Twin study defines shared features of human gut microbial communities: Variations linked to obesity

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Trillions of microbes make their home in the gut, where they help to break down and extract energy and nutrients from the food we eat. Yet, scientists have understood little about how this distinctive mix of microbes varies from one individual to the next.

Now, by cataloging the microbial species in the guts of lean and obese, identical and fraternal female twins and their mothers using a new generation of powerful DNA sequencers, researchers at Washington University School of Medicine in St. Louis have discovered that each individual carries a unique collection of bacteria, although the communities are more similar among family members.

When the scientists looked more deeply at the microbes' DNA, they found a striking similarity: The various collections of bacterial species carried a common set of genes that performed key functions to complement those performed by our human genes. The study is available in the advance online *Nature*.

"Although there are differences in who's there among our individual gut communities, these different assemblages of microbes carry a common core set of genes that perform key functions. These functions supplement those carried out by our human genes," says senior author Jeffrey I. Gordon, M.D., director of Washington University's Center for Genome Sciences.

Furthermore, when the study's lead author Peter Turnbaugh, a graduate student working in Gordon's lab, sequenced the microbial community DNA, or microbiome, of a subset of obese and lean twin pairs, he found that obese individuals had an increased representation of nearly 300 bacterial genes, many of which are devoted to extracting calories from food and processing nutrients. This new evidence supports Gordon's earlier research in mice that established a link between obesity and the efficiency of energy harvest from the diet by gut bacteria.

To compare gut bacterial communities both within and between families, Gordon and his colleagues obtained stool samples from 31 identical twin pairs, 23 fraternal twin pairs and 46 of their mothers. The twins were in their 20s and 30s and of European or African ancestry. Each twin pair was generally either lean or obese as defined by the Body Mass Index (BMI). All twins were born in Missouri, but they now live throughout the country. They are participants in the Missouri Adolescent Female Twins Study, a long-standing study of Missouri-born twins led by Washington University's Andrew Heath, Ph.D., professor of psychiatry, which is designed to decipher the influence of environment versus genetics on aspects of human health.

In the current study, each individual provided stool samples two months apart, enabling the researchers to track fluctuations in bacterial communities over time. The women had not taken antibiotics, which are known to alter the gut community, for at least six months.

Initially, the researchers sequenced a gene found in all microbes. This gene, 16S rDNA, functions as a barcode of life and can be used to catalog the species present in a microbial community without having to culture the bacteria.

Surprisingly, they did not find a single abundant bacterial species shared in the intestines of the study's 154 participants. While family members

were more likely to harbor similar collections of bacterial species, the degree of similarity was the same for identical as for fraternal twin pairs, regardless of whether they lived in the same house or in different regions of the United States, the researchers found.

"This suggests that early environmental exposures play a key role in determining which microbes colonize our intestinal tracts," Gordon says. "It appears that we acquire an enormous number of genes - in the form of our microbial genes - from our early environment. These microbial genes, together with our human genes, form our 'metagenome."

The current research is part of the ongoing human microbiome project, which seeks to not only catalog the microbial species and genes associated with healthy bodies and certain disease states, but to understand how our microbial communities function. Microbial cells are estimated to outnumber human cells by a factor of ten to one. Collectively, the microbes are estimated to carry far more than the 20,000 genes that make up the DNA that we inherit from our parents.

"This study opens many doors to areas that are important to explore," Gordon says. "But before we can confidently associate changes in our indigenous microbial communities with risk for certain diseases, it is very important that we define the normal variations that occur in these communities within and between individuals, and the factors that might drive these variations in our microbial ecology. We are interested in understanding how our modern lifestyles, changing cultural traditions, new technologies, and Western diets are shaping our gut microbiome. We should consider another dimension of human evolution, namely that which is occurring at the level of our microbiomes, as our societies undergo rapid transformation. We think that studying twins living in different parts of the world represents a particularly useful way to move this new area of research forward."

Citation: Turnbaugh PJ, Hamady M, Yatsunenko T, Cantarel BL, Duncan A, Ley RE, Sogin ML, Jones WJ, Roe BA, Affourtit JP, Egholm M, Henrissat B, Heath AC, Knight R and Gordon JI. A core gut microbiome in obese and lean twins. Online *Nature*.

Source: Washington University