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Colonic transit time relates to bacterial metabolism and mucosal turnover in the human gut

<u>Henrik M. Roager</u>¹, Lea B. S. Hansen², Martin I. Bahl¹, Henrik L. Frandsen¹, Vera Carvalho¹, Rikke J. Gøbel³, Marlene D. Dalgaard², Morten H. Sparholt⁴, Henrik Vestergaard³, Torben Hansen³, Thomas S. Pontén², H. Bjørn Nielsen², Oluf Pedersen³, Lotte Lauritzen⁵, Mette Kristensen⁵, Ramneek Gupta², Tine R. Licht¹.

¹National Food Institute, Technical University of Denmark, Denmark

²Department of Systems Biology, Technical University of Denmark, Denmark

³The Novo Nordisk Foundation Center for Basic Metabolic Research, Section of Metabolic Genetics, University of Copenhagen, Denmark

⁴Department of Radiology Bispebjerg and Frederiksberg Hospitals

⁵Department of Nutrition, Exercise and Sport, University of Copenhagen, Denmark

Little is known about how colonic transit time relates to human colonic metabolism, and its importance for host health, although stool consistency, a proxy for colonic transit time, has recently been negatively associated with gut microbial richness. To address the relationships between colonic transit time and the gut microbial composition and metabolism, we assessed the colonic transit time of 98 subjects using radiopaque markers, and profiled their gut microbiota by16S rRNA gene sequencing and their urine metabolome by ultra performance liquid chromatography mass spectrometry. Based on correlation analyses, we show that colonic transit time is associated with overall gut microbial composition, diversity and metabolism. A relatively prolonged colonic transit time associates with high microbial species richness and a shift in colonic metabolism from carbohydrate fermentation to protein catabolism as reflected by microbial metabolites in urine. This results in a number of potentially deleterious protein-derived metabolites. Additionally, longer colonic transit time correlates with metabolites likely reflecting reduced renewal of the colonic muccosa. Together, this suggests that a high gut microbial richness does not *per se* imply a healthy gut microbiota, and contributes to the understanding of the pathophysiology of diseases where increased transit time is a risk factor. Finally, our findings highlight the colonic transit time as an important physiological variable, which should be considered in gut microbiota and metabolomics studies.