

MICROBIOLOGIE, INFECTIOLOGIE ET IMMUNOLOGIE



CONFÉRENCE

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Resistant Starch Utilization by the Human Gut Microbiota

Starch is the most frequent nutritious polysaccharide consumed in the typical human diet and thus has a major impact on human health. However, not all the starch we consume can be degraded by human derived enzymes. The remaining fraction is termed resistant starch and serves as an important substrate for the gut microbiota, which returns some of the stored energy to their human host in the form of short chain fatty acids (SCFA) such as butyrate. These SCFA have important impacts on human health, particularly in their ability to modulate the immune system in the gut, reducing inflammation and its associated detrimental effects. Resistant starch consumption is known to have many beneficial effects, such as lowering the risk of becoming obese or developing diabetes. The ability to utilize starch or its derived components is predicted to be widespread among members of the gut microbiota, but little is known about how this translates to the degradation of resistant starch. Among the organisms known to flourish on diets rich in resistant starch are the cluster XIVA and cluster IV clostridia. The cluster XIVA clostridia contain several of the most important butyrate producers in the gut and butyrate is thought to be the most beneficial of the SCFA. *Eubacterium rectale* is a key member of the cluster XIVA group and serves as an important model organism. Cluster IV includes *Ruminococcus bromii*, an organism that has been found to be particularly adept at breaking down resistant starch. I have undertaken the study of the starch metabolizing systems of these two key organisms from the gut microbiota in order to gain insight into how resistant starch is utilized in the gut and how the various players in starch breakdown interact with one another. One thing these organisms have in common is a series of adaptations in their key extracellular enzymes that has allowed them to thrive within their respective niches in the starch ecosystem of the gut. Both organisms encode novel carbohydrate binding modules (CBMs) that may play an important role in the ability of these organisms to process starch in the complex and competitive gut environment. Additionally, *R. bromii* organizes its enzymes into multi-enzyme complexes termed amylosomes for their resemblance to the cellulosomes formed by some cellulose degrading organisms. Here I present the structural and biochemical characterization of these unique enzymes and their CBMs, providing a first look at how these key organisms interact with and degrade starch at the molecular level. I will then share my future research goals as I aim to determine the organisms responsible for resistant starch degradation in the human gut and the molecular mechanisms underlying this ability.

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