Diseases caused by bacterial pathogens in water still pose a significant threat to public health and the environment, especially in rural communities. Bacteria enter water bodies via animal and human fecal wastes and can survive in water systems, serving as a reservoir for future infections.

Maintaining a clean water supply and identifying contaminated water is a worldwide environmental challenge. Nonpoint-source pollution, such as agricultural runoff from pastures, cropland, and septic systems, accounts for more than half of the water quality impairments in the United States. Identification of nonpoint sources of pollution has been a challenge but is needed to effectively remediate or prevent contamination of water. Livestock serve as the source for a number of bacteria that cause illness in humans (E. coli, Salmonella, Campylobacter, etc.) and can increase these bacterial numbers without suffering from disease themselves. This adds to the amount of bacteria in the environment. Exposure of water to the feces of humans or wildlife is associated with different human health risks.

A recent study, published in the May–June 2013 issue of the *Journal of Environmental Quality*, focused on the Upper Sugar Creek watershed, a mixed-use watershed with many headwater streams, and one of the most contaminated waterways in Ohio. This watershed supports various types of land use that can serve as potential contaminant sources, including residential areas, crop fields, livestock operations, and natural forested areas. The headwater streams of this mixed-use watershed are suitable for examining bacterial contamination from human activity, agricultural activity, and/or wildlife.

To identify sources of fecal contamination, a method to determine the source of the bacteria called source tracking was evaluated. Detecting and measuring the most important fecal indicator bacteria aid in the assessment of the degree of contamination. New molecular techniques can assess bacterial contamination rapidly and accurately by detecting and measuring indicator bacteria that are difficult to grow in the laboratory.

In the current study, a team of researchers at the Ohio State University combined the new molecular techniques with microbial source tracking. Their target bacterium, known to be abundant in human and animal feces but which does not cause illness, was *Bacteroidales*. The team determined how *Bacteroidales* concentrations varied with space and time in the Upper Sugar Creek watershed and whether the *Bacteroidales* came from humans, ruminants (e.g., cows), or other sources. The group also investigated whether *Bacteroidales* predicted the presence of other bacteria in feces known to cause illness in humans.

The study revealed lower numbers of ruminant-specific (i.e., from agricultural origins) *Bacteroidales* markers in water samples collected between rainstorm events compared with *Bacteroidales* from humans. They found that the *Bacteroidales* contamination and thus had a significant positive relationship occurred between *Bacteroidales* and specific pathogenic bacteria E. coli.

What is learned from this study can be applied to other watersheds with mixed land uses, the authors say, and they recommend that assessment of health risks with fecal contamination be done using a complement of approaches. They believe the new molecular detection of *Bacteroidales* have great potential for predicting contamination of water by human and animal feces and for distinguishing whether the bacteria come from human or other animal sources.