***Cryptosporidium* and *Escherichia coli* (*E. coli*) concentrations in three southwestern rivers of Ghana**

Saeed Ibn Idris Kofi Yeboah [ac], Jane Tanner [a], Tomaž Urbič [b]

[a]Institute for Water Research, Rhodes University, Grahamstown, South Africa

[b]Faculty of Chemistry and Chemical Technology, University of Ljubljana, Večna Pot 113, SI-1000, Ljubljana, Slovenia

[c]Department of Civil and Environmental Engineering, University of Energy and Natural Resources, Sunyani, Ghana

Corresponding author: Saeed Ibn Idris Kofi Yeboah (saeed.yeboah@uenr.edu.gh /saeed.yeboah@ru.ac.za)

Abstract

Cryptosporidium and *E. coli* are the leading causes of diarrhoea and infant mortality worldwide. A better understanding of the sources, fate, and transport of these pathogens via rivers is vital for effective management of waterborne transmission, especially in sub-Saharan Africa, where rivers serve as critical domestic water sources yet receive increasing volumes of untreated waste. Modelling fate and transport of waterborne pathogens in river systems is critical for understanding microbial water quality and supporting public health and clean water goals. However, direct pathogen sampling in these basins is minimal, making modelling essential to fill the gaps. We present hydrological microbial modelling with SWAT to simulate river discharge and pathogen transport across the Tano, Ankobra, and Pra river basins in Ghana. Model performance for streamflow was satisfactory across all basins (R^2 = 0. 58–0. 90; NSE = 0. 60–0. 79). We found that point pollution sources, mainly from human faeces, were more dominant than diffuse sources for *E. coli* in the Ankobra and Pra basins, whereas Cryptosporidium contamination was controlled predominantly by diffuse agricultural pathways across all basins. Validation shows that SWAT medians mostly fall within the range of observed concentrations. The model generally produces *E. coli* concentrations that differ by less than 1 $\log_{10}$ CFU/100 mL from observed values, and Cryptosporidium concentrations that differ by approximately 0 0.2–0. 4 log10 oocysts L^{-1}. This is likely mainly due to the absence of recovery efficiency in the observations, which are consequently likely underestimated, particularly for Cryptosporidium. Sensitivity analysis indicates that microbial survival is most affected by changes in temperature-dependent decay, soil adsorption, and percolation rates. The findings of this study open up many new opportunities and avenues for research, including scenario analysis to examine the influence of global change and management strategies on bacterial and protozoan concentrations in rivers, as well as risk assessments to evaluate human health risks.

Keywords: *Cryptosporidium; Escherichia coli;* SWAT model; hydrological microbial modelling; source attribution; tropical river basins; Ghana

Advancing Modelling of Waterborne Pathogens in River Systems: Approaches, Process Representations, Challenges, and Key Considerations for a Changing World

Saeed Ibn Idris Kofi Yeboah [ab], Jane Tanner [a], Esther Boahen [b]
[a]Institute for Water Research, Rhodes University, Grahamstown, South Africa
[b]Department of Civil and Environmental Engineering, University of Energy and Natural Resources, Sunyani, Ghana
Corresponding author: Saeed Ibn Idris Kofi Yeboah (saeed.yeboah@uenr.edu.gh /saeed.yeboah@ru.ac.za)

Abstract

Modelling fate and transport of waterborne pathogens in river systems is critical for understanding microbial water quality and supporting public health and clean water goals. The reliability of these models depends on how accurately they represent faecal contamination pathways, environmental controls, and transport dynamics across diverse socio-environmental contexts. Approaches to modelling these complex relationships vary, and some aspects are difficult to reliably represent and can be subject to large uncertainties. We systematically evaluate 106 studies published between 2000 and 2025 to examine how riverine pathogen models conceptualise contamination sources, hydrological processes, and environmental drivers, and how these choices affect model applicability under changing climatic conditions. We find that some critical sanitation conditions, human and livestock waste sources, and land-use practices are often underrepresented or omitted, limiting model credibility, particularly in low- and middle-income regions where decentralised sanitation and informal drainage dominate. Many widely used models were developed in high-income contexts with different hydrological regimes, monitoring infrastructure, and sanitation standards, raising questions about their transferability to many Global South catchments. Our analysis further shows that increasing model complexity does not always improve predictive accuracy; simpler models can be effective when they capture the main faecal pathways and key controlling processes, especially in data-limited settings. Incorporating current and future climate change scenarios into riverine pathogen modelling is the way forward for effective water quality management given the sensitivity of pathogen fate and transport to climate factors. To conclude, pathogen-modelling must account for the full range of sanitation-related faecal pathways that govern microbial loading in many catchments if predictions are to remain credible. Our review paves the way for exciting new opportunities for advancing riverine pathogen modelling, guiding the development and application of models that are credible, transferable, and relevant to both current and future water quality challenges in a multitude of contexts.

Keywords: waterborne pathogens; river systems; fate and transport modelling; sanitation-related faecal pathways, climate change; Process representation; uncertainty analysis, developing nation contexts.