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The role of exercise as a driver for the structure and function of the human gut microbiome

Exercise is one of the most important life style factors triggering human health. However the exact modes of action are not well understood. Mainly data on the influence of exercise on the gut microbiome is missing. We explored the metagenomics and metabolomics of intestinal microbiota in healthy male participants during a 21 days bed rest study in a strictly controlled laboratory environment, with balanced fluid and dietary intakes, controlled circadian rhythm, microbial ambient burden and 24/7 medical surveillance. Inactivity resulted in a significant increase in the genus *Bacteroides* as well as in genes coding for proteins involved in iron acquisition and metabolism, cell wall, capsule, virulence, disease and defense and mucin degradation, such as beta-galactosidase (EC3.2.1.23), α -L-fucosidase (EC3.2.1.51), Sialidase (EC3.2.1.18) and α -N-acetylglucosaminidase (EC3.2.1.50). Bayesian network analysis was used to derive the first hierarchical model of initial deconditioning steps over time. The wash-out period (when subjects were released from bed rest conditions) corresponded to a profound life-style change (i.e. reintroduction of exercise) that resulted in stepwise amelioration of the negative physiological symptoms, indicating that exercise acted as an important parameter apparently preventing microbial physiology and activities in host mucin degradation and pro-inflammatory immune crosstalk.