IMPROVING COLONIC DEGRADATION OF RECALCITRANT FIBER BY PROCESSING AND ENZYME TECHNOLOGIES IN *VITRO*

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Abstract

The gut microbiota has been identified as crucial for health and disease. The composition and activity of the gut microbiota can be modulated with dietary components, including dietary fiber. Steering the kinetics of fiber fermentation is key to ensure health promoting effects of dietary fibers in animals and humans. This health effect is increasingly associated with microbial metabolites produced (amongst others: short chain fatty acids, SCFA), which should be ideally produced throughout the entire length of the colon. Moreover, in pigs, for efficient conversion of vegetal matter into pork, the degradation of complex carbohydrates and thereby absorption of energy rich SCFA, is considered to be rate limiting. The inability of microbial enzymes to open the cell wall matrix is the main reason for this recalcitrance. In vivo, the competition between degradation kinetics of fiber and fiber transit determines the actual SCFA yield, and hence increase in body weight. Previous efforts have revealed that common enzyme- and process technologies can solubilize fiber fractions but will not increase the extent of fermentation in vivo. For a breakthrough in this area, focus on isolated, recalcitrant fibers is required. In this project, we will study a pectin-rich fiber source, applying novel enzymes, to split cellulose and hemicellulose chains as present in recalcitrant fiber fractions. These technologically-treated fibers will subsequently be tested using a validated, dynamic in vitro model of the colon. Key words: gut microbiota, recalcitrant fibers, SCFA, in *vitro*