



Science
Societies

Capturing Multiple Sources of Antimicrobial Resistance in Groundwater

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Sampling groundwater from a private well in Kewaunee County, WI, in 2016. Photo by Joel Stokdyk.

Antimicrobial resistance is a global public health problem, contributing to more than 2 million infections per year in the U.S. alone. It has been characterized as a “OneHealth” problem because human, animal, and environmental factors are all believed to contribute. However, very few studies on antimicrobial resistance capture all three of these sectors simultaneously.

A research team working in Wisconsin's rural northeast examined the presence of antimicrobial resistance genes (ARGs)—the genetic basis of resistance in bacteria—in groundwater impacted by both residential septic systems and land applied dairy manure. They related ARGs detected in household wells to land use, rainfall, groundwater conditions, and well construction. They found that septic systems were the most common land use factor but also that ARGs with genetic markers for humans and cows were present at similar rates.

This study found that waste from humans and cows contributed equally to contamination of groundwater by ARGs in this setting. Mitigation efforts that consider both sources of antimicrobial resistance may be more effective than those that focus on a single source.

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