

THE METRO SYSTEM MAY MODULATE THE SKIN MICROBIOME AND RESISTOME BY ITS ENVIRONMENTAL EXPOSURES AND INNER- AND INTERCITY TRAFFIC FLOWS

Kang Kang^{1,2}, Jun Li^{1,2}, Gianni Panagiotou^{1,2}

¹Systems Biology & Bioinformatics Group, School of Biological Sciences, Faculty of Sciences, The University of Hong Kong, Hong Kong S.A.R., China

²Systems Biology & Bioinformatics Unit, Leibniz Institute for Natural Product Research and Infection Biology, Hans Knöll Institute, 07745 Jena, Germany

Skin functions as the primary interface between the human body and the external environment, therefore great attention is given to the disinfection of high-density urban environments to limit the spread of pathogens. Yet, we have little understanding of how the built microbiome varies within urban environments and what factors drive the diversity and risk of pathogenicity therein. We used shotgun metagenomic sequencing to profile the palm microbiome after contact with handrails within the Hong Kong Mass Transit Railway (MTR) system. Our sampling has covered different times (AM vs PM commute), over the course of 3 days and targeted distinct lines (8) which serve different urban centers in the city. Intraday sampling time was identified as the primary determinant of the variation and recurrence of the community composition, whereas human-associated species and clinically important antibiotic resistance genes (ARGs) –including *tetM*, *ermC* and *vanB*– were captured as PM signatures. Line-specific signatures were notably correlated with line-specific environmental exposures and civic characters, and losing their discriminatory power over time in the operating hours. For instance, high uniqueness was observed in the most topologically isolated line, which runs by a polluted river. The aquatic species and indicator organisms for sewage could also be identified as signature species of this line, in AM communities in particular. The only cross-boundary line appeared as an outlier in most analyses including the community diversity and dissimilarity. This line had the 2nd highest abundance of clinically important ARGs and community-wide dissemination potential, and the greatest intraday increments in the abundance of ARGs and clinically important ARGs (33.5% and 24.1%), suggesting a potential cross-boundary ARG transmission, especially tetracycline resistance.

Keywords: Microbial diversity, Microbiome signatures, Traffic flow, Public transit connectivity, Pathogenicity, ARG transmission and dissemination