Microbial interaction network reveals co-occurrence patterns across built environment microbiomes

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In the post-industrial era, rapid urbanisation has led to increased habitation in built environments. Microorganisms in these environments profoundly influence human health by directly altering physiological, immunological and mental development. By creating a barrier for natural exposure, contemporary built environments restrict the transmission of beneficial microorganisms and reduce microbial diversity, exacerbating chronic diseases such as allergies and asthma. Accounting for microbial composition during the design of built environments is crucial, not only to improve health outcomes but also to track disease outbreaks and potential biothreats. Recent advances in metagenomic sequencing have provided us with the microbial composition of our environments of interest. Deciphering microbial associations in these environments can provide valuable insights into the communities. In this study, through a systematic approach combining network biology and metabolic modelling, we explored microbial communities across different built environments, including hospital spaces, offices, and metro stations (MetaSUB), utilising approximately 600 shotgun samples. Our analysis revealed distinct and diverse microbial communities, with offices exhibiting the lowest diversity, followed by metro stations and hospitals. The hospital environment contained a significant fraction of nosocomial pathogens responsible for healthcare-associated infections (HAIs). Our co-occurrence network analysis demonstrated that despite similar microbial compositions, built environments harbour unique microbial interactions, highlighting the importance of the environment in shaping microbial interactions. Spatial microbial trajectory analysis indicated a convergence of microbial communities from hospitals and offices with those in metro stations, emphasising the role of public transport in microbial dissemination. Further, we investigated the microbial interactions that drive community structure. Utilising genome-scale metabolic models, we demonstrated metabolic dynamics within these microbial communities. We also seek to extend our study to understand how microbial invasion disrupts the stability of these communities and compare it with other built environments, including the International Space Station. These distinct microbial associations not only illuminate microbial adaptation and succession but also hold implications for infection control and environmental management.