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Relationship Between *Akkermansia muciniphila* Abundance and Exercise-Induced Fat Mass Reduction

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ABSTRACT

Background: Obesity is a major public health concern associated with type 2 diabetes, cardiovascular diseases, and NAFLD. Growing evidence implicates gut microbiota dysbiosis in these conditions. Akkermansia muciniphila, a mucin-degrading bacterium, is inversely associated with adiposity, inflammation, and insulin resistance. Physical activity improves metabolic health; however, outcome variability suggests the involvement of additional modulators, including the gut microbiota.

Aim: This review aimed to summarize the relationship between *A. muciniphila*, physical exercise, and fat mass reduction, and to examine underlying physiological and microbiological mechanisms.

Materials and Methods: A structured narrative review incorporating elements of systematic analysis was conducted. Databases (including PubMed) were searched for experimental and clinical studies assessing associations between A. muciniphila and metabolic parameters, the effects of exercise on gut microbiota, and mechanisms linking microbiota changes with metabolic outcomes. Both animal and human studies were considered.

Results: Animal studies consistently show that aerobic and moderate exercise increase A. muciniphila abundance, enhance microbial diversity, improve glucose tolerance, and reduce fat mass. Human studies show more variable results, with modest increases in A. muciniphila and metabolic improvements, particularly in overweight or metabolically impaired individuals. Proposed mechanisms include enhanced gut barrier integrity, immune modulation, increased short-chain fatty acid (SCFA) production, AMPK activation, and microbiota–adipose tissue cross-talk.

Conclusions: Physical activity modulates gut microbiota, with A. muciniphila serving as a potential mediator of exercise-induced fat loss and metabolic improvement. Although human evidence remains heterogeneous, targeting this bacterium through exercise and lifestyle interventions may support obesity prevention and metabolic health.

Key words: *Akkermansia muciniphila*, gut microbiota, obesity, type 2 diabetes, exercise, fat mass, metabolic health

CONTENTS

1. Introduction

Obesity is one of the foremost public health challenges globally, contributing to an elevated risk of numerous non-communicable diseases, including type 2 diabetes, cardiovascular disorders, non-alcoholic fatty liver disease, and certain types of cancer [1–3]. The most widely used clinical measure for assessing overweight and obesity is the Body Mass Index (BMI). According to the World Health Organization, a BMI ≥25 kg/m² defines overweight, while a BMI ≥30 kg/m² is classified as obesity [1]. Over recent decades, the global prevalence of overweight and obesity has risen sharply, reflecting the interplay of multiple factors, including excessive caloric intake, sedentary behavior, genetic predisposition, environmental influences, socioeconomic conditions, and epigenetic mechanisms [1,2].

Insufficient physical activity is recognized as a major modifiable risk factor for obesity. The WHO defines physical inactivity as insufficient bodily movement to meet established energy-expenditure recommendations. Physical activity encompasses all skeletal-muscle-driven movements, including daily tasks, commuting, occupational activities, and structured exercise [4]. Current WHO guidelines recommend adults perform 150–300 minutes of moderate-intensity or 75–150 minutes of vigorous-intensity aerobic activity per week, complemented by muscle-strengthening exercises [4]. Regular adherence to these guidelines promotes energy balance, improves cardiometabolic health, and reduces the risk of excessive fat accumulation. [4].

Beyond its direct effects on energy expenditure and body composition, physical activity is increasingly recognized as a key regulator of metabolic health through its influence on the gut microbiota. The gut microbiota is a complex ecosystem comprising trillions of microorganisms—including bacteria, archaea, fungi, and viruses—that inhabit the gastrointestinal tract. These communities contribute to digestion, nutrient metabolism, energy extraction, immune regulation, and intestinal barrier maintenance [5–7]. Alterations in microbiota composition or function, collectively termed dysbiosis, have been linked to obesity, insulin resistance, chronic inflammation, and metabolic syndrome [5–7].

Among microbial species influencing metabolic health, Akkermansia muciniphila has gained particular attention. This Gram-negative, strictly anaerobic bacterium belongs to the phylum Verrucomicrobiota and primarily colonizes the intestinal mucus layer, [8]. Its mucin-degrading activity supports mucus layer renewal and epithelial barrier integrity, while its metabolic byproducts serve as substrates for other microbes, enhancing ecosystem stability and diversity

[7,8,9]. Experimental and clinical evidence indicates that higher levels of A. muciniphila are associated with improved metabolic outcomes, including reduced body weight, better glucose regulation, lower systemic inflammation, and overall metabolic homeostasis [10–12].

Regular physical exercise has been shown to positively influence gut microbial diversity and the abundance of SCFA-producing bacteria, which are important for metabolic regulation, immune function, and intestinal barrier maintenance [7,13–15]. Physically active individuals often exhibit higher levels of beneficial microbes, including A. muciniphila, compared with sedentary populations [14,15]. These microbiota-related adaptations may partly account for the beneficial metabolic effects of exercise, including reductions in fat mass and improvements in insulin sensitivity.

Despite growing interest, the precise mechanisms connecting physical activity, A. muciniphila abundance, and fat mass reduction remain incompletely understood. Elucidating these interactions may provide insights into the biological pathways through which exercise exerts metabolic benefits and supports obesity prevention.

The aim of this review is to examine current evidence on the relationship between physical activity, *A. muciniphila* abundance, and exercise-induced fat mass reduction, with a particular focus on the underlying physiological and microbiological mechanisms.

2. Material and Methods

This review was conducted as a structured narrative review with elements of a systematic approach in order to comprehensively analyze the relationships between *Akkermansia muciniphila*, physical activity, and the regulation of fat mass and metabolic parameters.

Publications were included if they met the following general criteria: addressed gut microbiota in the context of body weight regulation, obesity, glucose metabolism, insulin sensitivity, inflammation, or other metabolic parameters. Examined the role of Akkermansia muciniphila in metabolic mechanisms, intestinal barrier integrity, host–microbiota interactions, microbial metabolite production, or cellular signaling pathways. Evaluated the effects of lifestyle interventions (including physical activity), dietary interventions, probiotic or prebiotic supplementation, or experimental manipulations on gut microbiota composition and metabolic outcomes. Represented experimental studies (animal or human), observational studies, mechanistic investigations, or review articles relevant to understanding the relationship between A. muciniphila, physical exercise, and metabolic regulation.

Only English-language peer-reviewed publications were considered. Selected institutional reports and documents from international organizations were also used to provide epidemiological background and contextual information. The following were excluded: non-peer-reviewed publications; conference abstracts, commentaries, and letters lacking original scientific data; studies unrelated to gut microbiota or metabolic regulation; and articles unavailable in full text.

3. Impact of *Akkermansia muciniphila* on Obesity and Body Composition

3.1 Evidence From Animal Models

Animal studies provide strong evidence that increasing the abundance of Akkermansia muciniphila can improve metabolic health in models of diet-induced obesity. In mice fed high-fat diets, supplementation or enrichment with this bacterium has been associated with attenuated weight gain, lower visceral fat, and enhanced glucose tolerance [12,16,17].

Mechanistically, *A. muciniphila* supports intestinal barrier function by maintaining mucus layer integrity and promoting tight-junction protein expression, limiting endotoxin translocation and contributing to metabolic homeostasis [12,16]. Probiotic co-supplementation, such as with *Lactobacillus acidophilus* LA5, can further enhance these effects, leading to additional reductions in fat mass and hepatic lipid accumulation [17].

Overall, preclinical studies indicate that *A. muciniphila* plays a crucial role in regulating body composition and metabolic outcomes, highlighting its potential as a target for microbiota-based interventions in obesity management [12,16,17].

3.2 Evidence From Human Studies

In humans, higher fecal abundance of A. muciniphila is generally associated with lower body fat, improved insulin sensitivity, and more favorable glucose and lipid profiles [10,11]. Individuals with elevated baseline levels often respond better to caloric restriction, suggesting that A. muciniphila may serve as a predictive marker of dietary intervention effectiveness [10]. Clinical trials with pasteurized *A. muciniphila* supplementation in overweight or obese volunteers have shown improvements in insulin sensitivity and certain metabolic markers, while preserving the bacterium's barrier-protective and immunomodulatory properties [11,13]. Lifestyle factors, including regular physical activity, also shape gut microbial composition. Physically active individuals typically exhibit higher microbial diversity and distinct microbial profiles compared with sedentary counterparts [14,15,18–20]. However, evidence that structured exercise alone consistently increases A. muciniphila in humans remains limited, with interindividual differences in baseline microbiota, diet, and lifestyle contributing to variability [10,14].

Collectively, human studies support the role of *A. muciniphila* as an important modulator of metabolic health. Strategies targeting diet, microbiota, or lifestyle factors—alone or in combination—may offer benefits for obesity management [10,11,14,15,19].

4. Effects of Physical Exercise on Gut Microbiota

Physical activity is recognized as an important determinant of gut microbial diversity and composition. Systematic reviews suggest that regular exercise can modify certain bacterial taxa, including A. muciniphila, although responses vary depending on exercise type, intensity, and individual baseline microbiota [14,15]. Observational studies consistently demonstrate that physically active adults exhibit greater microbial diversity than sedentary individuals, supporting a beneficial relationship between habitual activity and gut microbial ecology [15].

Animal models provide mechanistic support for these observations. Voluntary or controlled exercise in rodents reshapes the gut microbiota, prevents excessive weight gain, and improves metabolic outcomes such as glucose tolerance and lipid profiles, particularly under high-fat diet conditions [21].

Exercise also activates systemic metabolic regulators that may indirectly shape the gut environment. AMP-activated protein kinase (AMPK) coordinates energy homeostasis during physical activity, potentially creating conditions favorable to beneficial microbial shifts [22].

Human intervention studies indicate that structured exercise programs can induce measurable changes in microbial composition and function within weeks, Short-term endurance training has been associated with increased microbial diversity and alterations in metabolic pathways, although individual responses depend on baseline microbiota, dietary habits, and training characteristics [23,24].

Combining exercise with dietary interventions may further enhance microbiota-related benefits. For instance, prebiotic supplementation in adults at metabolic risk has been shown to increase *A. muciniphila* abundance and improve metabolic markers, suggesting a synergistic effect of diet and physical activity [25].

In summary, current evidence supports that physical activity modulates gut microbiota composition and function. The magnitude and direction of these changes are influenced by host characteristics, dietary patterns, and exercise-specific factors. Further research is needed to identify optimal exercise protocols for promoting beneficial microbial shifts and associated metabolic health outcomes [14,15,21–25].

5. Evidence from Animal Exercise Models

Preclinical studies indicate that structured exercise can directly affect the gut microbiota, including increasing the abundance of *Akkermansia muciniphila* in rodent models. A recent systematic review by Aguiar et al. (2024) reported that most rodent studies found higher levels of *A. muciniphila* in response to moderate aerobic exercise, such as treadmill running or voluntary wheel activity [14].

These findings suggest that exercise reliably modulates this bacterium in experimental settings, although the underlying mechanisms remain to be fully elucidated. Exercise-induced alterations in gut microbiota likely reflect complex host–microbe interactions that contribute to improved metabolic outcomes. [14,26].

Additional evidence demonstrates that aerobic exercise in rodents enhances microbial diversity and enriches beneficial taxa, including A. muciniphila, which is associated with improved metabolic health markers in preclinical studies [26]. Although translation to humans is not straightforward, these results reinforce the view that exercise can act as a modulator of the gut microbiota, highlighting its potential role in metabolic health interventions.

In summary, animal studies indicate that moderate physical activity increases *A. muciniphila* abundance and gut microbial diversity, supporting the concept that exercise-induced microbiota modulation may contribute to metabolic regulation [14,26].

6. Evidence From Human Exercise Interventions on *Akkermansia muciniphila*

Intervention studies in humans suggest that structured exercise may influence the gut microbiota, including the abundance of Akkermansia muciniphila, although responses are often variable. In one randomized controlled trial involving postmenopausal women with type 2 diabetes, a 12-week home-based exercise program led to measurable increases in fecal A. muciniphila. These changes were positively correlated with improvements in HDL cholesterol, physical fitness, and metabolic health markers, indicating that exercise can promote beneficial shifts in microbiota composition and metabolic parameters [27].

Despite this promising evidence, not all studies report consistent increases in A. muciniphila following exercise, highlighting the influence of factors such as baseline microbiota, diet, exercise type, duration, and intensity [14,15]. Interindividual variability suggests that the gut microbiota's response to exercise is highly personalized, with some individuals experiencing more pronounced microbial and metabolic changes than others.

Overall, current human research supports the notion that exercise can modulate the gut microbiota and potentially enhance metabolic health, but further well-controlled studies are needed to clarify the dose-response relationships, optimal exercise protocols, and interactions with diet and other lifestyle factors that affect *A. muciniphila* abundance [14,27].

7. Potential Mechanistic Pathways

The interplay between *Akkermansia muciniphila*, physical activity, and fat mass regulation involves several mechanisms that affect gut barrier integrity, microbial metabolites, immune function, and host metabolism. *A. muciniphila* contributes to intestinal barrier maintenance by promoting mucin turnover and enhancing tight junction protein expression, thereby reducing endotoxin leakage and attenuating the low-grade inflammation often associated with obesity [7–9,28].

Physical exercise can further support these effects by improving intestinal perfusion, stimulating epithelial renewal, and modulating gut microbial communities. [14,20,29,30]. Exercise-induced shifts in microbiota, including potential increases in A. muciniphila, may enhance the production of short-chain fatty acids (SCFAs), which are linked to improved insulin sensitivity, adipocyte metabolism, and overall energy homeostasis [7,18].

Additionally, components derived from A. muciniphila, such as extracellular vesicles and membrane proteins, can influence immune signaling and reduce pro-inflammatory responses [7,12,13]. Preclinical studies suggest these microbial factors may also affect gut permeability through AMPK-dependent pathways, although these mechanisms remain primarily supported by animal models [30].

The bacterium's mucin-degrading activity also supports microbial cross-feeding and ecosystem stability [8,9,25], and exercise-related changes in gut motility or the luminal environment may further facilitate these beneficial interactions, promoting a gut microbiome configuration favorable for metabolic health [14,25,29,31]. Collectively, these mechanisms suggest that A. muciniphila acts as an established mediator of gut barrier integrity and a potential mediator of exercise-induced metabolic adaptations.

8. Discussion

The current evidence highlights a complex relationship between A. muciniphila, physical activity, and fat mass regulation. In animal models, moderate aerobic exercise consistently increases the abundance of A. muciniphila, enhances microbial diversity, and improves metabolic outcomes, including reduced weight gain, lower visceral fat, and better glucose tolerance [14,16,26]. Mechanistic research indicates that A. muciniphila supports intestinal barrier function, mucin turnover, immune regulation, and reduced endotoxemia, collectively attenuating obesity-associated low-grade inflammation [7–9,28].

In human studies, structured exercise can alter gut microbial composition, with some trials showing increases in A. muciniphila linked to improved metabolic markers, such as HDL cholesterol and insulin sensitivity [10,14,15,27]. However, responses vary considerably across individuals, likely reflecting differences in baseline microbiota, dietary habits, exercise type, intensity, and duration [14,15,29].

Although mechanistic pathways such as AMPK activation and SCFA-mediated signalling are supported in preclinical models, extrapolation to humans should be approached with caution [23,30]. Overall, the findings suggest that A. muciniphila may serve as a mediator of exercise-induced metabolic benefits, yet the individual variability underscores the importance of personalized strategies for microbiota-targeted interventions.

9. Future Directions

Future research should focus on well-designed, longitudinal human studies to clarify which types, durations, and intensities of exercise most effectively modulate Akkermansia muciniphila and support metabolic health [14,15,29]. Standardization of exercise protocols and dietary interventions is essential to facilitate meaningful comparisons across studies. Combining physical activity with dietary strategies—including prebiotics, probiotics, or tailored macronutrient modifications—may amplify microbial and metabolic responses and warrants further investigation [19,25].

Mechanistic studies employing multi-omics approaches—such as metagenomics, metabolomics, and transcriptomics—could help identify predictors of individual responsiveness, thereby enabling more personalized obesity management strategies [3,10,31].

Exploring the interactions among gut microbiota, exercise, and host metabolism will deepen understanding of causal pathways and inform precision interventions that account for individual microbiota profiles, diet, and lifestyle factors.

10. Conclusions

Current evidence supports the role of *Akkermansia muciniphila* as a key contributor to metabolic regulation and a potential mediator of some beneficial effects of physical exercise on adiposity and metabolic health. Preclinical studies in animal models consistently demonstrate that aerobic exercise increases *A. muciniphila* abundance, enhances microbial diversity, and improves body composition and glucose metabolism [14,16,26].

In humans, structured physical activity can modify gut microbiota composition and positively influence metabolic markers. However, increases in A. muciniphila and reductions in fat mass are generally modest and variable, reflecting individual differences in microbiota composition, diet, and lifestyle [10,14,15,27]. Mechanistic insights highlight the importance of gut barrier integrity, immune modulation, and microbial metabolite production in mediating these outcomes [7–9,22,30].

Overall, combining exercise with dietary and lifestyle interventions holds promise for supporting metabolic health and obesity management, although effectiveness may vary between individuals. Future investigations integrating personalized approaches, standardized protocols, and mechanistic studies are essential to fully elucidate how A. muciniphila mediates exercise-induced metabolic benefits and to optimize interventions for obesity and related metabolic disorders.

Disclosures

Author's Contribution

Role	Authors
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Software	ACH, NK, KK
Validation	MP, AJ, MS, KF, ACH

Role	Authors
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Investigation	AM, ACH, AS
Resources	AJ, AS, AM, ACH
Data curation	NK, JŁ, KK
Writing – original draft preparation	MS, KK
Writing – review and editing	KK, MS, KF
Visualization	ACH, AM, AS, KF
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Declaration of the Use of Generative AI and AI-Assisted Technologies in the Writing Process

During the preparation of this manuscript, the authors utilized ChatGPT to assist with language editing and formatting. Following the use of this tool, the authors carefully reviewed and revised the material as necessary and assume full responsibility for the accuracy and integrity of the publication's substantive content.

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