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Co-occurrence of antimicrobial resistance genes and dissolved organic matter in groundwater along an urban–rural gradient in Uganda

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Groundwater is increasingly recognised as a reservoir for antimicrobial resistance genes (ARGs) [1,2], yet environmental controls on their occurrence and distribution in aquifers remain poorly understood [1,3], especially in rapidly urbanising regions of sub-Saharan Africa. Fluorescent dissolved organic matter (fDOM), especially protein-like fractions, can trace surface-derived inputs from sources that may be enriched in ARGs [4,5]. However, little is known about the co-occurrence of specific DOM components and ARGs in groundwater. Here, we quantified ARGs, mobile genetic elements (MGEs), 16S rRNA, bulk dissolved organic carbon (DOC), and fDOM across an urban–rural gradient in Jinja, Uganda, to explore these relationships. ARGs and MGEs were widespread, with MGEs most prevalent, and vancomycin resistance genes (*vanA/vanB*) and *sul1* among the most frequently detected ARGs, particularly in urban groundwater. Overall, resistome abundance and diversity were higher in urban groundwater, although considerable spatial variability was evident. Correlation and network analyses revealed co-occurrence among ARGs, MGEs, 16S rRNA, and multiple fDOM components. Among DOM components, tyrosine-like fluorescence showed the strongest positive associations with resistance genes, followed by bulk DOC and humic-like fractions. Specific MGEs (*e.g., IS1247*) and ARGs (*e.g., tetA*) co-occurred with multiple DOM components. However, total ARG abundance showed no consistent relationship with bulk DOC or fDOM, with high ARG occurrence largely confined to specific urban sites. These findings highlight spatial variability in groundwater resistomes and identify specific DOM components that co-occur with ARGs, reflecting localised environmental and anthropogenic influences.

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