



Research Paper

Dissemination of sulfonamide resistance genes in digester microbiome during anaerobic digestion of food waste leachate

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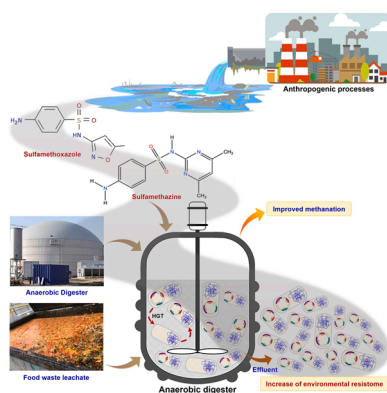
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HIGHLIGHTS

- Cumulative methane yields enhanced by 37 % under SAs loading compared to FWL alone.
- Methanosarcinales-led acetoclastic methanogenesis played a predominant role in methanation.
- Dissemination of *sul1* depended on *int1*-based HGT.
- Transmission of *sul2* was *int1*-independent.
- Methanogenesis was uninterrupted by the influence of SAs or ARGs.

GRAPHICAL ABSTRACT



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ABSTRACT

The preeminence of sulfonamide drug resistance genes in food waste (FW) and the increased utilization of high-strength organic FW in anaerobic digestion (AD) to enhance methane production have raised severe public health concerns in wastewater treatment plants worldwide. In this regard, the dissemination patterns of different sulfonamide resistance genes (*sul1* and *sul2*) and their impact on the digester core microbiota during AD of FW leachate (FWL) were evaluated. The presence of various sulfonamide antibiotics (SAs) in FWL digesters improved the final methane yield by 37 % during AD compared with FWL digesters without SAs. Microbial population shifts towards hydrolytic, acidogenic, and acetogenic bacteria in the phyla Actinobacteriota, Bacteroidota,

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