

Structural Comparison of *Faecalibacterium prausnitzii* α -glycosidases and Sucrase-Isomaltase

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The human gastrointestinal system is home to a very diverse microbiome that is made up of approximately 100 trillion microorganisms. This microbiome has a significant impact on human health, as it can influence the immune system, the central nervous system and the body's metabolism. *Faecalibacterium prausnitzii* is one of the most abundant microorganisms found in a healthy gut, where it makes up about 5% of the microbiome. This gastrointestinal microorganism produces 2 enzymes belonging to the glycoside hydrolase family 31, which will be referred to as Fp- α G1 and Fp- α G2. These α -glycosidases have notable structural similarities to the N-terminal subunit of sucrase-isomaltase. Sucrase-Isomaltase (SI) is a gastrointestinal enzyme found in humans, and is responsible for hydrolyzing carbohydrates with α -1,6, α -1,4 and α -1,2 glycosidic bonds. The objective of this project is to compare the enzymatic activity of *F. prausnitzii* α -glycosidases to the N-terminal subunit of SI, in order to investigate the structural similarities between the proteins. Real time kinetic assays and computational models will be used to identify structural features contributing to the differences in substrate affinity. These investigations into protein structure and enzymatic activity of the α -glucosidase proteins will provide a clearer insight on the structure and function of the Fp- α G1, Fp- α G2, and SI.