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Understanding the Relationship Between Bacteria and Obesity
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SAN DIEGO, CA – May 26, 2010 Research presented today sheds new light on the role bacteria in the digestive tract may play in obesity. The studies, which were presented at the 110th General Meeting of the American Society for Microbiology, paint a picture that may be more complex than originally thought.

“Work currently underway suggests that an interaction between genetic factors and the composition of the bacteria that inhabit the human gut may predispose certain individuals towards obesity. These results potentially provide insight into the mechanisms by which genetics may predispose some people to obesity. They could also help pave the way towards a future in which genetic screening in conjunction with individually tailored treatments could help people at risk for obesity to maintain a healthy weight,” says Margaret Zupancic of the Institute for Genome Sciences at the University of Maryland School of Medicine, who presented one of the studies.

Zupancic and her colleagues analyzed the gut bacterial communities of lean and obese individuals belonging to the Old Order Amish of Lancaster County, Pennsylvania – a population relatively homogenous in regard to both genetics and lifestyle. Initially they found no correlation between the composition of the gut bacteria and obesity, but when they factored in the genetic makeup of the participants, certain patterns began to emerge.

One pattern was a statistically significant correlation between whether the participant carried a given variant of the FTO gene (a gene associated with obesity) and the presence of certain bacterial groups in the digestive tract.

The researchers also found that in people with certain genetic variations in taste receptor genes, a low level of bacterial diversity in the gut correlated with a higher likelihood of obesity, while a high level of diversity correlated with a lower likelihood of obesity.

“While this work is still at a relatively early stage, results such as these could lead to applications such as probiotic or antibiotic-based treatments for obesity that could be individualized based on a person’s unique genetic and gut microbial makeup,” says Zupancic.

Another study from the Fred Hutchinson Cancer Research Center analyzed the gut microbes of women between 40 and 45 years of age. The researchers found a positive correlation between the population of one specific type of bacteria, *Bacteroidetes*, and body fat percentage in the participants.

Not all research presented at the meeting found differences in bacterial populations in the gut and obesity. One study, focusing specifically on children and childhood obesity failed to find identify any significant differences in the gut microbial communities of obese and normal-weight children.

The researchers subsequently analyzed the ability of the microbes to extract and convert dietary energy. They found higher levels of short-chain fatty acids in the feces of obese children.

"This suggests that although obese and normal-weight children have similar gut microbial communities, the gut microbes in obese children are more efficient at converting dietary substrates into energy," says Amanda Payne of the Institute of Food Health and Nutrition ETH, Zurich, Switzerland.

Short-chain fatty acids are converted into triglycerides and glucose by the liver, a process estimated to provide an additional 10% of dietary energy. The increased production of short-chain fatty acids by gut microbes in obese children could potentially supply more dietary energy, resulting in weight gain.

"While the importance of a balanced diet and regular exercise should not be discounted, our results may help contribute to the development of novel approaches in treating childhood obesity by modulating the composition and activity of the gut microbiota in order to reduce energy extraction from undigested food," says Payne.

About IGS

The Institute for Genome Sciences (IGS) at the University of Maryland School of Medicine is an international research center dedicated to advancing the use of genomics to improve healthcare. Led by Dr. Claire Fraser-Liggett, a preeminent genome scientist and microbiologist, IGS is located in a 10-acre BioPark on the University of Maryland Baltimore's campus. IGS scientists integrate genomics, bioinformatics and metagenomics into biomedical research. For more information, see www.igs.umaryland.edu.