

Study illuminates how humans digest fiber

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Humans owe their ability to digest fibre to a newly-discovered sequence of genes in a species of gut microbiota called Bacteroides ovatus, pictured here. Credit: Dr. Eric Martens, University of Michigan

New insight into how gut bacteria digest fibre could lead to advances in areas as diverse as health and environmentally-friendly biofuels.

Fibre is an essential part of a healthful diet, but our ability to benefit



from it is entirely dependent the bacteria living in our intestines. An international research team, which included scientists at Sweden's KTH Royal Institute of Technology, recently uncovered how one group of bacteria digest a major type of dietary fibre.

Until now, scientists were not sure exactly how complex sugars known as xyloglucans are broken down in the human gut. Xyloglucans account for a quarter of the dry weight of many common fruits and vegetables. The new study, which was published in the January 19 issue of *Nature*, sheds light on how a specific class of gut bacteria called Bacteroidetes break down the complex carbohydrates.

The researchers traced the molecular mechanism for the digestion of xyloglucans to a genetic sequence in one of the species of the bacteria, Bacteroides ovatus.

"Bacteroides ovatus and its complex system of enzymes provide a crucial part of our digestive toolkit," says Harry Brumer, who began the study four years ago with a research team at the Division of Glycoscience in the KTH School of Biotechnology. Brumer continued the work over the last two years at University of British Columbia, where he is a professor in the Michael Smith Laboratories and Department of Chemistry. The research partners also include University of York and the University of Michigan.

"This newly discovered sequence of genes enables Bacteroides ovatus to chop up xyloglucan, a major type of <u>dietary fibre</u> found in many vegetables – from lettuce leaves to tomato fruits. In fact, this system is so important, it is found in at least 92 percent of humans surveyed worldwide so far," Brumer says.

The findings can be useful to researchers developing new probiotic or dietary treatments for microbial imbalances that cause, or are a result of,



bowel diseases, he says.

"The probiotics field is a complex one, which includes many regulatory issues; but one could imagine making defined treatments based on specific microbes, based on their individual, inherent metabolic capacities, to improve the balance of the microbiota and overall human heath," he says.

The research may also prove useful for the future of biomass technology.

"The basic enzymology and structural biology gives new insight into the function of carbohydrate-active enzyme families, which can suggest ways to improve these biocatalysts for biomass utilisation, in such areas as materials or fermentation to chemicals and fuels," Brumer says.

The next step for the research team will include investigating whether these bacteria work in concert – or competition – with other <u>gut bacteria</u> to target <u>complex carbohydrates</u>. "Right now, we are excited to explore similar <u>complex</u> loci to find out how other common dietary polysaccharides are broken down," he says.

"Very little is known at the molecular level in this area, even for very common dietary carbohydrates."

More information: Johan Larsbrink, Theresa E. Rogers, Glyn R. Hemsworth, Lauren S. McKee, Alexandra S. Tauzin, Oliver Spadiut, Stefan Klinter, Nicholas A. Pudlo, Karthik Urs, Nicole M. Koropatkin, A. Louise Creagh, Charles A. Haynes, Amelia G. Kelly, Stefan Nilsson Cederholm, Gideon J. Davies, Eric C. Martens & Harry Brumer, "A discrete genetic locus confers xyloglucan metabolism in select human gut Bacteroidetes" *Nature* (2014) <u>DOI: 10.1038/nature12907</u>



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