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Similar Wastewater Microbiomes, Distinct Resistomes: A Comparative Metagenomic Analysis of German and Nigerian Wastewaters from Diverse Sources

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Environmental contamination links antimicrobial resistance (AMR) across human, animal, and environmental compartments, but how wastewater source and infrastructure shape resistomes remains unclear. We used metagenomics to compare communities and resistomes in municipal wastewater in Germany and municipal, hospital, and slaughterhouse wastewaters in Nigeria. Bacterial communities showed limited separation (ANOSIM $R=0.059$, $p=0.278$), indicating a shared wastewater microbiome baseline. In contrast, resistomes differed significantly (PERMANOVA $p=0.023$), showing that ARG profiles diverged more strongly than underlying communities. German samples showed a homogenized, diverse resistome ($H'=2.15-2.25$), dominated by aminoglycoside, bacitracin, beta-lactam, and MLS genes. Nigerian samples showed greater heterogeneity and hotspots exceeding 2.0 log₁₀ relative abundance, driven by sulfonamide and tetracycline genes. Despite this divergence, 634 ARG subtypes (53.9%) formed a shared resistome core, while 375 variants were detected only in Nigerian samples. Co-occurrence networks linked *erm(B)* and OXA-10 with opportunistic pathogen-containing genera such as *Acinetobacter*, *Klebsiella*, and *Pseudomonas*. These findings show that similar wastewater microbiomes can harbour distinct resistomes and identify wastewater source and infrastructure as determinants of environmental AMR distribution. Hotspots highlight the need for One Health surveillance that accounts for source-specific waste streams.

Keywords

Antimicrobial Resistance, Wastewater, Metagenomics

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No, I am not a Junior Scientist.

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