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GUT MICROBIOTA AS A REGULATOR OF FEMALE REPRODUCTIVE HEALTH AND EXERCISE ADAPTATION: MECHANISTIC AND CLINICAL PERSPECTIVES

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ABSTRACT

Introduction: The gut microbiota regulates host metabolism, immune function and endocrine signaling. In women, it may affect reproductive health through estrogen metabolism, inflammation and metabolic homeostasis. Physical activity also modifies microbiota composition, with potential effects on adaptation, recovery and performance.
Aim: This review summarized evidence on gut microbiota in female reproductive health and exercise adaptation, with emphasis on mechanisms and implications in physically active women.
Materials and Methods: A narrative review was conducted using PubMed, Web of Science and Scopus. Studies from 2012–2024 were included, especially reviews, meta-analyses and observational studies on gut microbiota, estrobolome, reproductive disorders, exercise and female athletes.
Results: Gut microbiota influences estrogen metabolism through the estrobolome and may affect systemic estrogen levels and reproductive function. Dysbiosis has been associated with PCOS and endometriosis, mainly through metabolic dysfunction and chronic low-grade inflammation. Physical activity may increase microbial diversity and short-chain fatty acid production, supporting metabolic efficiency and anti-inflammatory effects. Excessive exercise may im-pair intestinal barrier integrity and increase gastrointestinal symptoms, especially in athletes. Hormonal fluctuations, contraceptive use and energy availability may further modify microbiota composition.
Conclusions: Gut microbiota appears to link reproductive physiology and exercise adaptation in women. Current evidence supports associations between microbiota, hormonal regulation and metabolic function, but causal relationships remain unclear. Further longitudinal and interventional studies are needed to clarify mechanisms and support personalized strategies for female health and sports performance.

KEYWORDS

Gut Microbiota; Estrobolome; Female Reproductive Health; Exercise; Female Athletes; PCOS; Endometriosis

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1. Introduction

The human gut microbiota is increasingly recognized as a complex and dynamic ecosystem that plays a fundamental role in maintaining host homeostasis. Beyond its traditional involvement in digestion, it functions as a metabolically active organ capable of influencing systemic physiology through interactions with immune, endocrine, and metabolic pathways [15,20]. Microbiota-derived metabolites, including short-chain fatty acids (SCFAs), bile acid derivatives, and other signaling molecules, are now known to regulate key processes such as energy metabolism, inflammation, and hormonal signaling.

In recent years, growing attention has been directed toward the role of the gut microbiota in female reproductive health. Female physiology is characterized by cyclical hormonal fluctuations governed by the hypothalamic–pituitary–gonadal axis, making it particularly sensitive to systemic regulatory mechanisms. One of the most important links between the gut microbiota and reproductive function is the estrobolome—a collection of microbial genes involved in the metabolism of estrogens [1,8,13]. Through enzymatic activity, particularly β-glucuronidase-mediated deconjugation, gut bacteria regulate the enterohepatic circulation of estrogens, thereby influencing circulating hormone levels and reproductive processes.

Alterations in gut microbiota composition, commonly referred to as dysbiosis, have been increasingly associated with reproductive disorders. Polycystic ovary syndrome (PCOS) and endometriosis are among the most extensively studied conditions in this context. Both disorders are characterized by metabolic dysfunction, chronic low-grade inflammation, and hormonal imbalance, all of which have been linked to microbiota alterations [6,10,14,18,19]. Although these associations are well documented, the directionality and causality of these relationships remain subjects of ongoing investigation.

Parallel to these developments, physical activity has emerged as an important modulator of gut microbiota composition and function. Regular exercise has been associated with increased microbial diversity, enhanced production of SCFAs, and improved intestinal barrier integrity, all of which contribute to metabolic health and reduced inflammation [5,9,11,17]. These adaptations are particularly relevant in the context of exercise performance, as efficient energy utilization and recovery are critical determinants of athletic capacity.

However, the relationship between exercise and gut microbiota is not uniformly beneficial. High-intensity or prolonged physical activity may lead to gastrointestinal disturbances, increased intestinal permeability, and alterations in microbial balance [7,17]. These effects are especially relevant in athletes, where gastrointestinal symptoms are commonly reported and may negatively impact performance.

In females, the interaction between gut microbiota, reproductive function, and exercise adaptation is further complicated by sex-specific factors. Hormonal fluctuations across the menstrual cycle, the use of hormonal contraception, and variations in energy availability can all influence both endocrine function and microbiota composition [12,16]. In particular, low energy availability, frequently observed in physically active women, may contribute to disruptions in reproductive function and metabolic homeostasis, potentially affecting gut microbiota as well.

Despite increasing recognition of these interconnected systems, current research remains fragmented, with most studies focusing on individual domains rather than their integration. As a result, a comprehensive understanding of how gut microbiota regulates both reproductive health and exercise adaptation in females is still lacking.

Therefore, the aim of this review is to provide an integrated overview of current evidence on the role of gut microbiota as a regulator of female reproductive health and exercise adaptation, with particular emphasis on underlying mechanisms and clinical implications.

Additionally, increasing evidence suggests that host–microbiome interactions are highly context-dependent and influenced by environmental, nutritional, and physiological factors. This complexity highlights the need for integrative approaches that consider multiple regulatory systems simultaneously when evaluating female health and exercise adaptation.

2. Materials and Methods

This study was designed as a narrative review aimed at synthesizing current evidence on the role of gut microbiota in female reproductive health and exercise adaptation.

2.1. Search Strategy

A comprehensive literature search was conducted using PubMed/MEDLINE, Web of Science, and Scopus databases. The search included studies published between January 2012 and December 2024. Additional relevant studies were identified through manual screening of reference lists of selected articles.

The search strategy was based on combinations of the following keywords and Medical Subject Headings (MeSH): “gut microbiota,” “estrobolome,” “female reproductive health,” “polycystic ovary syndrome,” “endometriosis,” “exercise,” and “female athletes.” Boolean operators (AND/OR) were applied to refine the search.

2.2. Eligibility Criteria

Studies were included if they met the following criteria:

- published in peer-reviewed journals,
- written in English,
- focused on human subjects,
- addressed at least one of the following domains: gut microbiota, hormonal regulation, reproductive disorders, or exercise-related adaptations.

Systematic reviews, meta-analyses, randomized controlled trials, and observational studies were prioritized.

2.3. Study Selection and Data Extraction

Titles and abstracts were screened for relevance. Full texts of potentially eligible studies were then assessed. Data extraction focused on study design, population characteristics, microbiota-related outcomes, and key findings related to endocrine, metabolic, and inflammatory pathways.

2.4. Data Synthesis

Due to heterogeneity in study designs, populations, and outcome measures, a qualitative synthesis approach was applied. Emphasis was placed on consistency of findings, biological plausibility, and clinical relevance.

Particular attention was also given to studies providing mechanistic insights, allowing for a more comprehensive interpretation of the relationship between microbiota composition and functional outcomes.

3. Gut Microbiota and Female Reproductive Physiology

The gut microbiota plays a central role in regulating host physiology through interconnected metabolic, endocrine, and immune pathways. In females, these interactions are particularly relevant due to the tight regulation of reproductive function by hormonal signaling. Increasing evidence suggests that the gut microbiota contributes to reproductive physiology by modulating estrogen metabolism, systemic inflammation, and metabolic homeostasis [1,3,8,13,15,20].

One of the key mechanisms linking gut microbiota to reproductive health is the estrobolome, defined as the collection of microbial genes capable of metabolizing estrogens [1,8,13]. Through β-glucuronidase activity, intestinal bacteria deconjugate estrogen metabolites, enabling their reabsorption into systemic circulation via enterohepatic recirculation. This process directly influences circulating estrogen levels and plays a role in regulating ovulation, endometrial function, and menstrual cycle dynamics.

Microbial communities are also present along the female reproductive tract, suggesting that host–microbiome interactions may extend beyond the gut and involve multiple body sites relevant to reproductive health [4].

Alterations in gut microbiota composition may disrupt this balance. Reduced microbial diversity and changes in the abundance of specific bacterial taxa can impair estrogen metabolism, potentially contributing to hormonal dysregulation. Such disturbances have been associated with conditions characterized by altered estrogen signaling, including polycystic ovary syndrome (PCOS) and endometriosis [6,10,14,18,19].

In addition to hormonal regulation, the gut microbiota influences reproductive physiology through immune-mediated mechanisms. Dysbiosis has been associated with increased intestinal permeability, facilitating the translocation of bacterial endotoxins such as lipopolysaccharide into systemic circulation. This process activates inflammatory pathways, including toll-like receptor signaling, leading to chronic low-grade inflammation [17,19]. Inflammation is a recognized contributor to reproductive dysfunction, affecting ovarian steroidogenesis, follicular development, and endometrial receptivity.

Metabolic regulation represents another important pathway. Microbiota-derived metabolites, particularly short-chain fatty acids, contribute to energy homeostasis and insulin sensitivity [5,17]. These processes are closely linked to reproductive health, as metabolic disturbances can impair hormonal balance and ovulatory function, especially in disorders such as PCOS.

Overall, current evidence supports the concept that the gut microbiota contributes to female reproductive physiology through integrated endocrine, immune, and metabolic mechanisms. However, causal relationships remain to be clearly established.

These interactions emphasize the systemic nature of microbiota-related regulation and suggest that alterations in gut microbial composition may have far-reaching effects beyond the gastrointestinal tract.

Table 1. Key mechanisms linking gut microbiota, reproductive function, and exercise adaptation in females.

Domain	Mechanism	Physiological Effect	Clinical/Performance Relevance
Estrogen metabolism	Estrobolome (β-glucuronidase activity)	Regulation of estrogen recirculation	Hormonal balance, ovulation, menstrual function
Immune regulation	Increased intestinal permeability, LPS translocation	Chronic low-grade inflammation	PCOS, endometriosis progression
Metabolic function	SCFA production (acetate, propionate, butyrate)	Improved insulin sensitivity and energy metabolism	Metabolic health, exercise efficiency
Exercise adaptation	Increased microbial diversity	Enhanced metabolic flexibility and recovery	Improved endurance and performance

Domain	Mechanism	Physiological Effect	Clinical/Performance Relevance
High-intensity exercise	Reduced splanchnic blood flow, gut barrier disruption	Increased gut permeability	GI symptoms, impaired recovery
Female-specific factors	Hormonal fluctuations, contraception	Modulation of host–microbiome interactions	Cycle-related variation, metabolic changes
Energy availability	Low energy intake, altered diet	Reduced microbial diversity, SCFA production	RED-S, menstrual dysfunction, performance decline

4. Estrobolome and Hormonal Regulation

The estrobolome represents a critical interface between the gut microbiota and the endocrine system in females. It comprises microbial genes involved in the metabolism of estrogens, thereby influencing their systemic availability and biological activity [1,8,13].

Through enzymatic activity, particularly β-glucuronidase, gut bacteria deconjugate estrogen metabolites in the intestine, enabling their reabsorption via enterohepatic circulation [1,8,13]. This process plays a central role in maintaining hormonal homeostasis and regulating reproductive functions such as follicular development, ovulation, and endometrial proliferation.

Disruptions in microbial composition may alter estrobolome activity, leading to either increased or decreased estrogen availability. Elevated β-glucuronidase activity may enhance estrogen reabsorption and contribute to hyperestrogenic states, whereas reduced microbial diversity may impair estrogen recycling and lead to relative estrogen deficiency [1,8,13]. Both scenarios may negatively affect reproductive health.

Importantly, estrobolome activity is modifiable and influenced by external factors, including diet, antibiotic exposure, and physical activity [1,11]. These factors can alter microbial composition and consequently impact estrogen metabolism, highlighting the estrobolome as a dynamic link between environmental factors and endocrine regulation.

Despite strong mechanistic evidence, most data remain observational, and the direct clinical implications of microbiota-driven modulation of estrogen metabolism require further investigation [1,8].

This highlights the importance of maintaining microbial balance for optimal endocrine function and suggests that even subtle alterations in microbiota composition may have physiological consequences.

5. Clinical Models: PCOS and Endometriosis

5.1. Polycystic Ovary Syndrome

Polycystic ovary syndrome (PCOS) is one of the most extensively studied conditions linking gut microbiota with reproductive and metabolic dysfunction. Women with PCOS consistently exhibit reduced gut microbial diversity and alterations in microbial composition compared to healthy controls [10,14,18].

These alterations often include reduced abundance of short-chain fatty acid–producing bacteria and shifts in major bacterial phyla. Such changes have been associated with key features of PCOS, including insulin resistance, hyperandrogenism, and chronic low-grade inflammation [10,14].

Increased intestinal permeability associated with dysbiosis may facilitate the translocation of endotoxins such as lipopolysaccharide, activating inflammatory pathways and contributing to metabolic disturbances [17,19]. These processes may further exacerbate hormonal imbalance and ovarian dysfunction.

Additionally, gut microbiota may influence androgen metabolism and insulin sensitivity, suggesting that microbial dysregulation could contribute to both metabolic and reproductive abnormalities observed in PCOS.

Although microbiota-targeted interventions, including probiotics, have shown promising effects in improving metabolic parameters, current evidence remains limited and heterogeneous, preventing definitive conclusions regarding causality [14,18].

5.2. Endometriosis

Endometriosis represents another condition in which the interaction between gut microbiota, inflammation, and estrogen-dependent pathology is evident. Alterations in both gut and reproductive tract microbiota have been observed in affected women, often characterized by increased abundance of pro-inflammatory bacterial taxa [6,19].

The disease is associated with chronic inflammation and immune dysregulation. Increased intestinal permeability and systemic endotoxin exposure have been proposed as contributing factors to peritoneal inflammation and disease progression.

Microbiota-related alterations in estrogen metabolism may also play a role. Disruption of estrogen homeostasis may promote the growth and persistence of ectopic endometrial tissue.

Despite consistent associations, current evidence is largely observational, and it remains unclear whether dysbiosis is a cause or consequence of endometriosis.

5.3. Integrated Clinical Perspective

Both PCOS and endometriosis illustrate the complex interplay between gut microbiota, metabolic regulation, and reproductive health. A common feature of these conditions is chronic low-grade inflammation linked to microbiota alterations.

These findings support the concept that gut microbiota may contribute to reproductive dysfunction through interconnected endocrine, immune, and metabolic pathways. However, further longitudinal and interventional studies are required to establish causality. The main microbiota-related features of selected clinical models are summarized in Table 2.

Table 2. Gut microbiota alterations and clinical features in selected female reproductive disorders.

Condition	Microbiota alterations	Key mechanisms	Clinical features
PCOS	↓ diversity, ↓ SCFA-producing bacteria, altered Firmicutes/Bacteroidetes ratio	Insulin resistance, inflammation, androgen metabolism	Hyperandrogenism, anovulation, metabolic dysfunction
Endometriosis	↑ pro-inflammatory taxa, dysbiosis in gut and reproductive tract	Estrogen dysregulation, immune activation, inflammation	Chronic pain, infertility, ectopic endometrial growth
Female athletes (high load)	Variable diversity, potential dysbiosis with low energy intake	Increased gut permeability, reduced SCFA production	GI symptoms, menstrual disturbances, reduced performance

6. Exercise Adaptation and Gut Microbiota

Physical activity is an important modulator of gut microbiota composition and function. Regular exercise has been associated with increased microbial diversity and enrichment of beneficial taxa involved in short-chain fatty acid production [5,9,11].

Short-chain fatty acids play a central role in mediating these effects by influencing energy metabolism, mitochondrial function, insulin sensitivity, and inflammatory pathways [5,17]. These mechanisms are directly relevant to exercise performance and recovery.

Athletes often exhibit distinct microbial profiles compared to sedentary individuals, characterized by greater diversity and enhanced metabolic capacity [2]. These adaptations may reflect the physiological demands of regular training.

However, the effects of exercise are not universally beneficial. High-intensity or prolonged exercise may compromise gastrointestinal integrity by reducing splanchnic blood flow and increasing intestinal permeability [7,17]. This can lead to endotoxin translocation and inflammatory responses that may impair recovery and performance.

Gastrointestinal symptoms are frequently reported, particularly in endurance athletes, and may be associated with both physiological stress and microbiota alterations.

7. Female Athletes

Female athletes represent a unique population in which gut microbiota, endocrine regulation, and exercise adaptation interact dynamically. High training loads, dietary patterns, and fluctuations in energy availability may influence both reproductive function and microbiota composition [7,16].

Hormonal fluctuations related to the menstrual cycle and contraceptive use may further modulate host–microbiome interactions. While gut microbiota appears relatively stable across the menstrual cycle compared to other microbiomes, hormonal changes may still influence immune function and metabolic processes [12].

Gastrointestinal symptoms are common, particularly during high-intensity exercise. Mechanisms include reduced blood flow to the gastrointestinal tract, increased permeability, altered motility, and microbiota changes.

Energy availability is a key factor linking reproductive health and microbiota. Low energy availability may disrupt the hypothalamic–pituitary–gonadal axis, leading to menstrual disturbances. Although direct evidence linking energy deficiency to microbiota changes remains limited, dietary restriction and low fiber intake may reduce microbial diversity and SCFA production.

From a performance perspective, these interactions are clinically relevant, as impaired gut function may negatively affect nutrient absorption, hydration, and training capacity.

Moreover, female athletes often experience overlapping physiological stressors that may act simultaneously rather than independently. Training load, menstrual status, dietary intake, psychological stress, and recovery capacity can all influence gastrointestinal function and endocrine regulation. In this context, gut microbiota should be interpreted as one component of a broader physiological network rather than as an isolated determinant of performance.

This perspective is particularly relevant in athletes presenting with recurrent gastrointestinal symptoms, menstrual irregularities, or unexplained decreases in performance. Although routine microbiome testing is not currently supported by sufficient clinical evidence, awareness of gut-related mechanisms may help clinicians and coaches consider nutrition, recovery, and training load in a more integrated manner. Future studies should therefore examine female athletes using multidimensional models that include microbiota composition, dietary assessment, hormonal status, inflammatory markers, and performance outcomes.

8. Limitations of Current Evidence

Despite the growing body of research on the relationship between gut microbiota, female reproductive health, and exercise adaptation, several limitations should be acknowledged.

First, the majority of available studies are observational, which limits the ability to establish causal relationships. While consistent associations between microbiota composition and reproductive or metabolic outcomes have been reported, it remains unclear whether these alterations represent a cause or a consequence of underlying physiological changes.

Second, considerable heterogeneity exists across studies in terms of design, population characteristics, and microbiome analysis techniques. Differences in sequencing methods, bioinformatic pipelines, and taxonomic classification limit comparability and reproducibility of findings.

Third, female-specific data remain relatively limited, particularly in the context of exercise science. Many studies include mixed or predominantly male populations, with insufficient control for sex-specific variables such as menstrual cycle phase, hormonal contraception, or energy availability.

Another important limitation is the high inter-individual variability in gut microbiota composition. Factors such as diet, genetics, lifestyle, and environmental exposures contribute to substantial differences between individuals, which complicates generalization of results.

Finally, most studies focus on taxonomic composition rather than functional outcomes. There is a relative lack of research integrating metagenomics, metabolomics, and other multi-omics approaches that would allow for a deeper understanding of host–microbiome interactions.

Another limitation concerns the lack of standardized definitions and outcome measures across studies. Terms such as dysbiosis, microbial diversity, and gut barrier dysfunction are frequently used, but they are not always defined or measured in a consistent manner. This makes it difficult to compare findings between studies and to determine whether observed microbiota differences have direct clinical relevance. In the context of female reproductive health and athletic performance, this issue is particularly important because hormonal status, diet, training load, and gastrointestinal symptoms may all influence outcomes simultaneously.

Future studies should therefore include better-controlled designs with clearly defined clinical and microbiological endpoints. In female athletes, research protocols should account for menstrual cycle phase,

contraceptive use, energy availability, dietary intake, and training intensity. Such standardization would improve the interpretation of microbiota-related findings and support the development of more reliable clinical recommendations.

9. Discussion

This review integrates current evidence on the role of gut microbiota in female reproductive health and exercise adaptation. Overall, the findings support the concept that the gut microbiota acts as a central interface linking metabolic, endocrine, and immune pathways.

A key mechanism highlighted in this review is the estrobolome, which provides a direct connection between gut microbiota and estrogen metabolism. By influencing enterohepatic circulation of estrogens, microbial communities may contribute to the regulation of systemic hormone levels and reproductive function. This suggests that the gut microbiota may act not only as a downstream consequence of hormonal changes but also as a potential upstream regulator [1,8,13].

Inflammation emerges as a unifying pathway linking microbiota alterations with reproductive and metabolic dysfunction. Increased intestinal permeability and endotoxin translocation associated with dysbiosis may lead to chronic low-grade inflammation, which is implicated in conditions such as PCOS and endometriosis [17,19].

The relationship between exercise and gut microbiota further highlights the complexity of this system. Moderate physical activity appears to promote beneficial microbial adaptations, including increased diversity and enhanced production of short-chain fatty acids [5,9,11]. In contrast, excessive or high-intensity exercise may compromise gut barrier integrity and induce gastrointestinal symptoms, potentially impairing recovery and performance [7,17].

In female athletes, additional factors such as hormonal fluctuations, contraceptive use, and energy availability further influence these interactions [12,16]. Low energy availability, in particular, represents a critical factor linking metabolic stress, endocrine disruption, and potential microbiota alterations.

From a clinical perspective, these findings suggest that modulation of the gut microbiota may represent a potential strategy for improving both reproductive health and athletic performance. However, current evidence is insufficient to support specific clinical recommendations. Future research should prioritize longitudinal and interventional studies, integrating multi-omics approaches to better characterize causal relationships between gut microbiota, hormonal regulation, and exercise adaptation in female populations. Importantly, these interactions should not be interpreted in isolation, as microbiota-related effects are likely influenced by a combination of behavioral, nutritional, and physiological factors. This integrative perspective may help explain inconsistencies observed across studies and highlights the need for more standardized research protocols.

10. Additional Clinical and Translational Perspectives

An important implication of current research is the potential for microbiota-targeted strategies in female health and performance.

Dietary interventions represent one of the most accessible approaches. Diets rich in fiber and plant-based components are associated with increased microbial diversity and enhanced production of short-chain fatty acids, which may support both metabolic and reproductive health [5,11]. Conversely, low-fiber or highly processed diets may negatively affect microbiota composition.

Probiotic and prebiotic supplementation has also been investigated, particularly in metabolic conditions such as PCOS. Although some studies report improvements in insulin sensitivity and inflammatory markers, findings remain inconsistent, and optimal protocols have not yet been established [14,18].

Another key consideration is inter-individual variability. Gut microbiota composition is highly personalized, suggesting that responses to dietary and exercise interventions may differ significantly between individuals. This highlights the potential role of personalized, microbiome-informed approaches in the future.

From a clinical standpoint, incorporating gut microbiota into the broader assessment of female athlete health may provide additional insights into conditions such as menstrual dysfunction, gastrointestinal symptoms, and metabolic disturbances [16]. However, standardized diagnostic tools and clinical guidelines are currently lacking.

Overall, while the gut microbiota represents a promising therapeutic target, translation into clinical practice requires further high-quality evidence.

In practical terms, microbiota-oriented strategies should currently be viewed as supportive rather than primary therapeutic interventions. Dietary quality, adequate energy availability, sufficient fiber intake, and individualized training management remain the most realistic approaches for supporting gut microbial balance in physically active women. These strategies may be particularly important in athletes with high training loads, recurrent gastrointestinal symptoms, or menstrual disturbances. Potential microbiota-oriented strategies in physically active women are summarized in Table 3.

Table 3. Potential microbiota-oriented strategies in physically active women.

Strategy	Potential microbiota-related effect	Possible relevance for female health and performance
Adequate energy availability	Supports microbial diversity and metabolic stability	May help maintain menstrual function, recovery, and training adaptation
Fiber-rich diet	Promotes SCFA production and beneficial bacterial taxa	Supports metabolic health, anti-inflammatory effects, and gut barrier integrity
Individualized training load	Reduces risk of excessive gut permeability and GI symptoms	May improve recovery, performance consistency, and gastrointestinal tolerance
Probiotic/prebiotic supplementation	May modulate microbiota composition and inflammatory markers	Potential supportive role, but evidence remains insufficient for universal recommendations
Monitoring menstrual and GI symptoms	Helps identify broader physiological stress	May support early detection of low energy availability or impaired recovery

At the same time, caution is needed when interpreting commercial microbiome testing or generalized probiotic recommendations. Current evidence does not support a universal microbiota profile associated with optimal reproductive health or athletic performance. Therefore, future translational work should focus on identifying clinically meaningful microbial functions rather than isolated bacterial taxa. Such an approach may improve the usefulness of microbiome science in sports medicine, gynecology, and personalized nutrition.

Future clinical applications will likely depend on the integration of microbiome data with other biomarkers, including hormonal profiles, metabolic indicators, and lifestyle factors, to enable more precise and individualized interventions.

11. Conclusions

The gut microbiota appears to play an important regulatory role in female physiology by linking metabolic, endocrine, and immune pathways. Mechanisms involving the estrobolome, inflammation, and microbial metabolites contribute to the maintenance of hormonal balance and reproductive function.

Clinical observations in conditions such as polycystic ovary syndrome and endometriosis support the association between dysbiosis, chronic inflammation, and reproductive dysfunction. In parallel, physical activity has been shown to significantly influence gut microbiota composition, with moderate exercise promoting beneficial adaptations, whereas excessive training may contribute to gastrointestinal stress and impaired gut integrity.

In female athletes, the interaction between gut microbiota, hormonal status, and energy availability represents a complex and clinically relevant axis influencing both health and performance.

Despite increasing interest in this field, current evidence remains largely associative, and causal relationships are not yet fully established. Future research should focus on well-designed longitudinal and interventional studies, with particular emphasis on female-specific populations and integrative approaches combining microbiome science, endocrinology, and exercise physiology.

Advancing this field will likely require the development of personalized, microbiome-informed strategies that recognize the gut microbiota as a key determinant of female health and performance.

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