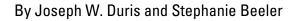


Fecal-Indicator Bacteria and *Escherichia coli*Pathogen Data Collected Near a Novel Sub-Irrigation Water-Treatment System in Lenawee County, Michigan, June–November 2007



In cooperation with Lenawee County Conservation District

Open File Report 2008-1025

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Conversion Factors

Multiply	Ву	To obtain
	Length	
inch (in.)	2.54	centimeter (cm)
foot (ft)	0.3048	meter (m)
meter (m)	3.281	foot (ft)
yard (yd)	0.9144	meter (m)
	Volume	
gallon (gal)	3.785	liter (L)

Temperature in degrees Celsius (°C) may be converted to degrees Fahrenheit (°F) as follows:

Small sample volumes are reported in milliliters (mL) and microliters (μ L); very small masses are given in nanograms (ng).

Bacteria concentrations are given in colony-forming units per 100 milliliters (CFU/100 mL).

[°]F=(1.8×°C)+32

Fecal-Indicator Bacteria and *Escherichia coli*Pathogen Data Collected Near a Novel Sub-Irrigation Water-Treatment System in Lenawee County, Michigan, June–November 2007

By Joseph W. Duris and Stephanie Beeler

Abstract

The U.S. Geological Survey, in cooperation with the Lenawee County Conservation District in Lenawee County, Mich., conducted a sampling effort over a single growing season (June to November 2007) to evaluate the microbiological water quality around a novel livestock reservoir wetland sub-irrigation system. Samples were collected and analyzed for fecal coliform bacteria, *Escherichia coli* (*E. coli*) bacteria, and six genes from pathogenic strains of *E. coli*.

A total of 73 water-quality samples were collected on nine occasions from June to November 2007. These samples were collected within the surface water, shallow ground water, and the manure-treatment system near Bakerlads Farm near Clayton in Lenawee County, Mich. Fecal coliform bacteria concentrations ranged from 10 to 1.26 million colony forming units per 100 milliliters (CFU/100 mL). *E. coli* bacteria concentrations ranged from 8 to 540,000 CFU/100 mL. Data from the *E. coli* pathogen analysis showed that 73 percent of samples contained the *eaeA* gene, 1 percent of samples contained the *stx1* gene, 21 percent of samples contained the *rfb*O157 gene, and 64 percent of samples contained the LTIIa gene.

Introduction

The management of animal wastes on dairy farms is commonly driven by the need of farmers to effectively manage nutrient content in soils where crops are grown, as well as to control and manage manure in a way that avoids negative effects on local surface water and ground water. Typically, the management of manure in and around a farm is locally controlled by use of comprehensive nutrient-management plans that define how manure will be handled on the farm under various conditions. To meet the guidelines of these management practices, the Bakerlads Farm, working with the U.S. Department of Agriculture and the Lenawee County Conservation District, in 2005 installed novel manure-management system called a Livestock Reservoir Wetland Sub-Irrigation System (LRWSIS) on the farmstead, which is near Clayton, Mich (fig. 1; all figures and tables are at back of report).

The U.S. Geological Survey (USGS), in cooperation with the Lenawee County Conservation District (LCCD) in Lenawee County, Mich., sampled nine sites (surface water and groud water) over a single growing season, from June to November 2007. The purpose of this study was to evaluate the microbiological water quality around the LRWSIS. By studying the populations of fecal coliform and *E. coli* bacteria and by characterizing the types of *E. coli* pathogens and other bacterial markers in manure sources, we can assess how manure-management practices may contribute to indicator and pathogen loading in environmental waters. This could lead to a better understanding of how and why bacterial indicators and pathogens might be found in other environmental settings affected by agriculturally influenced waters. In addition, this work builds on a growing body of work by the USGS Michigan Water Science Center related to understanding how manure management affects the transport of fecal indicator and pathogenic bacteria. Samples were collected and analyzed for fecal coliform bacteria, *Escherichia coli* (*E. coli*), and six genes from pathogenic strains of *E. coli*, including *E. coli* O157:H7. This report summarizes the results of this sampling.

Methods

Site Information

The LRWSIS directs dairy barn wash water and runoff from the entire facility into a primary settling reservoir. Once settled, the liquid waste is then transferred into an 80,000 gal constructed wetland via a 3-in. subsurface PVC pipe that bridges a small unnamed tributary to the South Branch of the River Raisin. The liquid waste from the influent pond of the constructed wetland is allowed to move via subsurface flow through a packed layer of sand and pea gravel, planted with wetland vegetation, into the subsurface irrigation holding pond. This water is then pumped directly into a closed subsurface tile irrigation system below a planted cornfield, where it supplies water and nutrients to the crop that is planted above.

Samples for this study were collected from nine locations in and around the Bakerlads Farm (table 1 and fig. 1). For flowing water, the tributary to the South Branch of the River Raisin was sampled at three locations: upstream from the sub-irrigated field and the LRWSIS, downstream from the sub-irrigated field, and downstream from the LRWSIS. For ground water, samples were collected from two piezometers within the cropped area of the sub-irrigated field and one piezometer 10 m from the bank of the tributary to the South Branch of the River Raisin. For ponded water, samples were collected from the primary settling pond, the influent pond of the wetland system, and the sub-irrigation holding pond of the wetland system to evaluate potential inputs to the ambient water. Samples were collected on nine dates over the 2007 growing season, from June 25 through November 27, 2007 (table 2).

Sample Collection

Samples were collected by the LCCD staff using standard USGS sampling procedures documented by the USGS National Field Manual (Myers, 2003). Each sample was evaluated for fecal coliform bacteria and *E. coli* and for six genes from pathogenic *E. coli*.

Bacteriological Indicator Organisms

Samples were examined for the presence of fecal-indicator bacteria by means of standard membrane filtration and serial dilution methods as indicated in Britton and Greeson (1989), whereas *E. coli* analysis followed protocols of the American Public Health Association and others (1998), method 9222D/9222G. Fecal coliform bacteria from the membrane filter with the most growth for each site and date were collected and suspended in 1 mL of phosphate buffered saline (PBS) with a final concentration of 15 percent glycerol. This fecal coliform stock (FC) was used for all subsequent analysis for pathogenic *E. coli*.

E. coli Gene Analysis

The FC stocks were analyzed by use of three polymerase chain reaction (PCR) methods. Deoxyribonucleic acid (DNA) was extracted from one-tenth of the volume of the FC stock, using alkaline polyethylene glycol (APEG) DNA extraction (Chomczynski and Rymaszewski, 2006). A volume of 100 μ L of FC stock was transferred to a volume of 1,000 μ L of APEG reagent and incubated at 55°C for 30 minutes, at which point it was stored at 4°C until PCR analysis for *E. coli* pathogen genes.

A volume of 1 μ L of DNA representing 1–100 ng of DNA was used to conduct all PCR analysis. Samples were analyzed for the gene responsible for the O157 type (rfbO157) as indicated by Osek (2003). The gene targeted by this assay is the gene responsible for the production of the specific antigen found on the surface of an E. coli O157 cell.

The samples were also analyzed for the pathogenic *E. coli* toxin genes *eaeA*, *stx2*, and *stx1* (Fagan and others, 1999; Sabat and others, 2000). The genes targeted by this assay are those required to confirm the presence of enterohemorrhagic *E. coli* in clinical samples (Nataro and Kaper, 1998; Fagan and others 1999). The method was modified to include analysis for a gene common to all *E. coli*, both pathogenic and nonpathogenic, which was used to confirm the presence of *E. coli* (Duris and others, 2003; Fogarty and others, 2005). The LTIIa gene, carried by some pathogenic *E. coli* strains common to bovine sources, was analyzed according to Khatib and others (2002) and Chern and others (2004). A summary of all genes and their common functions and associations can be found in table 3. All gene assays followed standard protocols (U.S. Environmental Protection Agency, 2004). All methods included positive controls and method blanks.

Results

Water-quality samples were collected on nine occasions from June to November 2007. A total of 73 water samples were collected within the surface water, shallow ground water, and manure-treatment system near Bakerlads Farm, in Lenawee County, Mich. Fecal coliform bacteria concentrations ranged from 10 to 1.26 million CFU/100 mL. *E. coli* bacteria concentrations ranged from 8 to 540,000 CFU/100 mL. Data from the *E. coli* pathogen analysis showed that 73 percent of samples contained the *eaeA* gene, 1 percent of samples contained the *stx1* gene, 21 percent of samples contained the *rfb*O157 gene, and 64 percent of samples contained the LTIIa gene. The EC gene that is common to all *E. coli* was present in 97 percent of samples. The data from the fecal-indicator bacteria testing at each site are presented in table 4 and figures 2–10. Data from the *E. coli* pathogen analysis are presented in table 4. Those samples that had countable *E. coli* but no detectable EC gene were considered not amplifiable by PCR and are noted in table 4.

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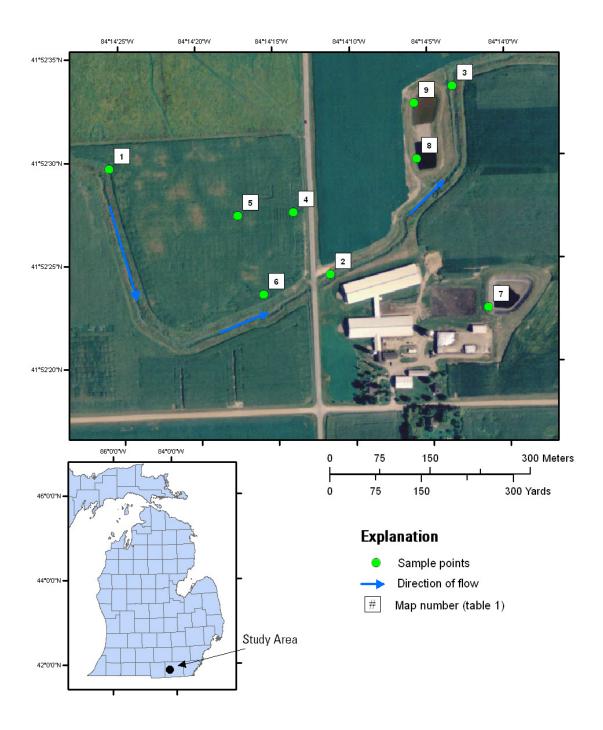


Figure 1. Sampling locations for fecal indicator bacteria and *E. coli* pathogen study, Lenawee County, Mich., 2007.

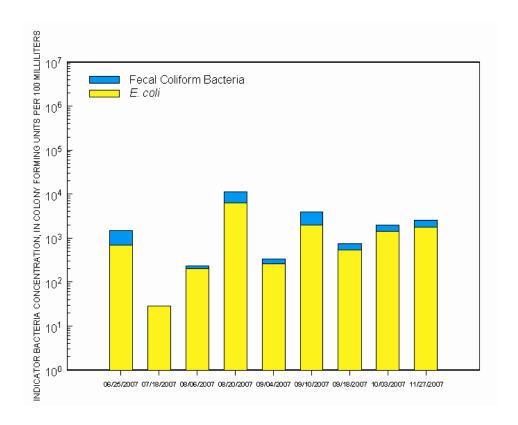


Figure 2. Fecal coliform bacteria and *Escherichia coli* concentrations by date for station 415233084140309 (D1), in Lenawee County, Mich., 2007.

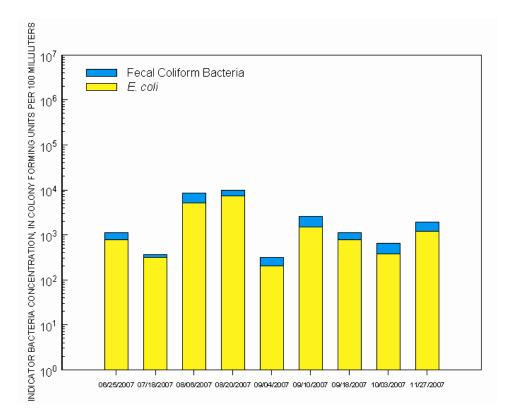


Figure 3. Fecal coliform bacteria and *Escherichia coli* concentrations by date for station 415224084141108 (D2), in Lenawee County, Mich., 2007.

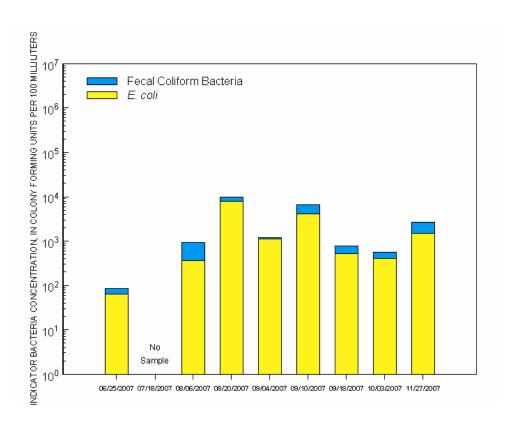


Figure 4. Fecal coliform bacteria and *Escherichia coli* concentrations by date for station 415230084142607 (D4), in Lenawee County, Mich., 2007.

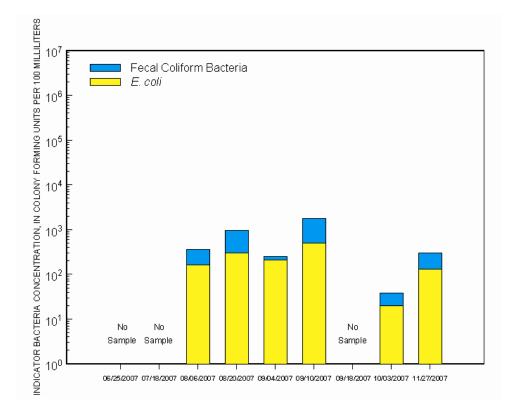


Figure 5. Fecal coliform bacteria and *Escherichia coli* concentrations by date for station 415224084141604 (W1), in Lenawee County, Mich., 2007.

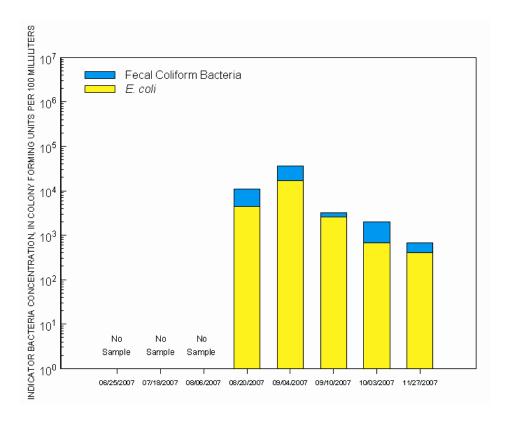


Figure 6. Fecal coliform bacteria and *Escherichia coli* concentrations by date for station 415227084141405 (W2), in Lenawee County, Mich., 2007.

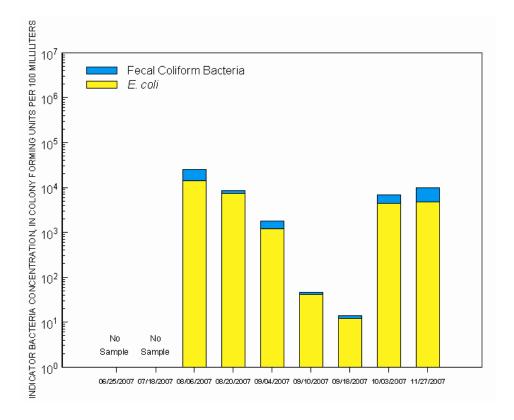


Figure 7. Fecal coliform bacteria and *Escherichia coli* concentrations by date for station 415227084141806 (W3), in Lenawee County, Mich., 2007.

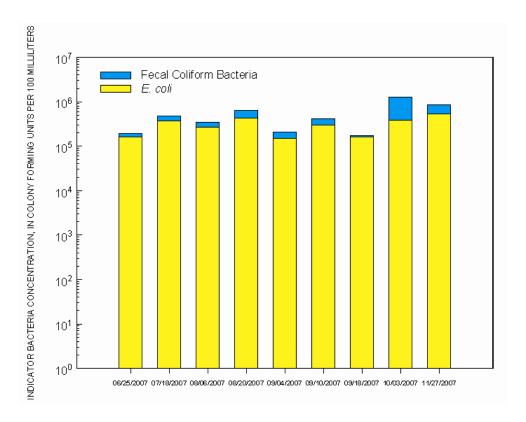


Figure 8. Fecal coliform bacteria and *Escherichia coli* concentrations by date for station 415223084140101 (P2), in Lenawee County, Mich., 2007.

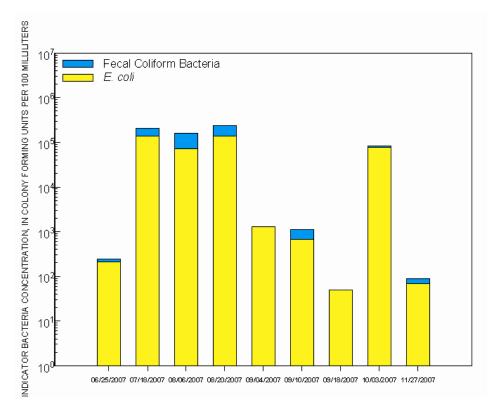


Figure 9. Fecal coliform bacteria and *Escherichia coli* concentrations by date for station 415230084140602 (P3), in Lenawee County, Mich., 2007.

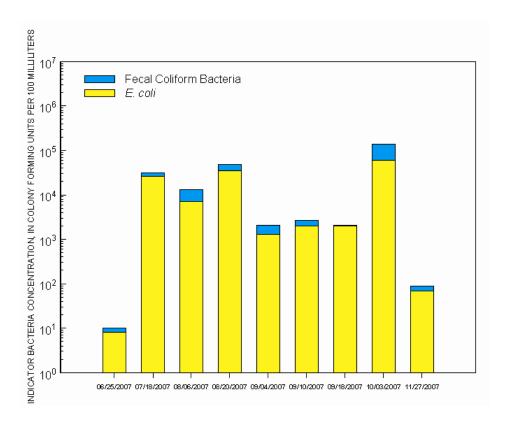


Figure 10. Fecal coliform bacteria and *Escherichia coli* concentrations by date for station 415233084140603 (P4), in Lenawee County, Mich., 2007.

Table 1. U.S. Geological Survey stations sampled in Lenawee County, Michigan.

[USGS, U.S. Geological Survey; ID, Identification]

USGS station ID	USGS field ID	Map number	USGS station name	Station type
415230084142607	D4	1	Tributary to South Branch River Raisin (site D4) near Clayton, MI	Surface water
415224084141108	D2	2	Tributary to South Branch River Raisin (site D2) near Clayton, MI	Surface water
415233084140309	D1	3	Tributary to South Branch River Raisin (site D1) near Clayton, MI	Surface water
415227084141806	W3	4	Unnamed Well W3 near Clayton, MI	Ground water
415227084141405	W2	5	Unnamed Well W2 near Clayton, MI	Ground water
415224084141604	W1	6	Unnamed Well W1 near Clayton, MI	Ground water
415223084140101	P2	7	Unnamed Storage Lagoon P2 near Clayton, MI	Place of use
415230084140602	P3	8	Unnamed Wetland Pond P3 near Clayton, MI	Place of use
415233084140603	P4	9	Unnamed Wetland Pond P4 near Clayton, MI	Place of use

Table 2. Sampling dates and conditions.

Sample number	Sampling date	Condition					
1	6/25/2007	4 days prior to treatment system start					
2	7/18/2007	Day 20 of system operation					
3	8/6/2007	Day 39 of system operation					
4	8/20/2007	Day 53 of system operation					
5	9/4/2007	Day 68 of system operation					
6	9/10/2007	Day 74 of system operation					
7	9/18/2007	Day 82 of system operation					
8	10/3/2007	10 days post system shutdown					
9	11/27/2007	37 days after field drained					

Table 3. Microbiological analytes and supplemental information for fecal-indicator-bacteria analysis. [*E. coli, Escherichia coli;* NA, Not Applicable]

Analyte	Category	Gene product	Importance
Fecal coliform	Indicator group	NA	Commonly used group of fecal indicator bacteria.
E. coli	Indicator group	NA	Commonly used species of fecal indicator bacteria.
eaeA	Gene	Intimin	Product causes tight binding of pathogenic <i>E. coli</i> to intestinal cells (Nataro and Kaper, 1998; Fagan and others, 1999).
stx1	Gene	Shiga toxin 1	Product causes intestinal cell death. <i>stx1</i> is associated with bovine sources (Nataro and Kaper, 1998; Fagan and others, 1999).
stx2	Gene	Shiga toxin 2	Product causes intestinal cell death. When found with <i>eaeA</i> is associated with human disease (Nataro and Kaper, 1998; Fagan and others, 1999).
EC	Gene	16s rRNA	Common to all <i>E. coli</i> , pathogenic and nonpathogenic (Fogarty and others, 2005).
rfbO157	Gene	O157 surface protein	Gene is marker for E. coli O157:H7 (Osek, 2003).
LTIIa	Gene	Heat labile toxin	Product causes diarrheal disease in calves, commonly associated with bovine sources (Khatib and others, 2002; Chern and others, 2004).

Table 4. Microbiological data collected in Lenawee County, Michigan. [USGS, U.S. Geological Survey; *E. coli, Escherichia coli*; EC, *E. coli* 16S ribosomal DNA gene that is common to all *E. coli*; +, gene present in sample; -, gene absent in sample; ns, no sample; na, not amplifiable with polymerase chain reaction]

			Colony forming units per 100 milliliters water Esc				Eschericha coli gene data					
USGS station ID	Field ID	Date	Fecal coliforms	E. coli	eaeA	stx2	stx1	EC	rfb	LTIIa		
415233084140309	D1	6/25/2007	1,500	700	+	-	-	+	-	+		
415224084141108	D2	6/25/2007	1,100	780	+	-	-	+	-	-		
415230084142607	D4	6/25/2007	84	64	+	-	-	+	-	-		
415223084140101	P2	6/25/2007	190,000	160,000	+	-	+	+	-	+		
415230084140602	P3	6/25/2007	240	210	+	-	-	+	-	-		
415233084140603	P4	6/25/2007	10	8	-	-	-	+	-	+		
415224084141604	W1	6/25/2007	ns	ns	ns	ns	ns	ns	ns	ns		
415227084141405	W2	6/25/2007	ns	ns	ns	ns	ns	ns	ns	ns		
415227084141806	W3	6/25/2007	ns	ns	ns	ns	ns	ns	ns	ns		
415233084140309	D1	7/18/2007	28	28	+	-	-	+	-	-		
415224084141108	D2	7/18/2007	370	310	+	-	-	+	-	+		
415230084142607	D4	7/18/2007	ns	ns	ns	ns	ns	ns	ns	ns		
415223084140101	P2	7/18/2007	480,000	370,000	+	-	+	+	-	+		
415230084140602	P3	7/18/2007	210,000	140,000	+	-	+	+	-	+		
415233084140603	P4	7/18/2007	31,000	26,000	+	-	+	+	+	+		
415224084141604	W1	7/18/2007	ns	ns	ns	ns	ns	ns	ns	ns		
415227084141405	W2	7/18/2007	ns	ns	ns	ns	ns	ns	ns	ns		
415227084141806	W3	7/18/2007	ns	ns	ns	ns	ns	ns	ns	ns		
415233084140309	D1	8/6/2007	230	200	-	-	-	+	-	-		
415224084141108	D2	8/6/2007	8,600	5,100	+	_	+	+	_	+		
415230084142607	D4	8/6/2007	930	370	+	-	-	+	-	+		
415223084140101	P2	8/6/2007	340,000	270,000	+	_	+	+	_	+		
415230084140602	P3	8/6/2007	160,000	73,000	+	-	+	+	-	-		
415233084140603	P4	8/6/2007	13,000	7,000	+	_	_	+	_	_		
415224084141604	W1	8/6/2007	360	160	+	-	-	+	-	-		
415227084141405	W2	8/6/2007	ns	ns	ns	ns	ns	ns	ns	ns		
415227084141806	W3	8/6/2007	25,000	14,000	na	na	na	na	na	na		
415233084140309	D1	8/20/2007	11,000	6,300	+	-	+	+	_	+		
415224084141108	D2	8/20/2007	10,000	7,400	+	-	+	+	+	+		
415230084142607	D4	8/20/2007	10,000	8,000	+	_	+	+	_	+		
415223084140101	P2	8/20/2007	630,000	430,000	+	_	+	+	+	+		
415230084140602	P3	8/20/2007	240,000	140,000	+	_	+	+	+	+		
415233084140603	P4	8/20/2007	49,000	35,000	+	_	_	+	_	+		
415224084141604	W1	8/20/2007	970	300	na	na	na	na	na	na		
415227084141405	W2	8/20/2007	11,000	4,500	+	_	_	+	_	+		
415227084141806	W3	8/20/2007	8,400	7,400	_	_	-	+	-	_		
415233084140309	D1	9/4/2007	330	260	+	_	_	+	_	+		
415224084141108	D2	9/4/2007	320	200	+	_	_	+	_	+		
415230084142607	D4	9/4/2007	1200	1,100	+	_	_	+	+	+		
415223084140101	P2	9/4/2007	210,000	150,000	+	_	+	+	+	+		
415230084140602	P3	9/4/2007	1,300	1,300	-	_	-	+	_	+		

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Table 4. Microbiological data collected in Lenawee County, Michigan.—Continued

[USGS, U.S. Geological Survey; *E. coli*, *Escherichia coli*; EC, *E. coli* 16S ribosomal DNA gene that is common to all *E. coli*; +, gene present in sample; -, gene absent in sample; ns, no sample; na, not amplifiable with polymerase chain reaction]

			Colony formi	ng units per						
			100 millilit	<u>ers water</u>	<u> </u>	<u>scheri</u>	cha co	<i>li</i> gen	e dat	<u>a</u>
HCCC -t-ti ID	Field ID	Date	Fecal	E. coli						
USGS station ID	Field ID		coliforms		eaeA	stx2	stx1	EC	rfb	LTIIa
415233084140603	P4	9/4/2007	2,100	1,300	-	-	-	+	-	-
415224084141604	W1	9/4/2007	250	210	+	_	-	+	-	+
415227084141405	W2	9/4/2007	36,000	17,000	+	-	-	+	-	-
415227084141806	W3	9/4/2007	1,800	1,200	+	-	-	+	-	+
415233084140309	D1	9/10/2007	3,900	2,000	+	-	+	+	-	+
415224084141108	D2	9/10/2007	2,600	1,500	+	-	+	+	+	+
415230084142607	D4	9/10/2007	6,500	4,100	+	-	-	+	-	+
415223084140101	P2	9/10/2007	410,000	300,000	+	-	+	+	+	+
415230084140602	P3	9/10/2007	1,100	670	+	-	-	+	-	-
415233084140603	P4	9/10/2007	2,700	2,000	-	-	+	+	-	+
415224084141604	W1	9/10/2007	1,800	500	+	_	-	+	_	-
415227084141405	W2	9/10/2007	3,200	2,600	_	-	-	+	_	_
415227084141806	W3	9/10/2007	46	42	_	-	-	+	_	+
415233084140309	D1	9/18/2007	730	530	_	_	_	+	_	_
415224084141108	D2	9/18/2007	1100	770	+	_	-	+	_	_
415230084142607	D4	9/18/2007	770	530	+	_	+	+	_	+
415223084140101	P2	9/18/2007	170,000	160,000	+	_	+	+	+	+
415230084140602	Р3	9/18/2007	50	50	_	_	_	+	_	_
415233084140603	P4	9/18/2007	2,100	2,000	_	_	_	+	_	+
415224084141604	W1	9/18/2007	ns	ns	ns	ns	ns	ns	ns	ns
415227084141405	W2	9/18/2007	ns	ns	ns	ns	ns	ns	ns	ns
415227084141806	W3	9/18/2007	14	12	_	_	_	+	_	+
415233084140309	D1	10/3/2007	2,000	1,400	+	_	_	+	_	_
415224084141108	D2	10/3/2007	660	380	+	_	_	+	_	_
415230084142607	D4	10/3/2007	570	410	+	_	+	+	_	+
415223084140101	P2	10/3/2007	1,260,000	390,000	+	_	+	+	+	+
415230084140602	Р3	10/3/2007	83,000	76,000	+	_	+	+	_	+
415233084140603	P4	10/3/2007	140,000	60,000	+	_	_	+	_	+
415224084141604	W1	10/3/2007	38	20	_	_	_	+	_	_
415227084141405	W2	10/3/2007	2,000	670	+	_	_	+	+	_
415227084141806	W3	10/3/2007	6,800	4,400	+	_	_	+	+	+
415233084140309	D1	11/27/2007	2,500	1,800	+	+	+	+	_	+
415224084141108	D2	11/27/2007	1,900	1,200	+	_	+	+	+	+
415230084142607	D4	11/27/2007	2,700	1,500	+	_	+	+	+	+
415223084140101	P2	11/27/2007	860,000	540,000	+	_	+	+	+	+
415230084140602	P3	11/27/2007	90	70	+	_	_	+	_	+
415233084140603	P4	11/27/2007	90	70	-	_	_	+	_	-
415224084141604	W1	11/27/2007	300	130	_	_	_	+	_	+
415227084141405	W2	11/27/2007	670	400	_	_	_	+	_	+
415227084141806	W3	11/27/2007	9,900	4,700	_	_	_	+	_	-
415233084140309	D1 Rep	8/6/2007	460	300	_	_	_	+	_	_
415223084140101	P2 Rep	8/6/2007	390,000	310,000	+	_	+	+	_	+
713223004140101	1 2 KCp	3/0/2007	370,000	510,000			Т	Т		Т

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