Flat Creek 3.1 to 4.1

**Section D.34 West Fork of Buck Creek 0.0 to 3.3****Waterbody ID:** KY506423\_01**Receiving Water:** Buck Creek**Impaired Use:** PCR**Support Status:** nonsupport**Indicator Bacteria:** *E. coli***HUC 12:** 051100050201**County:** McLean

In 2008 the Division of Water collected samples at two stations along this segment as part of a study of the Buck Creek watershed. Table D.44-1 summarizes information about the stations; Table D.44-2 provides a summary of the data collected from these stations.

**Table D.34-1 Division of Water Sample Site Locations**

Station Name	Latitude	Longitude	Stream Segment	River Mile
DOW03003007	37.52391	-87.16674	West Fork of Buck Creek 0.0 to 3.3	0.55
DOW03003008	37.54716	-87.13695	West Fork of Buck Creek 0.0 to 3.3	2.9

**Table D.34-2 Division of Water Sample Data Summary<sup>(1)</sup>**

Station Name	Indicator Bacteria	Number of Observations	Percent Exceeding WQC <sup>2</sup>	Minimum (colonies/100 ml)	Maximum (colonies/100 ml)	Average (colonies/100 ml)
DOW03003007	<i>E. coli</i>	5	40.00	105	580	286
DOW03003008	<i>E. coli</i>	5	60.00	168	1,500	607

<sup>(1)</sup>The full data set for samples collected from these stations may be obtained by submitting a request of records under the Kentucky Open Records Act (KORA) to [DEP.KORA@ky.gov](mailto:DEP.KORA@ky.gov) or by fax to 502-564-9232. The DEP KORA point of contact may also be reached at 502-564-3999.

<sup>(2)</sup>240 colonies/100 ml for *E. coli*.

The TMDL allocations for West Fork of Buck Creek 0.0 to 3.3 are presented in Table D.34-3. There are no KPDES-permitted discharges into this segment of West Fork of Buck Creek. The location of the segment within the Buck Creek watershed is shown in Figure D.34-1.

**Table D.34-3 West Fork of Buck Creek 0.0 to 3.3 TMDL Allocations<sup>(1)</sup>**

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

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

<sup>(2)</sup> $Q_S$  is the flow (ft<sup>3</sup>/s) in the segment.

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

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

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

<sup>(6)</sup>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.

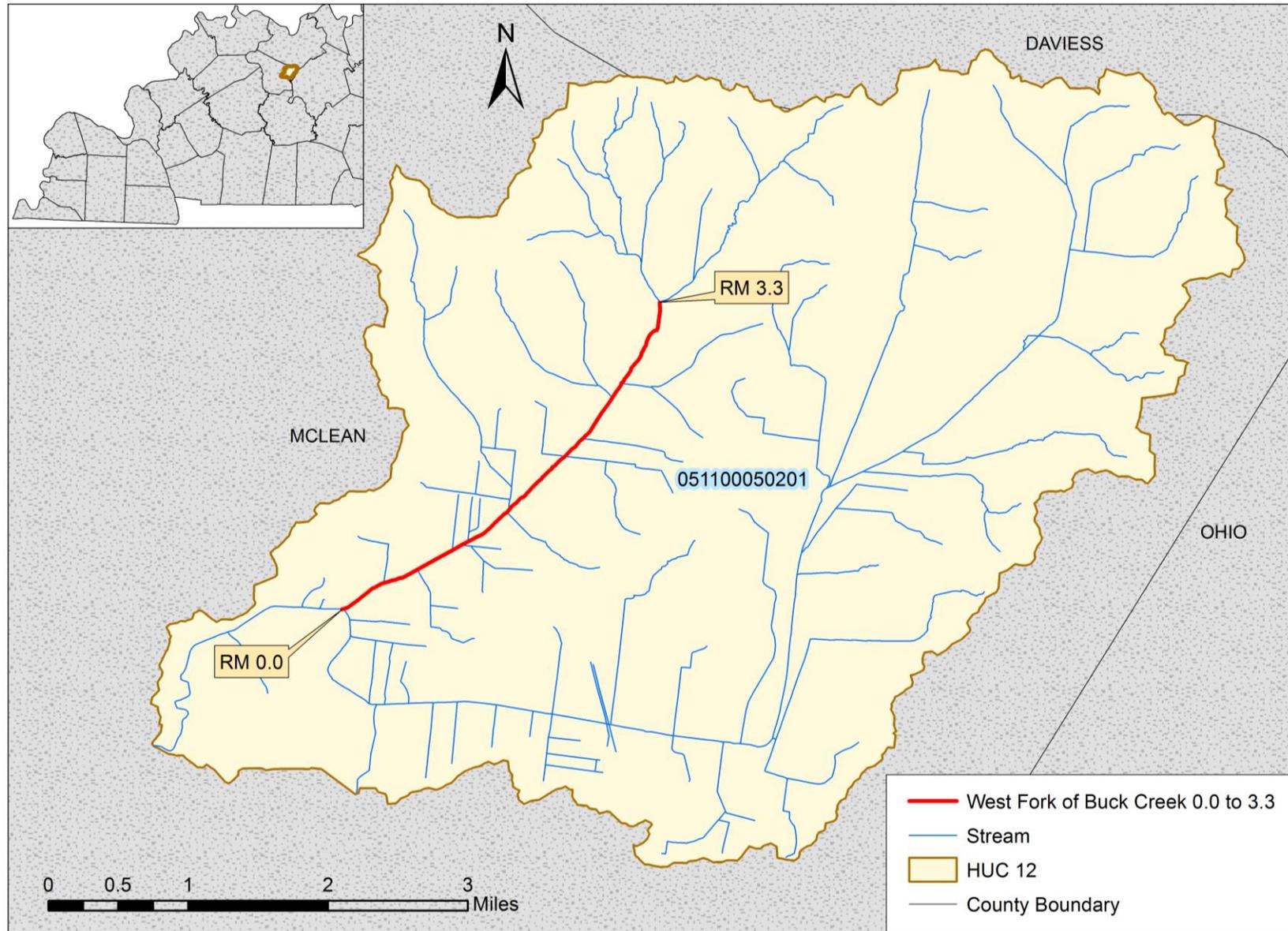


Figure D.34-1 Location of West Fork of Buck Creek 0.0 to 3.3