

The gut microbiome and its role in influencing running behavior in male rats

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Exercise has well-established physiological benefits, and a lack thereof often gives rise to health conditions. Exercise encompasses a spectrum of activities and varies on an individual level. Prior studies have established connections between our gut microbiome (GMB) and disease pathogenesis and behaviors. We explored the relationship between voluntary wheel running in male rats and GMB composition.

Each rat was randomly assigned into a running (n=8) and sedentary group (n=3). Initially, all rats had no access to a running wheel for one week, after which the running group had full access to the wheel for four weeks. Differences in running distance stratified the running group into high (n=3) and low (n=5) runners. We ran alpha/beta diversities with QIIME2 and analyzed the relationship between bacterial abundance and rungroup/time using generalized least square models.

Ruminococcaceae abundance increased (R²: 0.65, p <0.001), while *Peptostreptococcae* decreased with running distance (R²: -0.47, p: 0.006) in high runners only. *Peptostreptococcaceae* decreased with time (R²: -0.42, p: 0.012) with high runners, while a significant, yet weaker, relationship was observed in low runners (R²: -0.03, p: 0.0421). *Ruminococcaceae* ferments starch into short-chain fatty acids, which helps maintain gut barrier integrity. These findings demonstrate a relationship between GMB composition and behaviors such as running. Further investigation will help us understand what influences exercise variability among individuals.