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RESEARCH & COLLABORATION PROFILE

KEY WORDS: Metagenomics, Environmental Microbiome, Antibiotic Resistance Genes (ARGs), PM2.5, Biohydrogen, Environmental Health Data Science

Research Snapshot. Dr. Kang is an environmental microbiologist who studies how air pollution shapes airborne microbial communities and antimicrobial resistance. Her work combines PM sampling, DNA-based metagenomics (16S rRNA/ITS2) and qPCR of antibiotic resistance genes with statistical and network analysis of air pollutants, PM chemical composition and meteorology across Northeast Asia (Seoul, Ulaanbaatar, Noto). She also brings bioprocess experience in thermophilic dark fermentation of high-salt food waste for biohydrogen, and currently applies statistics and AI to environmental health data on air pollution, sleep and mortality.

RESEARCH EXPERTISE

- **Airborne microbiome analysis:** optimized DNA extraction from PM filters, 16S rRNA/ITS2 amplicon sequencing and functional prediction of bacterial and fungal communities.
- **Atmospheric antimicrobial resistance:** qPCR of ARGs, mobile genetic elements and heavy metals in size-fractionated PM, with their environmental drivers and bacterial hosts.
- **Environment–microbe association modeling:** correlation, multivariate and network analysis linking microbiomes to air pollutants, ions, organics (PAHs, DCAs, alkanes) and meteorology.
- **Anaerobic bioprocess & biohydrogen:** halotolerant thermophilic consortia, dark fermentation of food waste, GC/TCD and metagenomic tracking of succession.
- **Environmental health data science:** statistics and AI on air pollution, sleep and mortality datasets (R, Python).

RECENT RESEARCH HIGHLIGHTS

- **Atmospheric ARGs (Sci. Total Environ. 2026):** systematic review (2015–2025) showing winter peaks in absolute ARG loads, highest urban burdens (tetA, sul1), and ARG/MGE co-occurrence with *Pseudomonas* and *Acinetobacter*.
- **Size/season-resolved PM microbiome (JES 2026; FESE 2025):** higher microbial load and diversity in $PM_{>2.5}$, drug-resistance pathways in both fractions, and chemical (winter/spring) vs. meteorological (summer/autumn) drivers.
- **Halotolerant biohydrogen (Renew. Energy 2026):** moderate-salinity consortium gave the highest H_2 yield (130.1 mL·g-VS^{-1}), with succession toward halotolerant *Clostridium thermopalmarium* and *Heyndrickxia coagulans*.

POTENTIAL COLLABORATION RESEARCH

Best-fit collaborator areas: environmental & applied microbiology | bioenergy & bioconversion | public & environmental health

- **1. Microbial community analysis for bioconversion:** metagenomic and functional-gene profiling of mixed cultures (e.g., waste-derived substrates) to link community shifts with process performance.
- **2. Airborne AMR & One Health surveillance:** quantifying ARGs/MGEs in air, wastewater or livestock settings and identifying their environmental drivers and microbial hosts.
- **3. Air pollution & human health:** integrating PM chemistry, microbiome and ARG data with exposure–health datasets (respiratory, sleep and mortality outcomes).

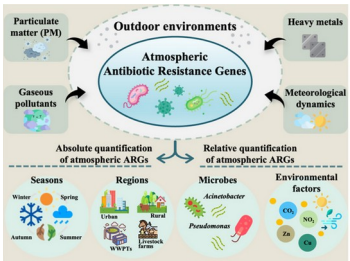
SELECTED RECENT PUBLICATIONS

- **Sci. Total Environ. 2026, 1052, 182322 —** Environmental determinants and microbial association of outdoor atmospheric ARGs.
- **Renew. Energy 2026, 271, 126022 —** Adaptive halotolerant communities for biohydrogen production from high-salt food waste.
- **J. Environ. Sci. 2026, 161, 400–410 —** Bacterial and fungal metagenomes of PM2.5 vs. TSP larger than PM2.5.
- **Front. Environ. Sci. Eng. 2025, 19(6), 75 —** Seasonal variability and atmospheric composition shaping PM2.5 bacterial and fungal communities.
- **Environ. Pollut. 2024, 348, 123834 —** PM2.5 chemical composition modulating microbial community dynamics in spring, Seoul.

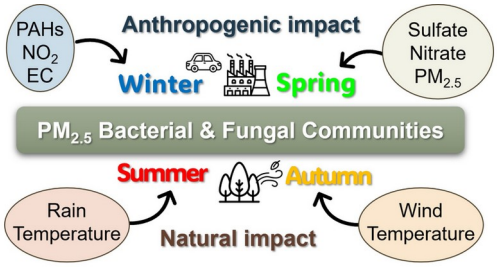
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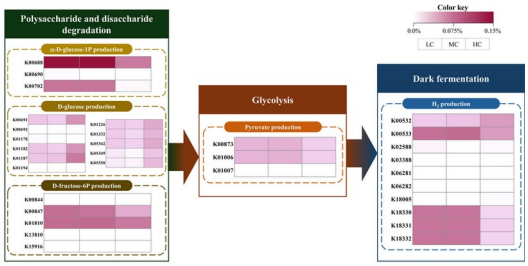
REPRESENTATIVE RESEARCH FIGURES / SCHEMES



(a) Atmospheric ARG drivers · STOTEN 2026



(b) Seasonal PM2.5 microbiome drivers · FESE 2025



(c) H2 dark-fermentation genes · Renew. Energy 2026