Intestinal bacteria may have a greater influence on us than was previously thought. In a study published in the journal *Nature* on 29 May, researchers at the Sahlgrenska Academy, University of Gothenburg, Sweden and Chalmers University of Technology, Sweden, show that patients with type 2 diabetes have an altered gut microbiota. Their findings have led to a new model to identify patients at increased risk of developing diabetes. (Credit: Image courtesy of University of Gothenburg)

The human body contains ten times more bacteria than human cells. Most of these bacteria comprise the normal gut microbiota. Our bodies thus contain a vast number of bacterial genes in addition to the genes in our own cells, and are collectively known as the metagenome.

Three Swedish, Gothenburg-based research groups led by Fredrik Bäckhed and Björn Fagerberg, Sahlgrenska Academy, University of Gothenburg, and Jens Nielsen of Chalmers University of Technology compared the metagenome of 145 women with diabetes, impaired glucose tolerance and healthy controls, and showed that women with type 2 diabetes have an altered gut microbiota.

Furthermore, healthy women have higher numbers of gut bacteria known to be producers of butyrate, a fatty acid that has previously been linked to beneficial health effect.

On the basis of these findings, the researchers developed a new model that can distinguish between patients with type 2 diabetes and healthy women by analysis of the metagenome. This model has better predictive value than the classical predictive markers used today, such as body-mass index and waist-hip ratio.

"By examining the patient's gut microbiota, we could predict which patients are at risk of developing diabetes. The big challenge is to find out whether the composition of the gut microbiota promotes the onset of age-related diabetes. If this is the case, this would indicate new opportunities to prevent the disease," says Professor Fredrik Bäckhed.

"In this study, we have developed new methods to analyze the metagenomic data and have been able to exploit..."
much more of the 'unknown' metagenome, that is, the bacteria that have not been previously mapped," continues Jens Nielsen, Professor of Systems Biology at Chalmers University of Technology. "The study is an excellent example of how novel technologies, developed in connection with Chalmers' initiative in life science, can assist in analyzing large amounts of data from the clinic."

The study Gut metagenome in European women with normal, impaired and diabetic glucose control was published in Nature on May 29.

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