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Murine Gut Microbial Communities Influenced by Physical Activity and Diet, But Not Gender

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The gut microbiota is known to be influenced by a myriad of environmental and genetic factors. Recently, our lab has shown the impact of host genotype and exercise on the selection of individual bacterial species in the mouse gut. **PURPOSE**: Here, we sought to examine changes to gut communities to voluntary wheel running (VWR) and very high fat (VHF, 60% fat) feeding over 12 weeks in male (M) and female (F) C57Bl/6Tac wildtype mice. **METHODS**: Following a two-week acclimation period, 224 mice were randomly assigned to one of four treatments for each sex (n=7/group): (1) control diet (10% fat) sedentary (CD-S); (2) VHF diet sedentary (VHF-S); (3) CD exercise (CD-X) & (4) VHF diet exercise (VHF-X). Throughout the study mice had ad libitum access to food, water and running wheels, where appropriate. Fecal samples were collected each week and analyzed by rRNA operon profiling to tract changes in gut communities over time by nanopore sequencing. **RESULTS**: 23 separate MinION runs yielded $2.64x10^7$ raw reads each collected over 24 hours and sized (3.7-6.0 kb) yielding $1.38x10^7$ rRNA operons. Sequence reads were screened against a ribosomal operon database (OpDB) using MegaBlast and yielded $1.16x10^7$ quality alignments (≥1000 bp) which were binned into 1,912 species dominated by *Lachnospiraceae bacterium 28-4.*, *Ruminococcus bromii* and *Parabcteroides spp*. β-diversity analysis showed clustering by activity for weeks 3 (p=0.001) and 4 (p=0.035) as well as for diet (p=0.001, p=0.005), where week 8 communities exhibited clustering by diet (p=0.001) only. Sex did not significantly affect β-diversity at all time points. Differential abundance testing showed increased abundance of *Turicibacter sanguinis* & *Paraclostridium bifermentans* in sedentary mice where *Muribaculum intestinale* & *Traorella massiliensis* spp. were more abundant in exercise mice. **CONCLUSION**: This preliminary data contributes to emerging evidence demonstrating the role of host activity and diet, but not gender, to alter gut microbial communities.

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