

Search for better biofuels microbes leads to the human gut

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University of Illinois microbiology professor Isaac Cann and his colleagues found bacterial enzymes in the human gut that can rival those of the cow rumen in their ability to break down the plant fiber hemicellulose for biofuels production. Credit: L. Brian Stauffer

Scientists have scoured cow rumens and termite guts for microbes that can efficiently break down plant cell walls for the production of next-generation biofuels, but some of the best microbial candidates actually may reside in the human lower intestine, researchers report.

Their study, reported in the *Proceedings of the National Academy of Sciences*, is the first to use biochemical approaches to confirm the hypothesis that microbes in the [human gut](#) can digest fiber, breaking it down into simple sugars in order to ferment them into nutrients that nourish human cells. These findings have significance for human health but also for biofuels production, since the same sugars can be fed to yeast to generate ethanol and other liquid fuels. The human microbes appear to be endowed with enzymes that break down a complex plant fiber component more efficiently than the most efficient microbes found in

the cow rumen, the researchers report.

Their work in cows led the researchers to the human microbes, said University of Illinois animal sciences and Institute for Genomic Biology professor Isaac Cann, who led the new analysis with his colleagues, animal sciences professor Roderick Mackie and M.D./Ph.D. student Dylan Dodd. Cann also is a microbiology professor and a principal investigator at the Energy Biosciences Institute. Dodd is now at Stanford University.

"In looking for biofuels microbes in the cow rumen, we found that *Prevotella bryantii*, a bacterium that is known to efficiently break down (the plant fiber) hemicellulose, gears up production of one gene more than others when it is digesting plant matter," Cann said.

When searching a database for similar genes in other organisms, the researchers found them in microbes from the human gut. The team focused on two of these human microbes, *Bacteroides intestinalis* and *Bacteroides ovatus*, which belong to the same bacterial phylum as Prevotella from the cow.

"We expressed the human gut bacterial enzymes and found that for some related enzymes, the human ones actually were more active (in breaking down hemicellulose) than the enzymes from the cow," Cann said.

When the researchers looked more closely at the structure of the human enzymes, they saw something unusual: many single polypeptide (protein) chains actually contained two enzymes, one of which was embedded in the other. Further analysis of the most important protein revealed that the embedded component was a carbohydrate-binding module (CBM), which, as its name implies, latches onto carbohydrates such as hemicellulose. This [enzyme](#) shreds the plant fiber hemicellulose so that other enzymes can work on it to break it

down into its unit sugars.

Working with U. of I. biochemistry professor Satish Nair, the [researchers](#) also noticed that the CBM "put a kink" in the fiber when it bound to it. This bending action may bring the fiber close to the other enzyme in the protein so it can get to work breaking the bonds between the sugars. Further research is needed to confirm this hypothesis, Cann said.

The study points to human microbes as a potentially potent source of microbes that can aid in biofuels production, Cann said.

"In addition to finding microbes in the cow rumen and termite gut, it looks like we can actually make some contributions ourselves," he said. "And our bugs seem to have some enzymes that are even better than those in the [cow](#) rumen."

More information: "Xylan utilization in human gut commensal bacteria is orchestrated by unique modular organization of polysaccharide-degrading enzymes", www.pnas.org/content/111/35/E3708.full

Provided by University of Illinois at Urbana-Champaign

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