Atomic view of bacterial enzymes that help human digestion

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A group of researchers at the University of Waterloo in Ontario, Canada has reached deep into the human gut, plucked out a couple enzymes produced by bacteria residing there and determined their biological activities and molecular structures—details that should shed new light on how we digest many of the foods we eat.

The question of how starch digestion works is one of great importance to human health because starch is a major component of the human diet. Plants make this polysaccharide molecule during photosynthesis as a way of storing energy, and foods like potatoes, wheat and rice are all rich in starch. It is a major source of dietary glucose, the main sugar the human body uses for fuel.

Dietary glucose and the physiology of starch digestion figures prominently in digestive and liver diseases, food intolerances, diabetes and obesity, and the new work has implications for all these conditions as well as other areas of human health.

In the last few years, scientists have come to appreciate the outsized role played in healthy gut physiology by a rich ecosystem of "good" bacteria residing in the gut—referred to collectively as the gut microbiome. Whenever we eat vegetables, enzymes produced by these bacteria break the starch molecules down into smaller component pieces, like glucose, which are then absorbed through the gut into the bloodstream.

The makeup of the organisms in the gut microbiome has been a hot topic

because of these linkages to human health, and earlier studies have shown how altering the microbiome of mice directly affects their weight, turning fat mice thin and vice versa. Major research projects started in the United States and elsewhere are aiming to identify and analyze all the micro-organisms in the human gut.

The University of Waterloo team, led by David Rose, has been working out the detailed molecular mechanisms for individual enzymes and other molecules involved in starch digestion. They are looking at component pieces of large complexes of molecules known as starch utilization systems, one of the two major systems in the intestinal microbiome helping to break down starch.

At the American Crystallographic Association (ACA) 2015 Meeting, which will be held in Philadelphia from July 25-29, 2015, Rose's graduate student, Marcia Chaudet will present biochemical activity data as well as crystal structures of two proteins known as GH31 enzymes that help to break down starch as part of these starch utilization systems.

"Based on the structures we have so far, we can make predictions about specificity," said Rose. "Such structural information can reveal subtle points about the physiology that would otherwise be hidden and may be impossible to predict. It can also guide the development of chemical compounds [a basic approach to pharmaceutical drug development]."

This is significant, he added, because if you can figure out which enzymes are primarily responsible for binding to and digesting starch, then you might be able to design drugs that would fine-tune that activity, allowing you to better regulate blood glucose levels and address diseases where this physiology is at play.

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