MICROBIOTA

Sewage comes up smelling like roses for microbiota research

Characterizing the human microbiome —to better understand its relationship with health and disease—is often achieved by assessing stool samples from individuals. In a novel strategy to develop a population-based approach, Newton and colleagues have used high-throughput 16S ribosomal (r)RNA sequencing to analyse sewage samples from 71 US cities.

Limited resources hamper the collection of enough individual samples to create meaningful population-level data. The investigators argue that sewage could be used as an alternative. Although only 15% of the sewage sample was of human origin, 97% of human faecal microbial rRNA oligotypes were identified. Having taken this into account when comparing sewage with individual stool results, a comparable microbial community was found in both datasets.

Within datasets, less variability existed between US city sewage samples than between individual stool samples. The main bacterial families found in each sewage sample were either Bacteroidaceae, Prevotellaceae or Lachnospiraceae plus Ruminococcaceae.

Could any population demographics be associated with the sewage microbial profile? A small proportion of the variability between city samples predicted (with an accuracy of 81–89%) whether the sample came from a lean or obese population.

The authors write that "comparative sewage analysis provides a unique opportunity to explore the relationship between fecal communities and lifestyle or demographic differences in human populations".

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Original article Newton, R. J. *et al.* Sewage reflects the microbiomes of human populations. *MBio* **6**, e02574-14 (2015)