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A glimpse into antimicrobial resistance in Berlin through wastewater surveillance

Inhalt

Antimicrobial resistance (AMR) is a growing threat to public health, and the European Union has introduced AMR monitoring regulations for wastewater (WW). Here, we implemented a multi-method approach to assess prevalence and circulation of antibiotic resistance genes (ARGs) in the Berlin metropolitan area. In October 2025, we collected samples from the Schönerlinde WW treatment plant. We profiled the resistome using two methods: i) metatranscriptomic molecular assessment and ii) culture-enriched metagenomics. Metatranscriptomic profiles revealed ARGs conferring resistance to various antibiotics in the influent samples. While these genes were co-abundant with environmental bacteria, they were also detected in plasmids common to clinically relevant bacteria. Although ARGs profiles showed a marked reduction following treatment, bacteria such as *Escherichia coli* and *Pseudomonas* could be enriched in selective media in samples taken before and after WW treatment, indicating their persistence in a viable state after treatment. The abundance of *E. coli* matched the overall occurrence of ARGs, while different *Pseudomonas* species correlated with clinically relevant genes. We demonstrate the potential of metagenomic approaches in AMR surveillance and the value of culture-enriched metagenomics in assessing the dissemination of clinically relevant ARGs through wastewater. This information is crucial for developing strategies to limit the spread of AMR in urban and suburban areas.

Keywords

AMR, Metatranscriptomics, Culture-enriched metagenomics, Wastewater

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No, I am not a Junior Scientist.

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