

# Airborne Pathogens and Antimicrobial Resistance Risks in Urban Food-Waste Treatment Systems

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Urban food-waste treatment plants (FWTPs) provide favorable niches for pathogen proliferation, yet the characteristics of airborne pathogens and associated antimicrobial resistance (AMR) risks within these systems remain poorly understood. Using amplicon sequencing, metagenomic analyses, and culture-based assays, we collected indoor and outdoor air samples from two large-scale FWTPs to characterize the composition, dynamics, and risks of airborne pathogens and the resistome. Airborne pathogens were highly prevalent in FWTP air, with significantly greater abundance and diversity than in urban ambient air. Although processing stages exhibited distinct community structures, key pathogens were consistently dominated by *Acinetobacter johnsonii* and *Ralstonia pickettii*, likely owing to their high aerosolization potential. Stochastic processes primarily governed pathogen community assembly—particularly indoors, where frequent industrial operations weakened deterministic selection imposed by environmental variables. Notably, PM<sub>2.5</sub> from FWTPs carried total antibiotic resistance gene (ARG) comparable to those of wastewater treatment plant (WWTP) PM<sub>2.5</sub>, but harbored a richer repertoire of multidrug-resistance (MDR) genes; the high prevalence of MDR genes serves as an effective indicator for defining the FWTP resistome. Source-tracking analyses, metagenome-assembled genomes, and culture experiments provided convergent evidence that *Acinetobacter*-dominated pathogens play pivotal roles in the emergence and dissemination of MDR genes, warranting priority attention when designing strategies to mitigate airborne ARGs. This work underscores the importance of urban food waste in disseminating pathogens and MDR genes and calls for a reassessment of food-waste-related air pollution from a public-health perspective.