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Probiotic modulation of symbiotic gut microbial–host metabolic interactions in a humanized microbiome mouse model

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The transgenomic metabolic effects of exposure to either *Lactobacillus paracasei* or *Lactobacillus rhamnosus* probiotics have been measured and mapped in humanized extended genome mice (germ-free mice colonized with human baby flora). Statistical analysis of the compartmental fluctuations in diverse metabolic compartments, including biofluids, tissue and cecal short-chain fatty acids (SCFAs) in relation to microbial population modulation generated a novel top-down systems biology view of the host response to probiotic intervention. Probiotic exposure exerted microbiome modification and resulted in altered hepatic lipid metabolism coupled with lowered plasma lipoprotein levels and apparent stimulated glycolysis. Probiotic treatments also altered a diverse range of pathways outcomes, including amino-acid metabolism, methylamines and SCFAs. The novel application of hierarchical-principal component analysis allowed visualization of multicompartamental transgenomic metabolic interactions that could also be resolved at the compartment and pathway level. These integrated system investigations demonstrate the potential of metabolic profiling as a top-down systems biology driver for investigating the mechanistic basis of probiotic action and the therapeutic surveillance of the gut microbial activity related to dietary supplementation of probiotics.

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