

Quantification of Pathogens and Sources of Microbial Indicators for QMRA in Recreational Waters

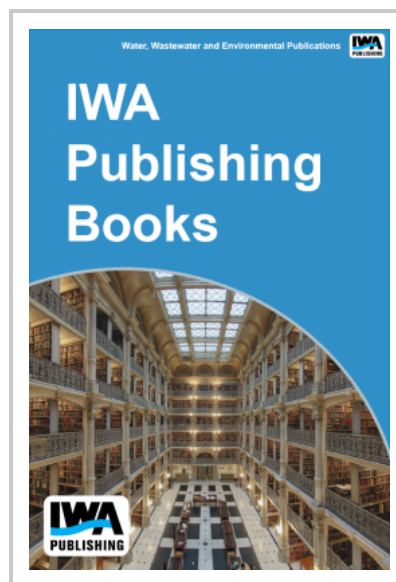
This study has increased knowledge about relationships between pathogen indicators, source identifiers and pathogens to support Quantitative Microbial Risk Assessment (QMRA) efforts and the implementation of revised recreational water quality criteria. Data gaps pertaining to waterborne pathogens and indicators in fecally-impacted discharges to recreational waters were identified and filled by targeted monitoring campaigns in three geographic regions. Study design involved simultaneous detection of pathogens in water samples using a combination of genetic, culture- and microscopy-based methodologies for *Salmonella*, *Campylobacter jejuni*, *Vibrio cholerae*, *Cryptosporidium*, *Giardia*, *Toxoplasma gondii*, adenoviruses, enteroviruses, noroviruses, rotaviruses, Bacteroidales, *Enterococcus*, and *Escherichia coli*.

The project team worked closely with experts and stakeholder groups in order to advance the understanding and applicability of QMRA for risk management purposes. QMRA analyses revealed Norovirus as the most dominant health risk followed by rotavirus. Norovirus and *Enterococcus* both had significant correlations with a number of pathogens in discharges.

Using qPCR data on the fecal source identifier Bacteroidales a new model can predict the true amount of human fecal contamination in a water sample by relating a human-associated genetic marker to a universal assay for fecal sources. The model output can then be used to implement and evaluate management options intended to restore microbial water quality.

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