Sewage provides insight into human microbiome

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A new study demonstrates that sewage is an effective means to sample the fecal bacteria from millions of people. Researchers say the information gleaned from the work provides a unique opportunity to monitor, through gut microbes, the public health of a large population without compromising the privacy of individuals.

Humans harbor tremendous amounts of bacteria in their gastrointestinal tract and gut bacteria serve important functions in healthy humans. Studies of the human microbiome, the collection of trillions of microbes living in and on the human body, have gained traction during the last decade. There is a great interest in identifying a "healthy microbiome" by identifying one or more bacterial community types that may be associated with healthy individuals, however financial considerations and privacy concerns limit the number of individuals who can be screened.

In a new study published in the January/February 2015 issue of the journal *mBio*, researchers from the Marine Biological Laboratory (MBL) and the University of Wisconsin-Milwaukee (UWM) School of Freshwater Sciences introduce the idea of using sewage as a population level pool that carries a signal for the microbiomes of humans.

Using oligotyping, a novel approach developed at the MBL, scientists compared the gut bacterial community profiles of 137 healthy adults provided by The Human Microbiome Project to the bacterial community profiles of more than 200 sewage influent samples collected from 71 U.S. cities.

In the paper led by UWM's Ryan Newton, researchers found that geographically distributed populations share a small core set of bacteria whose members represent various common community states within U.S. adults. The study uses the percent of obese individuals in a given city as a measure of lifestyle differences across cities, and demonstrates that the [bacterial community](#) structure is a good predictor, with 81 to 89 percent accuracy, of a city's estimated level of obesity. Lifestyle differences can reproducibly alter the human gut microbiome, and microbial community composition is a known indicator of obesity.

"This method is similar to trying to create a map of a geographical region," explains A. Murat Eren, an Assistant Research Scientist at the MBL, and one of the authors of the study. "The way we have been working with microbiomes of individuals has been similar to driving around and mapping the streets and structures of a city in a detailed manner. This approach takes our efforts to a much larger scale. In this sense it is similar to taking one big aerial picture of a city, trading off intricate details of a small number of well-described streets for broader insights and larger patterns."

The researchers say the use of oligotyping, which provides greater sensitivity, allowed them to better explain the distribution of very closely related bacterial organisms to compare microbiomes among 71 human populations.

"The sewage samples of 71 cities do not tell us anything specific about 'individuals' who live in those cities" says Eren. "However, only using sewage samples, we were able to differentiate these cities based on their estimated level of obesity. This approach can be beneficial to answer various public health questions while not compromising the privacy of individuals. For instance, microbial observatories plugged into sewage systems can keep us informed about the general health of large populations without being intrusive."

"This work fits into our long-term goal of developing better water pollution and public health assessments," says UWM professor and study co-author Sandra McLellan. "It's a great example of how new sequencing technologies and novel computational approaches can allow us to glean new information from complex environments."

The results of the oligotyping comparison of human gut to a sewage influent data were published on February 24, 2015 in *mBio*, an open access journal published by The American Society for Microbiology, by Eren, Joseph Vineis, Hilary Morrison, and Mitchell Sogin of the MBL's Josephine Bay Paul Center and Ryan Newton, Sandra McLellan, and Deborah Dila of the School of Freshwater Sciences, University of Wisconsin-Milwaukee. The team's research was supported was supported by a NIH grant R01AI091829-01A1 to Sandra McLellan and Mitchell Sogin.

More information: Newton RJ, McLellan SL, Dila DK, Vineis JH, Morrison HG, Eren AM, Sogin ML. 2015. Sewage reflects the microbiomes of human populations. *mBio* 6(2):e02574-14. DOI: 10.1128/mBio.02574-14.

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