

Update on the Southwest Wisconsin Groundwater and Geology Study August 1, 2019

Contacts:

Mark Borchardt, Mark.Borchardt@ARS.USDA.GOV, 715-387-4943

Joel Stokdyk, jstokdyk@usgs.gov, 715-384-9673

Ken Bradbury, ken.bradbury@wisc.edu, 608-263-7921

Iowa County: Katie Abbott, Katherine.Abbott@iowacounty.org, 608-930-9893

Grant County: Lynda Schweikert, Lynda.Schweikert@wi.nacdnet.net, 608-723-6377 #4

Lafayette County: Terry Loeffelholz, Terry.Loeffelholz@lafayettecountywi.org, 608-776-3836

The Southwest Wisconsin Groundwater and Geology (SWIGG) study aims to better understand the quality of groundwater accessed by private wells in Grant, Iowa, and Lafayette Counties, specifically as related to potential contamination from nitrate and microbiological contaminants. The overall goal is to provide data that can identify issues and guide potential solutions.

Current Objectives

- 1) Evaluate private well contamination using indicator bacteria (total coliform and *E. coli*) and nitrate based on randomized synoptic sampling events,
- 2) Identify the source of contamination in a subset of total coliform- and nitrate-positive wells once per season using microbial tests that distinguish between human, bovine, and swine fecal sources.

The first objective was completed through two synoptic (“snapshot”) sampling events (November 9-10, 2018 and April 12-13, 2019) that tested a total of 840 samples from randomly selected wells across the three-county region. Overall, 42% (November) and 27% (April) of sampled wells had evidence of contaminated groundwater (See Table 1).

Table 1. Percentage of wells positive for total coliform, *E. coli*, and high nitrate* for two sampling events.

| County | November event (301 wells tested) | | | | April event (539 wells tested) | | | |
|------------|-----------------------------------|----------------|---------------|---------------------------------|--------------------------------|----------------|---------------|---------------------------------|
| | Total coliform | <i>E. coli</i> | High Nitrate* | Total coliform or High Nitrate* | Total coliform | <i>E. coli</i> | High Nitrate* | Total coliform or High Nitrate* |
| Grant | 38 | 7 | 12 | 43 | 14 | 1 | 14 | 25 |
| Iowa | 26 | 3 | 13 | 33 | 14 | 1 | 13 | 25 |
| Lafayette | 40 | 3 | 27 | 55 | 23 | 4 | 21 | 36 |
| All | 34 | 4 | 16 | 42 | 16 | 2 | 15 | 27 |

*High nitrate exceeds the health standard of NO₃-N > 10 mg/L

The first of four sampling events for objective two was completed in April 9-13, 2019. Thirty-five wells were randomly selected from those previously testing positive for total coliform bacteria or with nitrate that exceeded the drinking water standard (10 mg/L). Samples were analyzed for pathogens and non-pathogenic microorganisms capable of distinguishing human wastewater and livestock manure (“microbial source tracking”). We sent homeowners their results this week; all participants will remain confidential.

We detected contamination of fecal origin in 32 of 35 wells, including microorganisms that indicate human wastewater (30 wells), cattle manure (17 wells), and swine manure (5 wells; see

Table 2). We also detected microorganisms capable of causing illness in 13 wells; we will call these homeowners to provide more information.

Table 2. Results from the first round of well testing for pathogens and microbial source tracking. Only organisms we detected are listed; see complete list in Table 3.

| Microbe group | Microorganism | No. Positive Wells |
|------------------------------|-----------------------------------|--------------------|
| Human-specific pathogens | <i>Cryptosporidium hominis</i> | 1 |
| | Human adenovirus groups A-F | 2 |
| | Human enterovirus | 1 |
| Human or livestock pathogens | <i>Cryptosporidium parvum</i> | 2 |
| | <i>Cryptosporidium</i> spp. | 4 |
| | Rotavirus group A (NSP3 gene) | 3 |
| | Rotavirus group A (VP7 gene) | 1 |
| | <i>Salmonella</i> (invA gene) | 7 |
| | <i>Salmonella</i> (ttr gene) | 5 |
| Human wastewater | <i>Bacteroidales</i> -like Hum M2 | 6 |
| | Human <i>Bacteroides</i> | 29 |
| Bovine manure | Bovine polyomavirus | 1 |
| | Ruminant <i>Bacteroides</i> | 16 |
| Swine manure | Pig-1- <i>Bacteroidales</i> | 3 |
| | Pig-2- <i>Bacteroidales</i> | 3 |
| Pathogen* | | 13 |
| Any microorganism* | | 32 |

*The value for Pathogen and Any microorganism are less than the sum of individual microorganisms because some wells were positive for more than one microorganism.

The evidence of fecal material from both human and livestock sources is clear from these data, but there is not a straight-forward step from these results to health risk. We expect the percentage of wells that test positive to differ in subsequent sampling events because weather and land use change over time. We emphasize that it's too soon to assess which contamination source (septic systems or livestock) is more prevalent. Finally, our tests only identify fecal sources of contamination, like wastewater and manure, and do not capture other potential contaminants or sources of contamination, like fertilizers.

Different wells will be randomly selected for the next sampling rounds. The next round is scheduled for August. The temporal component of the study design is important to capture to capture a full picture of groundwater quality and factors related to contamination.

As part of the study we will assess well construction and geological characteristics (e.g., well age, depth to bedrock) that affect total coliform and nitrate contamination. We are currently locating well construction reports for sampled wells to compile well characteristics. We will begin the statistical analyses after the sampling campaign is completed.

The Southwest Wisconsin Groundwater and Geology study is a collaborative effort among Grant, Iowa, and Lafayette Counties and researchers from USDA, USGS, and WGNHS, with

additional funding from Lafayette Ag Stewardship Alliance and the Iowa County Uplands Watershed Group.

Table 3. List of pathogens and microorganisms tested to identify contamination source. Of these, only organisms we detected are included in Table 2.

| Pathogens | |
|----------------------------------|--|
| Pathogen type | Microorganism |
| Only found in humans | <i>Cryptosporidium hominis</i> |
| | Human adenovirus groups A-F |
| | Human enterovirus |
| | Human polyomavirus |
| Found in humans or livestock | Norovirus genogroup I |
| | <i>Campylobacter jejuni</i> |
| | <i>Cryptosporidium parvum</i> |
| | <i>Cryptosporidium</i> species |
| | <i>Giardia lamblia</i> group B |
| | Hepatitis E virus |
| | Norovirus genogroup II |
| | Pathogenic <i>E. coli</i> |
| | Rotavirus group A (NSP3 gene) |
| | Rotavirus group A (viral protein gene) |
| | Rotavirus group C |
| | <i>Salmonella</i> (<i>invA</i> gene) |
| | <i>Salmonella</i> (<i>ttr</i> gene) |
| | Shiga toxin1-producing bacteria |
| Shiga toxin2-producing bacteria | |
| Microbial source tracking | |
| Contamination source | Microorganism |
| Human wastewater | <i>Bacteroidales</i> -like Hum M2 |
| | Human <i>Bacteroides</i> |
| Bovine manure | <i>Bacteroidales</i> -like cow M2 |
| | <i>Bacteroidales</i> -like cow M3 |
| | Bovine adenovirus |
| | Bovine enterovirus |
| | Bovine polyomavirus |
| Ruminant <i>Bacteroides</i> | |
| Porcine manure | Pig-1- <i>Bacteroidales</i> |
| | Pig-2- <i>Bacteroidales</i> |
| | Porcine adenovirus |
| | Porcine epidemic diarrhea virus |