

Linking the genotype of the host with rumen bacterial communities in sheep

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Divergent genetic selection for wool growth as a single trait has led to major changes in sheep physiology, including variations on rumen microbial protein production and uptake of amino nitrogen in portal blood. This study was conducted to determine if sheep with different genetic merit for wool growth under commercial conditions have distinct rumen bacterial populations. Eighteen Merino wethers were separated into groups of contrasting estimated breeding values for clean fleece weight (CFW; Low-FW and High-FW) and fed an oaten:lucerne chaff diet at two levels of intake (LI; 1.0-M or 1.5-M maintenance) for two seven-weeks periods in a crossover design. Bacterial diversity, in filtered rumen fluid collected by esophageal intubation, was characterised using 454 amplicon pyrosequencing of the V3/V4 regions of the 16S rRNA gene. Data was analysed using Mothur, Acacia, Qiime and SAS software packages. Bacterial diversity estimated by Phylogenetic distance, Chao1 and Observed species did not differ significantly with CFW or LI; however, the Shannon diversity index differed ($P=0.0432$) between High- (7.67) and Low-FW sheep (8.02). High-FW animals had a higher ($P=0.0342$) proportion of Bacteroidetes (71.9 vs 66.5%) and a lower ($P=0.0359$) proportion of Firmicutes (26.6 vs 31.6%) than Low-FW animals. Twenty-four specific OTUs, belonging to Firmicutes and Bacteroidetes phyla, were shared among all the samples, whereas thirty-seven specific OTUs varied significantly in presence/abundance ($P<0.05$) between Low-FW and High-FW and fifty varied ($P<0.05$) between 1.0-M and 1.5-M. It appears that genetic selection for fleece weight induces differences in rumen bacterial diversity that persist across different feeding levels.

Modulation of Gut Microbiota during Probiotics-Mediated Attenuation of Metabolic Syndrome in High Fat Diet-Fed Mice

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Structural disruption of gut microbiota and associated inflammation are important etiological factors in high fat diet (HFD)-induced metabolic syndrome (MS). Three candidate probiotic strains, *Lactobacillus paracasei* CNCM I-4270 (LC), *L. rhamnosus* I-3690 (LR) and *Bifidobacterium animalis* subsp. *lactis* I-2494 (BA) were individually administered to HFD-fed mice (10^8 cells / day) for 12 weeks. Each strain attenuated weight gain and macrophage infiltration into epididymal adipose tissue, and markedly improved glucose-insulin homeostasis and hepatic steatosis. UniFrac principal coordinate analysis on 454 pyrosequencing of fecal bacterial 16S rRNA genes showed the probiotic strains shifted the structure of the HFD-disrupted gut microbiota toward that of lean mice fed a normal (chow) diet. Redundancy analysis revealed that abundances of 83 operational taxonomic units (OTUs) were altered by probiotics. Forty-nine altered OTUs were significantly correlated with one or more host MS parameters and were designated "key" OTUs which may mediate the mitigation of MS by probiotics. Thirteen of the 15 key OTUs that were negatively correlated with MS phenotypes were promoted, and twenty-six of the 34 key OTUs that were positively correlated with MS were reduced by at least one of the probiotics, but each strain changed a distinct set of key OTUs. LC and LR increased cecal acetate but did not affect circulating lipopolysaccharide-binding protein; in contrast, BA did not increase acetate, but significantly decreased adipose and hepatic TNF- α gene expression. These results suggest that *Lactobacillus* and *Bifidobacterium* differentially attenuate obesity comorbidities in part through strain-specific impacts on MS-associated phylotypes of gut microbiota in mice.