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THE ROLE OF PHYSICAL ACTIVITY IN MODULATING THE GUT MICROBIOTA AND ITS CONSEQUENCES FOR INTESTINAL HOMEOSTASIS AND METABOLISM - A SYSTEMATIC REVIEW

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ABSTRACT

Introduction: The gut microbiota is increasingly recognised as an important regulator of immune function, metabolic processes, intestinal barrier integrity, and gut–brain communication. Both lifestyle factors and dietary habits, including the intake of fermented foods and probiotics, have been shown to influence its composition.

Objective: Our aim is to demonstrate how exercise can increase gut microbial diversity, which can be beneficial for athletes' performance, exercise capacity and recovery.

Materials and methods: The study is based on a variety of analyses from 1997 to 2026 that were found using PubMed and Google Scholar.

Results: Regular physical activity is associated with increased gut microbiota diversity, including a higher abundance of bacteria such as Akkermansia, Veillonella, Prevotella, Bifidobacterium, and Lactobacillus. These changes are linked to improved intestinal function, enhanced athletic performance, and more efficient muscle recovery. In contrast, prolonged or excessive high-intensity exercise may impair intestinal integrity and contribute to dysbiosis.

Conclusion: Physical activity promotes a greater diversity of gut microbiota, which can improve bowel function, athletic performance, muscle recovery and appetite regulation. However, the available evidence suggests that training load and recovery strategies should be carefully balanced to avoid potential negative effects on gastrointestinal health.

KEYWORDS

Gut Microbiota, Physical Activity, Microbiome, Athletes, Physical Performance, Gut Health

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Introduction

The gut microbiota is a complex community of microorganisms residing in the digestive tract, consisting of thousands of bacteria, viruses, and some eukaryotes. It plays an important role in enhancing the immune system, especially gastrointestinal (GI) barrier integrity, as well as nutrient uptake, vitamin synthesis and energy harvest [1, 2]. It also influences brain–gut communication, which can benefit mental health by improving cognitive performance and stress tolerance [3].

Lifestyle and diet are among the factors that influence gut health, which explains the growing interest in consuming naturally occurring probiotic bacteria found in fermented dairy-based products and pickles [4].

Regular exercise has been associated with increased gut microbiota diversity [1,3,2]. The composition and activity of gut microbiota that contribute to the efficient extraction of energy from food can provide metabolic benefits for athletes during high-intensity exercise and support faster recovery. The use of probiotics, which is becoming increasingly popular, leads to increased microbial diversity and the growth of health-promoting species. They also reduce the frequency of respiratory infections and relieve GI symptoms in athletes [3]. Better immunity means greater training efficiency.

On the other hand, athletes' restrictive diets containing low fibre may be harmful to the composition of the gut microbiota. Furthermore, excessive and/or prolonged high-intensity exercise may not be beneficial for intestinal health, causing increased intestinal permeability and hypoperfusion [1].

Methodology

This systematic review is based on numerous peer-reviewed studies conducted between 1997 and 2026, with a particular focus on the relationship between gut microbiota and physical activity. Information was obtained from PubMed and Google Scholar using the search terms 'gut microbiota', 'gut microbiota and sport', and 'gut microbiota and exercise', which generated 11,494 results.

Results

Physical activity is one of the important factors that influence intestinal bacterial flora. Increased diversity of microorganisms, including Akkermansia, Veillonella, Prevotella, Bifidobacterium and Lactobacillus, has been observed in physically active people. Athletes also benefit from this diversity, experiencing improved intestinal epithelial integrity, slower gastric emptying, enhanced athletic performance and reduced recovery time for damaged muscles. This is caused by the metabolic products of these bacteria [2, 3, 5-16]. However, prolonged high-intensity physical exertion can lead to dysbiosis [17, 18].

Discussion

The human GI tract hosts a complex ecosystem comprising bacteria, archaea, and eukaryotes, collectively referred to as the ‘gut microbiota’. This microbiota plays an important role in maintaining intestinal homeostasis and may contribute to disease prevention. The majority of microorganisms are found in the digestive tract, and their total population can reach 100 trillion cells, which is ten times more than the number of human cells. A total of 2,172 species of bacteria were isolated and classified into 12 different phyla, of which 93.5% belonged to the following: *Proteobacteria*, *Firmicutes*, *Actinobacteria* and *Bacteroidetes*. Furthermore, 386 species of these bacteria have been categorised as strictly anaerobic and are inhabited by the GI tract [19, 20]. The composition of the human gut microbiota is influenced by a number of factors, including host genetics, age, delivery method, antibiotic utilisation, diet, and lifestyle [1]. The subject of lifestyle, categorised as either sedentary or active, and its impact on the gut microbiome is not yet extensively researched, but a growing number of studies are addressing this issue.

A greater diversity of microorganisms, particularly *Akkermansia*, *Veillonella*, and *Prevotella*, has been observed in physically active individuals and athletes compared to those leading a sedentary lifestyle [3].

Akkermansia muciniphilla is a bacterium that has been demonstrated to degrade mucin, in the same way impacting its turnover. Furthermore, research has indicated an inverse correlation between the number of bacteria and obesity, as well as metabolic disorders [8]. The degradation of mucin produces short-chain fatty acids (SCFAs) including acetate and propionate. SCFAs are a substrate for colonocytes and support epithelial integrity. In addition, SCFAs improve the metabolic profile by slowing gastric emptying, increasing satiety, and stimulating L cells in the intestine to secrete glucagon-like peptide-1 (GLP-1), consequently impacting insulin secretion and glucose metabolism [15]. In order to maintain intestinal homeostasis, it is imperative to regulate the level of *A. muciniphilla*. An excess of this bacterium can lead to excessive degradation and thinning of the mucus, while a deficiency can result in thickening of the mucus, which can, in turn, lead to inflammation, bacterial translocation, and colonic pathologies [15]. Everard et al. demonstrated that restoring its presence or increasing its abundance correlates with strengthening the intestinal barrier, leading to an improvement in the metabolic profile [8]. However, Clarke et al. postulate that their study demonstrates that both a protein-rich diet and physical activity may have an impact on the increase in bacterial biodiversity. This finding underscores the necessity for further research to identify these factors. They also pointed out that lower microbiota diversity is linked to a greater incidence of diseases such as autism, GI diseases, and inflammatory characteristics associated with obesity [5].

Scheiman et al. observed a correlation between *Veillonella atypica* and athletic performance. In their studies conducted on mice, they observed that strain of *Veillonella* participate in the conversion of lactate to propionate. Propionate has been demonstrated to increase heart rate, VO2 max, and to affect blood pressure in mice. In humans, it has been shown to increase resting energy expenditure and lipid oxidation fasting [9]. Antibiotic treatment causes depletion of the gut microbiota. Okamoto et al. showed that mice after two weeks of antibiotic treatment had lower endurance on a treadmill than untreated controls, which highlights the importance of proper gut microbiota for exercise performance. They also observed on mice that the gut microbiome in the cecum and colon uses dietary fiber to produce SCFAs, the most important of which are acetate, propionate, and butyrate. Acetate is the most significant of SCFAs, with a prevalence in plasma that is predominantly attributable to intestinal origin. It serves as the primary energy source for skeletal muscles at least during endurance exercise [10].

The most significant source of SCFAs is a microbiome dominated by *Prevotella* species. They suggest that consuming fermentable dietary fiber before endurance exercises improves skeletal muscle performance in athletes due to the acetate produced, although further research is needed [10]. In their study of the gut microbiome of cyclists, Petersen et al. used the metagenomic whole genome shotgun (mWGS) method, thereby identifying a high prevalence of *Prevotella*. However, the researchers did not ascertain whether this abundance was associated with a diet high in carbohydrates, the use of various over-the-counter vitamins, or the duration and intensity of exercise [11]. Prevotella has been observed in two distinct groups: rural communities outside the West and people with a plant-based diet that is rich in fibre and polysaccharides [14].

Queipo-Ortuño et al. evaluated the composition of the gut microbiota in rats depending on their nutritional status and physical activity. The researchers observed a positive correlation between the number of *Bifidobacterium* and *Lactobacillus* and serum leptin levels. Leptin, a hormone secreted by adipocytes, exerts its influence upon the central nervous system, thereby modulating appetite and food intake. It has been established that both *Bifidobacteria* and *Lactobacillus* possess the capacity to produce organic acid lactate, which is subsequently converted into butyrate. Butyrate has been demonstrated to induce mucin synthesis, improve intestinal integrity, reduce bacterial transport through the epithelium, and lower serum levels of ghrelin, an appetite-stimulating hormone [16].

Probiotics can shorten the recovery time of muscles damaged by exercise and enhance physical performance. Jäger et al. showed that, after a two-week supplementation of *Bacillus coagulans* BC30 and casein, recreationally trained men had a better recovery status after 24 and 72 hours than those who only consumed casein [12]. The taking of *Lactobacillus gasseri* CP2305 by runners resulted in better recovery time and mental condition in comparison with the intake of a placebo [13].

The enrichment of the bacterial GI community is not only caused by the overall healthy lifestyle of athletes. Endurance training also causes adaptive changes in athletes' organisms, such as decreased blood flow, tissue hypoxia and increased transit, which can all lead to changes in the GI tract [2]. A study by Rosa et al. found that lifelong regular aerobic physical activity prevented oxidative ageing of intestinal muscles in mice [6]. Clarke et al. demonstrated that athletes also have a more diverse gut microbiota, as well as lower inflammatory markers and improved metabolic markers, compared to controls [5]. Furthermore, Estaki et al. proposed that exercise could provide an adjuvant therapy for combatting diseases associated with dysbiosis [7].

However, high-intensity exertion can also have deleterious effects on the gastrointestinal system, manifesting in heightened intestinal permeability. This, in turn, can give rise to inflammatory responses and gastrointestinal symptoms, as evidenced in long-distance runners [17]. Prolonged high-intensity physical activity can also cause dysbiosis. In the study of the gut microbiome of ultramarathon runners, Sato and Suzuki observed an increase in the abundance of *Faecalibacterium prausnitzii*, *Eubacterium rectale*, and *Blautia luti*, which produce anti-inflammatory butyrate, while Collinsella aerofaciens associated with pro-inflammatory states, increased [18].

Conclusions and summary

The available evidence indicates that regular physical activity influences the composition of the gut microbiota, particularly by increasing microbial diversity. These changes are associated with improved intestinal epithelial integrity, enhanced athletic performance, and more efficient muscle recovery following exercise. Alterations in gut microbiota may also affect appetite-regulating hormones, including leptin and ghrelin, which could contribute to better energy balance and long-term metabolic health in physically active individuals. At the same time, the findings reviewed here highlight that excessive or prolonged high-intensity exercise may adversely affect gastrointestinal function and microbial balance, potentially leading to dysbiosis. Therefore, an appropriate balance between training load, recovery, and nutritional support appears to be essential for maintaining gut health in athletes.

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