Huawei Zeng

Grand Forks Human Nutrition Research Center
USA

Oncogenic signatures and inflammatory colon in diet-induced obese mouse models

Abstract:

Adoption of an obesogenic diet such as a high-fat diet (HFD) results in obesity, bacterial dysbiosis, chronic inflammation, and cancer. Primary bile acids (BAs) play critical roles in cholesterol metabolism, lipid digestion, and host-microbe interaction. However, HFDs increase secondary BAs (e.g., deoxycholic acid (DCA) and lithocholic acid (LCA) in the colon), are risk factors for colonic inflammation and cancer. Gut bacteria and their metabolites are recognized by interleukin-1 (IL-1R)/toll-like receptors (TLRs) which are essential to maintain intestinal homeostasis; host extracellular microRNAs (miRNAs) can alter bacterial growth in the colon. Characterization of the underlying mechanisms may lead to identifying fecal oncogenic signatures reflecting colonic health. We hypothesize that a HFD accelerates the inflammatory process, oncogenic metabolites, and disease-related gut microbiome in the colon. With diet-induced obese mouse models, we found that the concentrations of plasma interleukin 6 (IL-6), inflammatory cell infiltration, β-catenin, and cell proliferation marker (Ki67) in the colon were elevated > 60% in the HFD (45 % energy fat) group compared to the control (16 % energy fat) group. Furthermore, the content of Alistipes bacteria, the Firmicutes/Bacteroidetes ratio, microRNA-29a, and DCAs and LCAs (secondary BAs with oncogenic potential) were 50% greater in the feces of the HFD group compared to the control group. In summary, our multimodal profile data may represent a unique HFD-induced oncogenic signatures for colon health in a diet-induced mouse model. A greater understanding of these mechanistic action may open new avenues for seeking noninvasive colonic biomarkers.

Biography

Zeng was born and grew up in Xiamen, China. He obtained B.S. and M.S. degrees in Biology from Xiamen University. He attended the University of Wyoming, where he earned a Doctor of Philosophy degree in Molecular Biology in 1996. After graduation, Dr. Zeng spent three and half years as a postdoctoral researcher at the National Institutes of Health (Bethesda, MD) investigating steroid hormone-induced gene expression. Dr. Zeng joined the scientific staff of the USDA-ARS Grand Forks Human Nutrition Research Center (GFHNRC) as a Research Molecular Biologist in November 1999.