

GENOME WATCH

Surveying what's flushed away

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This month's Genome Watch highlights the use of metagenomics to survey urban waste waters as a proxy for studying the gut microbiota in the local population and discusses how predictive models based on this data could inform public health.

The development of global-scale initiatives to characterize the human gut microbiome, like the Human Microbiome Project¹ or the Metagenomics of the Human Intestinal Tract (MetaHIT) consortium², is enabling us to better understand associations between its compositional variability and the development of diseases such as cancer, obesity and inflammatory bowel diseases. Most efforts to characterize the gut microbiota use faecal samples as the starting material, however, the increasing awareness of the microbiota in the built environment is expanding our potential to understand human health from a holistic perspective by acquiring samples from our environment.

Today, more than a half of the human population live in cities, so studying microbial dynamics in urban environments is being considered for public health. Indeed, the

MetaSUB consortium³ have performed extensive metagenomic surveys of public transport systems to analyse the spread of pathogens and antibiotic resistance.

Tons of human waste that pass through municipal sewage systems each day could be used to gain a broad overview of the gut microbiota of large populations living in urban areas. In a recent study, Newton et al.⁴ analyzed the waste waters of 71 cities in the United States using 16S ribosomal RNA (rRNA) amplicon sequencing and concluded that sewage can be used as a proxy for studying microbiomes in human populations. After filtering out reads belonging to non-faecal bacteria, the authors recaptured most (97%) of the oligotypes (taxonomic units of organisms that are classified according to primary DNA sequence) that are present in individual stool samples and found that the relative abundances of species correlated between sewage-derived and individual stool samples. Also, sewage bacteria were found to be a good predictor of the incidence of obesity. Specifically, higher *Bacteroides* spp. and lower *Faecalibacterium* spp. abundances were observed in cities with a higher percentage of individuals with obesity. These results suggest that gut bacteria present in sewage can be used as population-level biomarkers for demographics and public health.

Amplicon sequencing is useful for studying the diversity of microbial communities, but shotgun metagenomics enables their functions to be investigated. Hence, the strategy used by Newton et al.⁴ may be enhanced by integrating functional profiles inferred from shotgun metagenomics or whole-genome sequencing data, providing more information about virulence, antibiotic resistance or metabolic traits in the gut microbiota of human populations. Indeed, a recent study by Garza et al.⁵ reconstructed genome-scale metabolic models from over 1,500 human-associated bacteria and then integrated

metagenomics data from different body sites to predict metabolomes. Using this approach, the authors recapitulated the observed differences between the oral, skin, faecal and vaginal microbiota from the relative counts of predicted metabolites. Additionally, consistent correlations were observed after comparing predicted and measured metabolomes, supporting the application of metagenome-guided modeling to infer phenotypic traits from diverse environments.

In summary, the development of methods to investigate gut bacteria in waste water using multiomics data could be useful for public health initiatives. The routine application of these approaches brings us closer to the concept of smart cities, which could detect environmental changes in real time, like the production of enterotoxins or antibiotic metabolites. Also, these tools could inform us of dietary habits, the use of drugs or any measurable parameter just from the composition and functional patterns of the environmental, human-associated microbiota.

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Competing interests

The authors declare no competing interests.

