

Increased use of Quaternary Ammonium Disinfectants during the SARS-CoV-2 Pandemic – a Driver of Antimicrobial Resistance in the Environment?

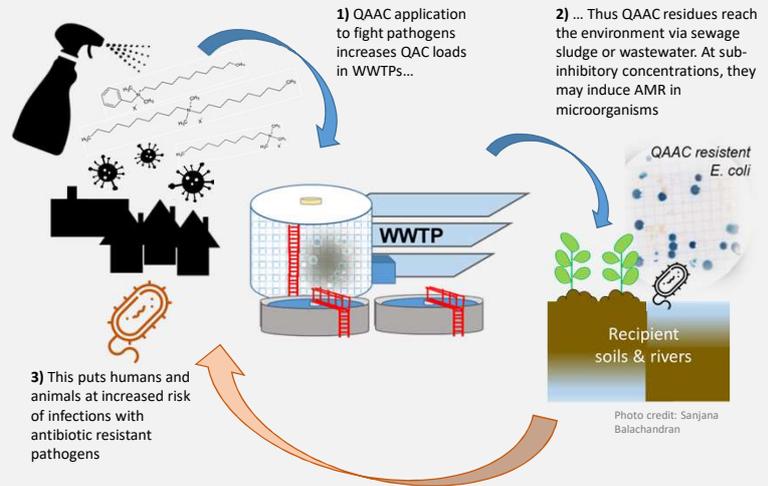
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Background

- During the SARS-CoV-2 pandemic disinfectant use increased around the world¹. While intended to minimize virus transmission, disinfectants could contribute to the spread of antimicrobial resistance (AMR)^{1,2,3}.
 - Many disinfectants contain **quaternary alkylammonium compounds (QAACs)**. With potential to induce resistance adaptations in microorganisms at sub-inhibitory concentrations³, QAACs could select for **cross- and multi-resistance** against commonly used therapeutic antibiotics.
 - **Wastewater treatment plants (WWTPs)** are known hot spots for the spread of AMR into the environment⁴.
- AMR is projected to cause 10 million annual deaths by 2050⁵. This calls for investigation of its potential drivers in the environmental – including increasing residues of QAACs.**



Hypotheses

- 1) QAAC concentrations in WWTPs (influent, activated sludge, dewatered sludge and effluent) and suspended particles in downstream surface waters rose after the onset of the the SARS-CoV-2 pandemic.
- 2) Elevated QAAC concentrations in the environment enhance QAC- and multi-resistance development in potentially pathogenic and environmental bacteria. Particle-attached bacteria are especially affected due to co-localization with adsorbing QAACs.
- 3) Increased QAAC concentrations in soils and surface waters inhibit microbial degradation of antibiotics, with unknown effects for the selection of resistant bacteria.

Materials and Methods

Sampling before and after pandemic begin

- Three Hessian WWTPs (rural and urban)
- the German rivers Saar, Mulde and Rhine, each with varying wastewater content (provided by the Environmental Specimen Bank)

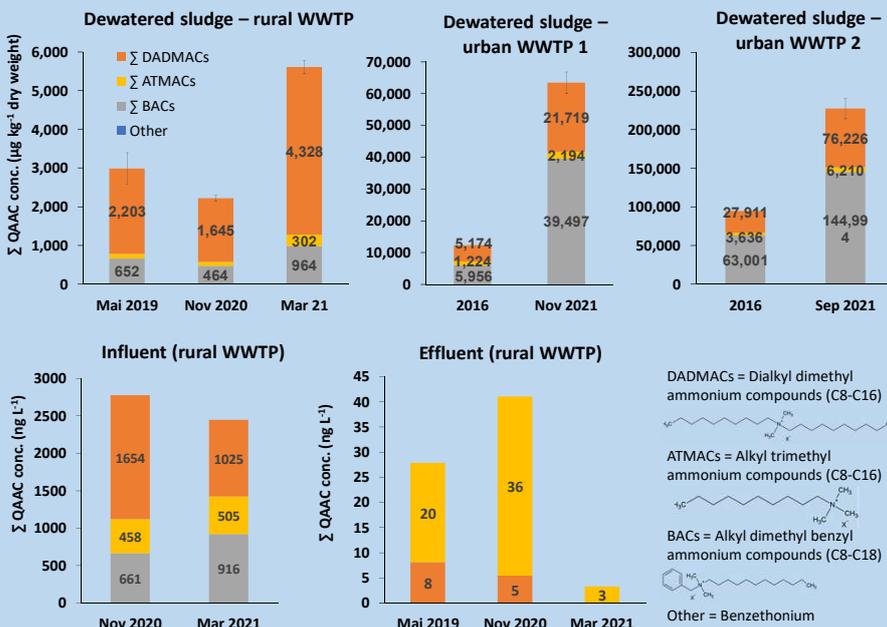
Quantification of QAAC concentrations

- Matrix-tailored solid phase extraction of QAACs^{6,7}
- Analysis of 18 QAAC homologues by high performance liquid chromatography-tandem mass spectrometry⁶

Identification of hot spots

- Serial filtration - size fractionation to differentiate truly-dissolved from particle- attached QAACs and microorganisms

Preliminary Results



Key findings

- 1) QAACs were present at varying concentrations in sewage sludge, influent and effluent of all three WWTPs
- 2) DADMACs and BACs dominated in sewage sludge, ATMACs in effluent -> possibly due to differences in hydrophilicity
- 3) Total QAAC concentrations in dewatered sewage sludge increased up to fivefold in 2021 compared to pre-pandemic years, but no clear trend for the effluent
- 4) Probably additional effect of seasonal variation in rainfall, temperature, and microbial activity

➤ Effects of SARS-CoV-2 pandemic on QAAC concentrations were visible across all studied WWTPs

Open Questions

- Are altered QAAC concentrations correlated with a change in resistance gene abundance and microbial diversity?
- How are QAAC concentrations and the resistome in riverine suspended particulate matter affected by the pandemic?
- How do elevated QAAC concentrations in soil and surface waters affect microbial activity?

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