

ASSESSING PATHOGENS IN A DRINKING WATER SOURCE: INVESTIGATIONS IN THE GRAND RIVER WATERSHED

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WHY DID WE DO THIS RESEARCH?

Source water characterization is an important component in the multi-barrier protection of drinking water, and accurate data on pathogens is critical for treatment design, monitoring and risk assessment. This study determined pathogen loadings from the Grand River watershed and measured pathogen occurrence and concentrations in river water. Baseline and peak pathogen concentrations were measured through frequent sampling and over a long time period. The project also developed new methods for pathogen detection and characterization, with a focus on molecular (nucleic-acid-based) methods that are specific for living cells. Pathogen sources were assessed, including human and animal influences. The study also evaluated farmer incentives for implementing source water protection initiatives.

Results from this project are relevant to municipal drinking water providers, conservation authorities, watershed researchers, farmers, and federal and provincial environment and public health agencies.



HOW WAS THE RESEARCH CONDUCTED?

River water samples were collected from various locations, and pathogens and water quality parameters were monitored. Sub-typing methods were developed and used to identify potential contaminant sources (animal, wildlife, human). Agricultural surveys and literature data were used in models to predict the loading and transport of three types of pathogens important for drinking water (*Cryptosporidium*, *Campylobacter*, and *E. coli* O157).

WHAT ARE THE IMPLICATIONS FOR STAKEHOLDERS AND DECISION MAKERS?

- Pathogen concentrations fluctuated considerably and were rarely correlated with water quality indicators. Therefore, water treatment systems must ensure that removal of peak pathogen concentrations can be continuously achieved.
- Both point and non-point sources are important contributors of pathogens and need to be considered for source water protection.
- Data from these projects have been used for risk assessment studies to ensure that drinking water treatment processes are robust.
- The approaches, methods and results from this study are applicable to other watersheds in Canada.

WHAT WERE THE RESULTS?

- *Cryptosporidium*, *Giardia* and *Campylobacter* were frequently detected throughout the watershed.
- *E. coli* O157:H7, *Salmonella* and human enteric viruses were rarely detected.
- Pathogens were detected at low but highly variable concentrations and were poorly related to commonly used water quality indicators and weather events.
- Molecular-based methods provided accurate data on cell concentrations, and newly developed methods could rapidly detect viable cells.
- Sub-typing methods identified that pathogens from both animal and human sources were present.
- Modeling analysis showed cattle and other farm animals were important contributors to pathogen loading.
- Models predicted that tile drainage was important for pathogen loading in the watershed.
- A farmers' decision to participate in watershed protection measures was mostly influenced by the value of the grant combined with performance incentives.

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