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Microbial Drivers of Halogenated Contaminant Cycling in Landfill Leachate

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Landfills harbour complex microbial communities that control leachate geochemistry, yet their role in contaminant transformation remains poorly understood. Leachate contains many priority contaminants including per- & polyfluoroalkyl substances (PFAS), polychlorinated biphenyls (PCBs), and halogenated flame retardants (HFRs), many of which persist and pose environmental risks. Despite microbes harbouring metabolic pathways that can transform these pollutants, their contributions in landfills are not well-characterized. In this study, we couple geochemical analyses of landfill leachate to whole-community DNA sequencing to examine how microbial community structure and pollutant transformation pathways respond to gradients of halogenated pollutants in landfills.

Leachate from four Ontario landfills (BF, DV, HG, Q) was collected in late 2023 and analyzed for chemical classes including, PFAS, PCBs, and HFR. DNA was extracted for 16S rRNA amplicon and shotgun metagenomic sequencing. Metagenome-assembled genomes were taxonomically classified and functional genes were annotated using custom databases developed for halogenated compounds. Ordinations, vector fitting, hierarchical clustering, and regression analyses were used to evaluate relationships between microbial composition, functional potential, and contaminant concentrations to identify potential microbial drivers of landfill biogeochemistry.

Across landfill sites, halogenated contaminant profiles spanned an order-of-magnitude gradient, site Q exhibiting the most distinct PFAS and PCB profiles. Microbial community structure and functional gene analysis showed site-specific clustering aligned with contaminant composition, indicating that composition, rather than total load, structured microbial assemblages. Functional ordinations mirrored taxonomic patterns, suggesting shifts in metabolic potential along contaminant gradients. Reductive dehalogenase (RDase) genes had higher abundances of a couple genes in less contaminated sites, whereas higher contaminated sites had greater diversity of low-abundance genes. RDase gene abundance did not significantly correlate with total PCB or PFAS concentrations, however, we did see statistically significant negative correlations with some individual PFAS compounds.

Landfill microbial communities shift in response to differences in halogenated contaminant composition and harbour widespread dehalogenation potential. These findings suggest that contaminant identity shapes microbial structure and function in landfills. By integrating geochemistry and genomics, this study provides new insights into the microbial processes that influence the fate and toxicity of persistent pollutants. Furthermore, this highlights the potential for leveraging intrinsic microbial functions in future bioremediation strategies.