Advances in Microbial Genomics and Ecology: Unveiling the Hidden Dynamics of Non-Tuberculous Mycobacteria in Built Environments

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Exploring microbial life in built environments is increasingly important for understanding human health. This presentation highlights genetic and ecological approaches to studying the transmission pathways of non-tuberculous Mycobacterium (NTM) species, particularly in residential settings. Non-tuberculous mycobacteria, common in water sources and households, can cause infections, mainly in elderly women and immunocompromised individuals. Understanding their environmental reservoirs and transmission pathways is crucial since they do not spread human-to-human.

Our research uses advanced genomic techniques to analyze bioaerosol samples from urban and rural settings. High-volume air samplers and long-read sequencing technologies identify microbial communities. We also examine the impact of environmental factors such as CO_2 levels, temperature, and particulate matter on indoor microbial dynamics.

We have sequenced bioaerosol samples from urban and rural areas, showing significant differences in microbial community composition and diurnal variations in bioaerosol concentrations, which affect infection risks. Parameters like CO_2 levels and temperature significantly influence indoor microbial counts. Real-time monitoring indicates the need to consider viable particulate matter when assessing ventilation's effects on microbial dynamics. Genome-wide association studies (GWAS) have identified specific genomic regions in NTM that differ in recombination frequency and type, contributing to understanding their evolutionary dynamics. Surveys of drinking water treatment plants in Hiroshima reveal various NTM species, with water treatment processes, including chlorine levels, affecting microbial community structures.

Our analysis of NTM in built environments highlights the need for precise and holistic methods to assess bioaerosol impacts on public health. We aim to standardize sampling and analytical procedures, improving risk assessments and informing public health interventions.

We plan to expand sampling efforts, enhance questionnaire methodologies, and conduct GIS analyses with more patient data. International and interdisciplinary collaboration will be crucial for advancing microbial genomics and ecology.

Keywords: Non-tuberculous Mycobacteria, Bioaerosol, Microbial Genomics, Indoor Air Quality, Environmental Microbiology