

## *CONFÉRENCE*

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#### **Using customized DNA microarrays for microbial pathogen detection and source tracking in assessing water quality.**

In assessing water quality, fecal pollution monitoring is of great significance for public health as the major source of waterborne pathogens is derived essentially from the large number of pathogenic microorganisms associated with contaminating fecal material. Considering that over 60% of emerging infectious disease events are caused by the transmission of an infectious agent from animals (zoonoses), with 75% of these originating from wildlife, fecal source tracking assumes even greater importance.

Due to the plethora of fecal-associated pathogens, the microbiological quality of water is primarily monitored using fecal indicator organisms, such as total coliforms, fecal coliforms, *Escherichia coli*, enterococci and *Clostridium perfringens* yet this approach provides little information as to the pathogenicity of the specific organism as well as the contamination source.

Comprehensive analyses of complex DNA samples with regards to microbial biodiversity, single isolate genotyping, microbial virulence assessment and source tracking requires a multitude of gene queries. Exploitation of the parallel processing power of custom designed DNA microarrays provides a powerful way to address this problem through the probing of numerous gene targets simultaneously. This presentation will discuss the design and deployment of custom DNA microarrays to detect and evaluate the potential virulence of water pathogens and the source identification of animal fecal contamination in Canadian watersheds.

**Vendredi 24 février 2012 à 11 h 30**  
**Pavillon Claire McNicoll, salle Z-255**

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