Research on Removal and Risk Control of Antibiotics and Resistance Genes in Landfill Leachate

Xiaosong He

Antibiotic resistance poses a significant threat to public health, and landfill leachate serves as a major reservoir for pharmaceuticals and personal care products (PPCPs) as well as antibiotic resistance genes (ARGs). Here, we conducted multi-sample analyses of the fate and driving mechanisms of PPCPs and ARGs in common landfill leachate treatment processes (“MBR+NF/RO,” “pretreatment + two-stage DTRO,” “biological treatment + AOP,” “pretreatment + MVR,” and “pretreatment + UF + RO + UV disinfection”) to comprehensively evaluate their associated risks. Results indicate that among all processes, “pretreatment + two-stage DTRO” achieves highly efficient and stable removal of 93.06–100% of PPCPs while significantly reducing the association between bacterial communities and ARGs in influent. The highest concentrations of ARGs in leachate were observed for multidrug resistance, macrolides, aminoglycosides, glycopeptides, bacillopeptides, and chloramphenicol, with “pretreatment + MVR” demonstrating the most stable removal efficiency for these ARGs. Key potential host bacteria carrying ARGs in the influent were Pseudomonadota, Bacillota, and unclassified_Bacteria, while only Pseudomonadota dominated in the effluent. “pretreatment + two-stage DTRO,” “pretreatment + MVR,” and “pretreatment + UF + RO + UV disinfection” reduced plasmid-encoded ARGs, but the absolute concentration of chromosomally encoded ARGs increased in all effluents. Furthermore, biological factors (microbes and MGEs) were the primary drivers of ARG presence, indicating that reducing microbial biomass and MGEs effectively enhances ARG removal rates. Our findings highlight that MGEs not only transmit ARGs across treatment processes but also significantly elevate their expression levels, providing crucial data for effective antibiotic resistance surveillance within the One Health framework.