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Physical Activity and the Gut Microbiota: Mechanisms and Clinical Relevance - literature review

Karolina Pracoń (KP)
1 Military Clinical Hospital with Outpatient Clinic: Lublin, Lublin, PL
karolinapracon1@gmail.com
https://orcid.org/0009-0001-9934-7279

Maria Pietrzak (MP)
Stefan Cardinal Wyszynski Regional Specialized Hospital in Lublin, Krasnicka 100, 20-718 Lublin, Poland
marysiapietrzak2@gmail.com
ORCID: https://orcid.org/0009-0002-5751-3248

Aneta Chawryło (AC)
Stefan Cardinal Wyszynski Regional Specialized Hospital in Lublin, Krasnicka 100, 20-718 Lublin, Poland
chawrylo.anet2503@gmail.com
ORCID:https://orcid.org/0009-0003-2412-6900

Marcela Łupina-Romaniuk (ML-R)
University Clinical Hospital No. 4 in Lublin, Poland, Doktora Kazimierza Jaczewskiego 8, 20-954 Lublin, Poland marcela.lupina2000@gmail.com https://orcid.org/0009-0003-1821-7910

Dominika Piecuch (DP)
1 Military Clinical Hospital with Outpatient Clinic in Lublin
aleje Racławickie 23, 20-049 Lublin, Poland
piecuchdominika24@gmail.com
https://orcid.org/0009-0005-7836-4810

Karolina Oleksińska (KO)
Stefan Cardinal Wyszynski Regional Specialized Hospital in Lublin, Krasnicka 100, 20-718 Lublin, Poland
karolinaolek19@gmail.com
ORCID: https://orcid.org/0009-0004-3046-9835

Gabriela Świetlicka (GŚ)
Medical University in Lublin, Lublin, Poland
gswietlicka00@gmail.com
ORCID https://orcid.org/0009-0005-7746-4879

Paulina Pietraś (PP)
University Clinical Hospital No. 1 in Lublin, Poland
Stanisława Staszica 16, 20-081 Lublin, Poland
paulina.pietras1929@gmail.com
https://orcid.org/0009-0004-9124-5149

Michał Stolarczyk (MS)
Independent Public District Hospital in Łęczna
Krasnystawska 52, 21-010, Łęczna, Poland
michal_stolarczyk200@wp.pl
https://orcid.org/0009-0009-7704-1154

Julia Kołodziejczyk (JK)
University Clinical Hospital No. 4 in Lublin, Poland, Doktora Kazimierza Jaczewskiego 8, 20-954 Lublin, Poland
julkak00@wp.pl
https://orcid.org/0009-0009-2526-0937

Corresponding Author

Karolina Pracoń (KP)

karolinapracon1@gmail.com

Abstract

Background:

The gut microbiota is an integral component of human homeostasis, participating in the regulation of metabolic, immunological, and neuroendocrine processes. Alterations in its composition and function have been associated with the development of numerous chronic diseases, thereby increasing interest in lifestyle factors that can modulate the intestinal microbial ecosystem. Among these factors, physical activity has emerged as a potentially important determinant of gut microbiota composition and function.

Aim:

This narrative review aimed to evaluate current evidence regarding the effects of physical activity on the composition and function of the gut microbiota, with particular emphasis on underlying biological mechanisms, clinical relevance, and the limitations of the available scientific evidence.

Materials and Methods:
A literature search was conducted using the PubMed database. Observational, interventional, experimental, and review studies investigating the relationship between physical activity and the gut microbiota were included.

Results:

Current evidence suggests that regular moderate physical activity may promote beneficial alterations in the gut microbiota, including increased microbial diversity, enhanced abundance of short-chain fatty acid (SCFA)-producing bacteria, and improved intestinal barrier integrity. In contrast, prolonged and intensive exercise may contribute to transient gastrointestinal disturbances, increased intestinal permeability, and enhanced inflammatory responses. Interpretation of the available findings is complicated by the substantial influence of confounding factors, particularly diet, pharmacotherapy, body composition, and training status.

Conclusions:

Physical activity is an important modulator of the gut microbiota; however, the nature of this relationship remains complex and multifactorial. Current evidence supports the hypothesis that regular moderate exercise may exert beneficial effects on the intestinal microbial ecosystem, although further well-designed studies are required to establish causal relationships and clarify their clinical implications.

Key words: gut microbiota, gut microbiome, physical activity, exercise, dysbiosis, short-chain fatty acids

1. Introduction

The gut microbiota is a complex ecosystem of microorganisms inhabiting the human gastrointestinal tract and plays a fundamental role in maintaining host homeostasis. Its functions extend beyond local digestive processes and include participation in nutrient metabolism, regulation of immune responses, maintenance of intestinal barrier integrity, and bidirectional communication between the gastrointestinal tract and other organ systems [1–5]. Over the past decade, the gut microbiota has become one of the most intensively investigated areas of biomedical research due to its potential involvement in the pathogenesis of numerous chronic disorders, including obesity, type 2 diabetes mellitus, cardiovascular disease, inflammatory bowel disease, and neuropsychiatric conditions [2–5].

Physical activity is among the most extensively documented modifiable lifestyle factors contributing to metabolic and overall health [3–9]. Increasing evidence suggests that at least some of these beneficial effects may be mediated through alterations in the composition and metabolic activity of the gut microbiota [6–9].

Most studies investigating the relationship between exercise and the gut microbiota indicate that physically active individuals exhibit distinct microbial profiles compared with sedentary populations [10–13]. These differences are frequently characterized by greater microbial diversity and increased abundance of bacterial taxa associated with favorable metabolic outcomes [10–13].

Importantly, the influence of exercise on gastrointestinal health is not universally beneficial. While regular moderate physical activity appears to support intestinal homeostasis, prolonged and high-intensity exercise has been associated with impaired intestinal barrier function, gastrointestinal symptoms, and transient unfavorable alterations in the gut microbial environment [19,20,24].

Despite the rapid expansion of research in this field, the current body of evidence remains insufficient to clearly define the clinical significance of exercise-induced changes in the gut microbiota or their practical applications in health promotion and disease prevention.

Therefore, the aim of this review is to critically evaluate current evidence regarding the effects of physical activity on the gut microbiota, with particular emphasis on biological mechanisms, clinical relevance, and limitations of existing research.

2. Materials and Methods

This study was conducted as a narrative review of the literature.

A comprehensive literature search was performed using the PubMed, Scopus, and Web of Science databases. Publications available up to March 2026 were considered for inclusion.

The search strategy included combinations of the following keywords: gut microbiota, gut microbiome, physical activity, exercise, exercise training, athletes, short-chain fatty acids, gut–brain axis, gut–muscle axis, intestinal permeability, dysbiosis, and probiotics.

Observational, interventional, experimental, and review studies investigating the effects of physical activity on the gut microbiota were included in the analysis. Preference was given to peer-reviewed publications published in English.

Due to the narrative nature of the review, no formal assessment of methodological quality or quantitative synthesis of results was performed.

3. Results

3.1. Biological Significance of the Gut Microbiota

The gut microbiota constitutes a dynamic microbial ecosystem that performs essential metabolic, immunological, and protective functions within the host [1–5]. The predominant bacterial phyla in the human gastrointestinal tract include *Firmicutes*, *Bacteroidetes*, *Actinobacteria*, and *Proteobacteria* [1,2].

One of the primary functions of the gut microbiota is the fermentation of indigestible dietary components, particularly dietary fiber, leading to the production of biologically active metabolites, including short-chain fatty acids (SCFAs) [2,15,16]. These metabolites play important roles in energy metabolism, maintenance of intestinal barrier integrity, and modulation of immune responses.

In addition, the gut microbiota contributes to host defense against pathogenic microorganisms and participates in the development and regulation of both innate and adaptive immunity [1–5]. Consequently, disturbances in microbial composition and function, commonly referred to as dysbiosis, have been associated with a wide range of chronic diseases.

3.2. Mechanisms Underlying the Effects of Physical Activity on the Gut Microbiota

The influence of physical activity on the gut microbiota is likely mediated through multiple interconnected biological mechanisms [6–9].

Regular moderate exercise may enhance intestinal barrier integrity, reduce chronic low-grade inflammation, and promote a favorable intestinal metabolic environment [6–8]. Exercise-induced improvements in insulin sensitivity, body composition, and systemic metabolic regulation may further contribute to alterations in microbial composition and function [3,6,15].

Physical activity may also affect intestinal transit time, mucosal immune activity, and the production of metabolites that shape the gut microbial ecosystem [6–9]. However, the effects of exercise appear to be dose-dependent. While moderate physical activity is generally associated with beneficial adaptations, prolonged and high-intensity training may exert adverse effects on gastrointestinal physiology and microbial homeostasis [19,20,24].

3.3. Gut Microbiota in Physically Active Individuals

Observational studies suggest that physically active individuals exhibit distinct gut microbial profiles compared with sedentary populations [10–13].

Most investigations have focused on changes in microbial diversity, bacterial abundance, and alterations in the relative proportions of the dominant phyla *Firmicutes* and *Bacteroidetes*.

Available evidence indicates that the effects of similar exercise interventions may vary according to age, dietary habits, training status, and other population-specific characteristics.
Furthermore, different exercise modalities, including voluntary and forced exercise models, may induce distinct microbial adaptations. One of the most consistently reported findings is an increase in microbial richness and diversity among individuals who engage in regular physical activity.

The *Firmicutes/Bacteroidetes* ratio has been positively associated with body mass index (BMI) and has been proposed as a potential marker of obesity-related dysbiosis [13]. Exercise may promote an increase in the relative abundance of *Bacteroidetes* while reducing the proportion of *Firmicutes* [13,23].

Some evidence suggests that the beneficial effects of exercise on the gut microbiota may be more pronounced when physical activity is initiated early in life. However, these adaptations appear to be reversible and may gradually diminish following cessation of regular exercise [13,23].

Interpretation of these findings requires caution because physical activity frequently coexists with numerous confounding factors, including dietary patterns, body composition, and other health-related behaviors [7–9].

3.4. Gut Microbiota in Athletes

Athletes represent a unique study population because intensive training is accompanied by multiple factors that may independently influence the gut microbiota, including specialized dietary practices, nutritional supplementation, low body fat levels, and substantial physiological stress [10,19,21,24].

Several studies have reported greater microbial diversity in athletes compared with non-athletic controls [10,21]. Among the most intriguing findings are observations concerning bacteria belonging to the genus *Veillonella*, which are capable of metabolizing exercise-derived lactate into propionate [14].

This observation has led to the hypothesis that microbial lactate metabolism may contribute to exercise performance by influencing host energy metabolism. Although biologically plausible, the practical significance of this mechanism remains uncertain and requires further investigation.

Current evidence does not support viewing the athlete microbiome as a simple model of beneficial training adaptation. Rather, the observed microbial characteristics likely reflect a complex interaction between exercise, diet, supplementation, and broader lifestyle factors [8,21,24].

3.5. Short-Chain Fatty Acids as Potential Mediators of Exercise-Induced Effects

Short-chain fatty acids, particularly butyrate, propionate, and acetate, are among the most frequently proposed mediators linking physical activity to beneficial metabolic outcomes [15,16].

SCFAs are produced through microbial fermentation of indigestible dietary substrates, primarily dietary fiber [2,15]. Butyrate serves as a major energy source for colonocytes and plays a crucial role in maintaining intestinal barrier integrity. Propionate and acetate are involved in energy metabolism, lipid homeostasis, and immune regulation [15,16].

Several studies have reported increased abundance of SCFA-producing bacteria in physically active individuals [11–13]. Experimental evidence has also suggested a potential relationship between microbial fermentation and metabolic adaptations associated with exercise training [15].

However, SCFA production is strongly influenced by dietary substrate availability, particularly fiber intake. Consequently, observed changes may reflect the combined effects of physical activity and dietary habits rather than the isolated effects of exercise itself [2,5,7,8].

3.6. The Gut–Brain Axis

The gut microbiota participates in bidirectional communication between the gastrointestinal tract and the central nervous system, commonly referred to as the gut–brain axis [17].

This complex network involves neural, endocrine, immune, and metabolic pathways. One of the proposed mechanisms underlying gut–brain communication is the ability of intestinal microorganisms to influence the metabolism and availability of neuroactive compounds, including serotonin, dopamine, norepinephrine, and gamma-aminobutyric acid (GABA).

The vagus nerve represents a major neural pathway linking the gastrointestinal tract with the brain and is considered a key component of gut–brain signaling. In addition, microbial metabolites and immune mediators may influence brain function either directly or indirectly through systemic circulation.

Inflammatory processes may also contribute to gut–brain interactions. Impairment of intestinal barrier integrity can facilitate the translocation of bacterial endotoxins into the bloodstream, promoting systemic immune activation and potentially affecting neurological function [17,19,20].

In the context of physical activity, the gut–brain axis is of particular interest because regular exercise influences stress responses, immune regulation, and energy metabolism [6,17]. Nevertheless, a substantial proportion of the available evidence originates from mechanistic and preclinical studies, and the clinical relevance of these observations remains incompletely understood [17].

3.7. The Gut–Muscle Axis

The concept of the gut–muscle axis has emerged as a relatively new area of research, describing bidirectional interactions between the gut microbiota and skeletal muscle physiology [8,18].

Several mechanisms have been proposed to explain this relationship, including modulation of nutrient bioavailability, amino acid metabolism, mitochondrial function, and the production of microbial metabolites capable of influencing muscle tissue [8,15,18].

Particular attention has been directed toward SCFAs, which may contribute to energy metabolism, anti-inflammatory responses, and maintenance of metabolic homeostasis [15]. Experimental studies have suggested that alterations in gut microbial composition may influence muscle function and exercise adaptation.

However, the strongest evidence supporting the gut–muscle axis currently derives from animal and mechanistic studies. Human clinical data remain limited, and the practical significance of these findings has yet to be fully established [8,18].

Although the gut–muscle axis represents a biologically plausible and promising concept, current evidence does not justify considering the gut microbiota as a direct therapeutic target for improving physical performance or training adaptations [8,21].

3.8. Effects of Intensive Exercise on the Gastrointestinal Tract and Gut Microbiota

The relationship between physical activity and gastrointestinal health appears to be nonlinear. While regular moderate exercise may promote intestinal homeostasis, prolonged and high-intensity training can exert adverse effects on both gastrointestinal function and the gut microbiota [6–9,19,20,24].

One of the principal mechanisms involves the redistribution of blood flow from the splanchnic circulation to exercising skeletal muscles. Sustained intestinal hypoperfusion may result in mucosal ischemia, enterocyte damage, and increased intestinal permeability [19,20].

As a consequence, bacterial translocation and systemic inflammatory responses may occur, potentially compromising both gastrointestinal and overall physiological function [17,19,20].

These effects are particularly relevant among endurance athletes, in whom gastrointestinal symptoms such as nausea, abdominal pain, bloating, and diarrhea are frequently reported [19,21,24].

Additional contributing factors may include chronic psychological stress, inadequate recovery, dehydration, heat stress, and cumulative training load [20,24].

Collectively, current evidence suggests that the effects of exercise on gastrointestinal health are dose-dependent. Greater training volume or intensity does not necessarily translate into greater biological benefit, and excessive exercise may compromise intestinal homeostasis [8,19].

3.9. Diet, Pharmacotherapy, and Targeted Modulation of the Gut Microbiota

The effects of physical activity on the gut microbiota should be interpreted within the broader context of factors that strongly influence the intestinal ecosystem, particularly diet and pharmacotherapy [2,5,7,8].

Dietary patterns among athletes often differ substantially from those observed in sedentary individuals, making it difficult to isolate the independent effects of exercise on the gut microbiota. Diets rich in fat and simple sugars have been associated with rapid quantitative and qualitative alterations in microbial composition, including increased abundance of *Firmicutes* and *Proteobacteria* and reduced representation of *Bacteroidetes* [9,27,28].

Similarly, high-protein, low-carbohydrate dietary patterns have been linked to reduced abundance of *Bifidobacterium* species [9,27,28]. These findings underscore the importance of considering dietary habits when interpreting exercise-related microbial adaptations.

Prebiotics and probiotics have been proposed as potential strategies for modulating the gut microbiota in physically active populations [9,15,29]. Several studies have demonstrated that supplementation with *Lactobacillus* strains may increase their abundance within the intestinal microbiota and may be associated with reduced markers of muscle damage and oxidative stress during exercise and recovery [13].

However, evidence regarding improvements in physical performance remains inconsistent. Enhanced exercise capacity has been reported in some studies but not in others, limiting the ability to draw definitive conclusions regarding ergogenic benefits [13].

At present, available evidence does not support the routine use of probiotics or prebiotics as evidence-based interventions for improving athletic performance [13,21,22].

Pharmacotherapy represents another important factor influencing gut microbial composition. Particular attention has been directed toward antibiotics, nonsteroidal anti-inflammatory drugs (NSAIDs), and proton pump inhibitors (PPIs) [9].

Antibiotic treatment may reduce microbial diversity, disrupt ecological balance within the intestinal microbiome, and promote the selection of antibiotic-resistant bacterial strains. These alterations may favor the proliferation of proteolytic bacteria and contribute to disturbances in intestinal fermentation processes, potentially leading to gastrointestinal symptoms [9].

NSAIDs may damage the small intestinal mucosa, increase intestinal permeability, and negatively affect microbial composition [9]. Long-term use of PPIs, commonly prescribed for gastroesophageal reflux disease or as prophylaxis during NSAID therapy, has also been associated with alterations in gut microbial communities and an increased risk of small intestinal bacterial overgrowth (SIBO) [9].

4. Discussion

Current evidence suggests that physical activity can influence both the composition and functional activity of the gut microbiota; however, the nature of this relationship appears to be considerably more complex than initially suggested by early observational studies [7–9].

One of the most consistently reported findings is the greater microbial diversity observed among physically active individuals compared with sedentary populations [10–13]. Although microbial diversity is frequently considered a marker of gut health, its interpretation should be approached with caution. Increased diversity alone does not necessarily indicate improved physiological function, nor does it establish a direct causal relationship between exercise and health outcomes [8,9].

A major challenge in interpreting existing evidence is the difficulty of separating the effects of physical activity from other lifestyle-related factors. Physically active individuals typically differ from sedentary individuals with respect to dietary habits, body composition, metabolic profile, socioeconomic status, and overall health behaviors [5,7–9]. Consequently, many of the observed microbial differences may reflect the combined influence of multiple factors rather than the isolated effects of exercise.

A similar limitation applies to studies conducted on athletes. Although athletes often exhibit greater microbial diversity and distinct microbial profiles, they also differ substantially from the general population in terms of nutritional practices, supplementation strategies, training volume, and physiological adaptations [10,21]. Therefore, athlete populations cannot be considered a simple model for investigating the independent effects of exercise on the gut microbiota.

Another important observation emerging from current research is the nonlinear nature of the relationship between physical activity and gastrointestinal health. Moderate exercise appears to promote intestinal homeostasis and favorable microbial adaptations, whereas excessive or prolonged training may compromise intestinal barrier integrity and increase the risk of gastrointestinal dysfunction [6,19,20]. These findings suggest that the biological effects of exercise on the gut microbiota are highly dependent on training intensity, duration, and individual physiological responses.

The gut–brain axis and gut–muscle axis represent particularly promising areas of investigation. Experimental and mechanistic studies indicate that microbial metabolites may influence neurological function, energy metabolism, inflammation, and skeletal muscle physiology [17,18]. However, the majority of available evidence remains indirect, and the clinical relevance of these pathways has not yet been firmly established.

Recent interest has also focused on the possibility of using the gut microbiota as a biomarker of exercise adaptation or physical performance. Although certain microbial signatures have been associated with athletic status and training adaptations, current evidence remains insufficient to define a specific “athlete microbiome” or to support microbiota-based interventions aimed at enhancing performance [8,21].

Taken together, existing data support the concept that the gut microbiota may act as a mediator of some beneficial effects of physical activity. Nevertheless, the current body of evidence remains inadequate for drawing definitive conclusions regarding causality, clinical significance, or practical applications in sports and preventive medicine.

5. Limitations

Several limitations of the current evidence base should be acknowledged.

First, available studies are characterized by substantial methodological heterogeneity, including differences in study populations, exercise protocols, dietary assessment methods, and microbiome analysis techniques [7–9]. These inconsistencies complicate direct comparisons across studies and limit the generalizability of findings.

Second, many studies have not adequately controlled for important confounding variables such as dietary intake, pharmacotherapy, body composition, age, and other lifestyle factors that may independently influence gut microbial composition [5,7].

Third, a considerable proportion of the available literature consists of observational studies, which preclude the establishment of causal relationships between physical activity and microbiota-related outcomes. Furthermore, many mechanistic insights are derived from animal models and experimental studies, whose findings may not be directly applicable to human populations [8,17].

Finally, differences in sequencing technologies, bioinformatic pipelines, and microbiome characterization methods contribute additional variability to the existing literature, further complicating the interpretation of the available evidence.

6. Clinical Implications

Current evidence suggests that regular moderate physical activity may represent an important lifestyle factor supporting gastrointestinal and overall health through its potential influence on the gut microbiota [6–9].

Healthcare professionals should recognize that exercise-induced microbial adaptations are influenced by multiple interacting factors, particularly diet, pharmacotherapy, and training status. Consequently, recommendations aimed at promoting gut health should consider these factors alongside physical activity.

Individuals participating in high-intensity or endurance-based exercise should be aware of the potential risk of gastrointestinal symptoms and exercise-induced disturbances in intestinal barrier function [19–21]. Appropriate nutritional strategies, adequate hydration, recovery management, and avoidance of unnecessary pharmacological interventions may help minimize these adverse effects.

At present, there is insufficient evidence to recommend targeted modulation of the gut microbiota through probiotics, prebiotics, or other microbiome-directed interventions as a routine strategy for improving athletic performance or exercise adaptation [21,22]. Further high-quality clinical studies are required before such approaches can be incorporated into evidence-based practice.

7. Conclusions

Physical activity is an important factor influencing the composition and function of the gut microbiota; however, this relationship is multifactorial and highly context-dependent.

Current evidence suggests that regular moderate exercise may promote favorable alterations in microbial diversity, intestinal barrier function, and the abundance of bacteria associated with beneficial metabolic effects. In contrast, prolonged and intensive exercise may compromise gastrointestinal homeostasis and contribute to adverse microbial and physiological changes.

Although the gut microbiota represents a promising area of research in exercise science and preventive medicine, substantial gaps in knowledge remain. Further well-designed longitudinal and interventional studies are needed to clarify causal mechanisms, identify clinically meaningful outcomes, and determine the practical significance of microbiota modulation in the context of health and physical performance.

Disclosure

Author's Contributions Statement

Conceptualization: Karolina Pracoń

Methodology: Aneta Chawryło, Dominika Piecuch

Check: Karolina Oleksińska, Michał Stolarczyk

Resources: Maria Pietrzak, Marcela Łupina-Romaniuk

Data Curation: Gabriela Świetlicka, Paulina Pietraś

Writing-rough preparation: Julia Kołodziejczyk, Karolina Pracoń

Writing-review and editing: Aneta Chawryło, Maria Pietrzak

Supervision: Marcela Łupina-Romaniuk, Gabriela Świetlicka

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Conflict of Interest Statement

The authors deny any conflict of interest.

Declaration of the use of AI:

In preparing this work, the authors used ChatGPT to improve the language, readability, andtext formatting. After using this tool, the authors reviewed and edited the content as necessaryand accept full responsibility for the substantive content of the publication

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