H124 Inferring Patterns of Occupancy From Human Microbial Signatures

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After attending this presentation, attendees will better understand current methods used to match humans to places they have inhabited and objects they have interacted with through shared microbial signatures. This presentation will educate attendees about the extent to which the skin microbial community of occupants shapes the microbial ecology of built environments.

This presentation will impact the forensic science community by incorporating modern methods in microbial ecology and bioinformatics into forensic applications and developing the concept of human microbial fingerprints.

This presentation will discuss three recent large-scale studies of temporal microbial interaction between humans and the built environment focusing on: (1) personal homes; (2) on hospital rooms; and, (3) on the shifting microbial signatures on shoes that accompanies a change in location.

Human skin and respiratory cavities harbor a vast array of microbial consortia that can be readily dislodged and transferred to their surrounding environment. Such communities are extremely diverse, with great variation both between individuals and between different body sites of the same individual, yet they are sufficiently stable over time that interpersonal variation exceeds temporal variation, even across sampling intervals of many months. The idea that individuals harbor a unique "*microbial fingerprint*" has been well supported by the vast number of microbial surveys that have accompanied the rise of high-throughput sequencing technology, and such "fingerprints" have been shown to have great predictive power in both medical diagnostics and the emerging field of microbial forensics, which utilizes microbial signatures to determine interactions between individuals and objects.

In this study of home-associate microbial communities, residents were successfully matched to their homes based on similarity between the microbial communities of their skin and home surfaces. Further, the relative contribution of different residents, including pets, to different surface types was also able to be determined. This study was even able to predict when a resident of a home had left for travel by determining when their microbial signal diminished or vanished.

In a second ongoing study of hospital rooms, the methods developed for the home study are being applied to a system in which the resident of the environment is constantly changing. The unique features of hospital rooms, such as their intensive cleaning and highly regulated temperature and humidity, allowed for testing of a number of hypothesis regarding the strength and persistence of human microbial signatures in built environments.

Finally, the results of a study on the forensic applications of shoe-associated microbes in determining where someone has recently walked will be presented. In this study, it was found that supervised learning techniques could easily distinguish which of two study participants a shoe sample was taken from, and that models trained on floor samples alone were able to correctly identify which participant a shoe sample was taken from. Major shifts in shoe-associated microbiota with a change in environment were also able to be detected and correlation in shoe and floor microbial communities could be used to match the study participant to their location at different time points. This same study also collected shoe and phone samples from 89 different participants at three different scientific conferences and was largely able to match participants from individual conferences based on microbial similarity, suggesting widespread microbial interaction between individuals temporarily inhabiting the same space.

These three studies represent some of the largest efforts yet to employ novel high-throughput sequencing methods to microbial forensics in built environments. This presentation will elucidate the extent to which current methods are able to match individuals to spaces they have inhabited and will discuss both the limitations and potential of these methods to impact forensic science.

Trace Evidence, Forensic Microbiology, Molecular Forensics

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