

Physical Activity, Gut Microbiota and Gut-Brain Axis

Subjects: [Sport Sciences](#)

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Physical activity (PA) can impact significantly the gut microbiota composition and diversity, and could also produce modifications in the gut microbiota that can mediate and induce mental health benefits. The PA favors bacterial strains that can promote physical performance and that can induce beneficial changes in the brain.

cognitive functions

anxiety

depression

microbiome

overweight

elderly

athletes

sports

fitness

overtraining

1. Introduction

In recent years, research on the interaction between gut microbiota (GM) and health has expanded considerably. High-throughput sequencing has favored and facilitated research on GM in multiple aspects ^[1]. Indeed, humans have specific microbial profiles at the oral, skin, reproductive organ, gastrointestinal and fecal levels ^{[2],[3]}. In particular, the human gastrointestinal (GI) tract has a microbial diversity of up to 100 trillion microorganisms, predominantly bacteria but also archaea, viruses, and parasites. The GM encodes more than three million genes that produce hundreds of metabolites ^[4]. Only recently, the effect of the physical activity (PA) on the GM has been more thoroughly investigated, although considerable difficulties persist in structuring research protocols capable of limiting the various confounding elements as much as possible. Most evidence shows that a sedentary lifestyle is associated with a higher incidence of chronic diseases ^{[5],[6],[7]}, on which PA can play a preventive and therapeutic role through different mechanisms. Recently, the potential effects produced on GM have been proposed as another modality through which PA can perform beneficial functions on host health ^[8].

Although there is no gold standard for gut health, and its definition remains uncertain ^{[9],[10],[11]}, the interaction between host PA can favor the growth of beneficial bacteria and gut cells that maintain the integrity of the intestinal surface, which acts as the first defense against pathogens. In return, the selected bacteria synthesize molecules capable of modifying the metabolism and immune functions of the host ^[12]. Furthermore, disruption of the gut barrier is considered one of the mechanisms of major depression and other cognitive and behavioral alterations, with the gut-brain axis (GBA) playing a role in mediating these processes ^[13]. In this context, PA seems able to influence this two-way communication interaction through the GBA ^[14].

2. Physical Activity and Gut Microbiota in Preclinic Studies

It is now quite clear that, in animal models, exercise initiates significant changes in the GM. In agreement with Kang et al. [15], Denou et al. [16] found an increased bacterial diversity in diet-induced obesity (DIO) mice fed a high fat diet (HFD) following forced treadmill running (FTR). In contrast to Kang et al. [15], using a high-intensity interval training (HIIT) protocol did not result in a reduction in body mass, suggesting the possibility of different bacterial changes based on the exercise modality used. Ribeiro et al. [17] highlighted that the use of a medium-low intensity exercise (50% of maximal velocity) induces insignificant changes in the GM to counteract the effects of a prolonged HFD. It has been found [18] that forced exercise (FWR) results in a significant up-regulation of the *Ruminococcus gnavus* species, a bacterium capable of degrading the intestinal mucosa and thus penetrating its inner and outer layers, exposing intestinal epithelial cells to immunogenic bacterial proteins and thus exacerbating intestinal inflammation [19]. However, the regulation of mucin, the glycoprotein that makes up intestinal muscle, and the bacterial dynamics involved in relation to exercise have been little investigated. Of note is the increase in the *Anaerotruncus* genus, a butyrate-producing bacterial group that colonizes the outer layer of the colonic mucosa and is phylogenetically related to *Fecalibacterium prausnitzii*, a known butyrate producer in humans [20], [21]. These bacteria often feed on lactate, acetate, or other intermediates produced by other bacterial strains, and so it is possible that the activity-induced changes in so-called lactate producers (e.g., lactobacilli) and butyrate producers (e.g., *Anaerotruncus*) are related by a cross-feeding phenomenon. The period of life in which exercise is carried out would also appear to be important, thus representing age as a determining factor in the regulation of the GM. Using germ-free (GF) mice, an early sensitive period has been identified during which the absence of an intact GM reflects physiological consequences such as the exaggerated activity of the hypothalamic-pituitary-adrenal (HPA) axis that can only be partly normalized by the introduction of *Bifidobacteria infantis* if administered during the early period of life [22]. This evidence reveals that the framework of GM during development can strongly influence the health of the host throughout life. Furthermore, just as physiological systems during development are remarkably malleable and sensitive to change, likewise the GM is more plastic in the early stages of life [23], [24] and, consequently, the microbial ecosystem present during the early period of life may be more sensitive to environmental changes due in part to its lower stability and diversity than in adulthood. Mika et al. [25] hypothesize and note that exercise undertaken during early life (EL) may have a greater impact on GM than that undertaken in adulthood, corroborated recently by another study [26]. They also observe a lower species richness in juvenile than in adult rats. A similar condition was observed in humans by Yatsunen et al. [27], supporting the idea that it is precisely this condition of the young GM that encourages greater changes within it, unlike in the adult GM where the greater microbial complexity may make it more resistant to changes induced by environmental factors. Li et al. [28] note that HFDs can induce an increase in circulating Lipopolysaccharide (LPS) levels which are related to the onset of osteoarthritis [29]. PA (VWR) seems able to remodel the GM by increasing its diversity and consequently reducing LPS levels in the blood and synovial fluid. Yuan et al. [30] find out negative effects of excessive exercise on the GM showing a reduced α -diversity and β -diversity compared with the control group.

3. Physical Activity and Gut Microbiota in Human Studies

Clarke et al. [31] performed the first study on athletes and greater richness and α -diversity were observed in the athletes than in the control groups, in agreement with Mörkl et al. [32]. Microbial diversity is positively associated

with protein intake, suggesting that exercise and diet are drivers of gut bacterial diversity. In the athletes' group, an increase in butyrate-producer phylum (Firmicutes) and genus (*F.prausnitzii*) was observed [20],[21]. Furthermore, athletes and LBG show increased Akkermansiaceae family and Akkermansia genus, associated with metabolic disorders [33]. Castellanos et al. [34], using data collected through their previous observational study [35] identified bacterial taxa considered to be 'key' microorganisms for the structure of the GM since the pathogenicity of certain bacteria is not always and only related to their abundance but also to other factors such as interactions with other microorganisms. No changes were found after three weeks of HIIT protocol, indicating that short-term HIIT protocol does not impact the fecal bacterial community and that progress in the cardiorespiratory fitness (CRF) does not lead to modification of GM in the short term [36], similarly to Moitinho-Silva [37]. Durk et al. [38] supporting other similar work in both animal models and humans [39],[32],[18], found that the PA can be a factor that positively affect the human GM. Bycura et al. [40] in contrast to Quiroga et al. [41], where aerobic and resistance exercises were analyzed separately, observed that only aerobic activity causes an initial significant change within the GM that subsequently decreases until it becomes irrelevant. Petersen et al. [42], found a significant correlation between the presence of the genus *Prevotella*, with concomitant upregulation of brain chain amino acids (BCAAs), and the time spent training (>11 h/week) in both professionals and amateurs. A decrease in *Bacteroides* and, among 30 cyclists, an increase in the genus *Akkermansia* was noted, as already observed [31]. It was also observed that the increased presence of *Prevotella* correlates with certain carbohydrate and amino acids (AAs) metabolic pathways, including the biosynthesis of BCAAs [43]. Morishima et al. [44] found that in endurance runners, some bacteria associated with gut inflammation (*Haemophilus*, *Rothia*, and *Ruminococcus ganvus*) were more abundant. Counterintuitively, *Fecalibacterium*, known as a beneficial butyrate producer, was also more abundant in the endurance runners (ER) group. This could be explained by the fact that an abnormal intestinal environment prompts the *Fecalibacterium* to produce succinate, a risk factor for diarrhea and loose stools [45], and not butyrate. This suggests that prolonged high-intensity exercise may lead to a form of dysbiosis in the athlete. One study [46] attempted to assess whether endurance activity can modulate GM in elderly men and whether these changes are associated with specific cardiometabolic conditions in the host. While genus *Oscillospira*, associated with reduced BMI [47],[48], increases, species *Clostridioides difficile* decreases. Furthermore, changes in these taxa were correlated with changes in several cardio-metabolic risk factors such as systolic and diastolic blood pressure. Researchers found that after six months of combined training, seven high-intensity and eight moderate-intensity exercises [49], *Oscillospira*, *Bifidobacterium*, and *Anaerostipes*, health-related genus [50],[51], were increased. Quiroga et al. [41] found that a combined endurance and strength training can alter GM composition and function in obese subjects by significantly reducing the phylum Proteobacteria, corroborating the results obtained by Munukka et al. [52] and the class Gammaproteobacteria. These results suggest the presence of a negative bacterial profile related to the state of obesity that can be positively modified by PA.

4. Physical Activity, Gut Microbiota and Cognitive Ability

According to Gubert et al. [53], considering the concomitant intestinal dysbiosis present in several neurodegenerative diseases and the impact that PA or exercise can have on the intestinal microbiome and neuronal degeneration, a triangulation between these aspects seems plausible to assess whether PA can

contribute to the modulation of neurodegeneration through GM. Kang et al. [15] showed that mice subjected to a 16-week training protocol reported an improvement in memory associated with the increase in the Firmicutes:Bacteroidetes ratio induced by exercise. One hour per day of exercise can increase the relative abundance of the family Lachnospiraceae, which is negatively correlated with anxiogenic behavior and is capable of producing butyrate (SCFA), a molecule that over-regulates Brain-Derived Neurotrophic Factor (BDNF) expression in the hippocampus and frontal cortex, supporting the survival of existing neurons and stimulating the formation of new neurons and synapses [54]. Thus, according to the authors, this association between induced changes in certain GM phyla and families and memory improvement could be used as a biomarker for exercise-induced effects at a cognitive level. Experimental data have shown that GM modifications induced by an aerobic activity, specifically characterized by an increase in certain bacteria (e.g., *Lactobacillus plantarum* and *Streptococcus thermophile*), are capable of inducing the synthesis of serotonin, a molecule that protects against symptoms of anxiety and depression [55]. Abraham et al. [56] extrapolated findings that seem to indicate the ability of exercise to improve cognitive function and some markers of Alzheimer's disease (AD); using transgenic mice (APP/PS1) subjected to a 20-week treadmill exercise protocol, they note a significant improvement in the Morris Maze Test, which assesses spatial memory, and a reduction in β -amyloid plaques, one of the main aspects involved in AD [57], supporting what was previously observed by Lin et al. [58]. Near these plaques, an increase in microglia, important for brain development by providing structural and metabolic support to neurons and involved in neuroplasticity and regulation of neural repair [59], is found, underlining the neuroprotective effect of exercise. This appears to be associated with the abundance of some bacterial strains (Eubacteria, Roseburia) and the reduction of others, so these results suggest that the cognitive effects of exercise may be mediated through GM alteration, reducing the levels of microbes involved in disease exacerbation and promoting the abundance of those bacteria capable of producing SCFAs that appear beneficial.

5. Conclusion

A PA performed voluntarily appears to attenuate intestinal inflammation, in contrast to a forced activity that instead increases this condition in animal models. Vigorous endurance exercise can negatively affect the GM framework in humans; furthermore, only aerobic activities can alter the GM structure, probably because of the positive correlation between CRF and microbial diversity. PA can stimulate bacterial community richness by altering SCFAs-producing species, as well as favoring the colonization of health and athletic performance-promoting strains (e.g., *A. muciniphila* and *Veillonella*). PA seems able to regulate cognitive conditions (e.g., anxiety and depression) and functionality (e.g., Alzheimer's and Parkinson's Disease) through modifications of microbial composition and subsequently the production of certain protective molecules, to date in animal models.

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