EGU21-14863
https://doi.org/10.5194/egusphere-egu21-14863
EGU General Assembly 2021

Microbiological requirements for safe drinking water production at a large river impacted by human wastewater: a scenario analysis

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Background: Rivers are important sources for drinking water supply, however, they are often impacted by wastewater discharges from wastewater treatment plants (WWTP) and combined sewer overflows (CSO). Reduction of the faecal pollution burden is possible through enhanced wastewater treatment or prevention of CSOs. Few methodological efforts have been made so far to investigate how these measures would affect the long-term treatment requirements for microbiologically safe drinking water supply under future changes.

Objectives: This study aimed to apply a new integrative approach to decipher the interplay between the effects of future changes and wastewater management measures on the required treatment of river water to produce safe drinking water. We investigated scenarios of climate change and population growth, in combination with different wastewater management scenarios (i.e., no upgrades and upgrades at WWTPs, CSOs, and both). To the best of our knowledge, this is the first study to investigate this interplay. We focussed on the viral index pathogens norovirus and enterovirus and made a cross-comparison with a bacterial and a protozoan reference pathogen (Campylobacter and Cryptosporidium).

Methods: We significantly extended QMRAcatch (v1.0 Python), a probabilistic-deterministic model that combines virus fate and transport modelling in the river with quantitative microbial risk assessment (QMRA). To investigate the impact of climatic changes, we used a conceptual semidistributed hydrological model and regional climate model outputs to simulate river discharges for the period 2035 – 2049. We assumed that population growth leads to a corresponding increase in WWTP discharges. QMRAcatch was successfully calibrated and validated based on a four-year dataset of a human-associated genetic MST marker and enterovirus. The study site was the Danube in Vienna, Austria.

Results: In the reference scenario, approx. 98% of the enterovirus and norovirus loads at the study site (median: 10^{10} and 10^{13} N/d) originated from WWTP effluent, while the remainder was via CSO events. The required log reduction value (LRV) to produce safe drinking water was 6.3 and 8.4 $\log_{10}$ for enterovirus and norovirus. Future changes in population size, river flows and CSO events did not affect these treatment requirements, and neither did the prevention of CSOs. In contrast, in the scenario of enhanced wastewater treatment, which showed lower LRVs by 2.0 and 1.3 $\log_{10}$, climate-change-driven increases in CSO events had a considerable impact on the treatment requirements, as they affected the main pollution source. Preventing CSOs and installing enhanced treatment at the WWTPs together had the most significant positive effect with a reduction of LRVs by 3.9 and 3.8 $\log_{10}$ compared to the reference scenario.

Conclusions: The integrative modelling approach was successfully realised. The simultaneous consideration of source apportionment and concentrations of the reference pathogens were found crucial to understand the interplay among the effects of climate change, population growth and pollution control measures. The approach was demonstrated for a study site representing a large river impacted by WWTP and CSO discharges, but is applicable at other sites to support long term water safety planning.