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

Roager, Henrik Munch; Hansen, Lea Benedicte Skov; Bahl, Martin Iain; Frandsen, Henrik Lauritz; Carvalho, Vera; Gøbel, Rikke J.; Dalgaard, Marlene Danner; Plichta, Damian Rafal; Sparholt, Morten; Vestergaard, Henrik; Hansen, Torben; Sicheritz-Pontén, Thomas; Nielsen, Henrik Bjørn; Pedersen, Oluf; Lauritzen, Lotte; Kristensen, Mette; Licht, Tine Rask

Publication date:
2016

Document Version
Publisher's PDF, also known as Version of record

Link back to DTU Orbit

Citation (APA):
Abstract for 13th NuGOweek 2016, “Phenotypes and prevention – the interplay of genes, life-style factors and gut environment”
September 5-8, 2016
Copenhagen, Denmark

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

Henrik M. Roager1, Lea B. S. Hansen2, Martin I. Bahl1, Henrik L. Frandsen1, Vera Carvalho1, Rikke J. Gøbel1, Marlene D. Dalgaard2, Damian R. Plichta2, Morten H. Sparholt4, Henrik Vestergaard3, Torben Hansen3, Thomas Sicheritz-Pontén2, H. Bjarne Nielsen2, Oluf Pedersen2, 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 by 16S 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 higher urinary levels of potentially deleterious protein-derived metabolites. Additionally, shorter colonic transit time correlates with metabolites likely reflecting increased renewal of the colonic mucosa. Together, this suggests that a high gut microbial richness does not per se imply a healthy gut microbial ecosystem and points at colonic transit time as a highly important factor to consider in microbiome and metabolomics studies.