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Role of Gut Microbiome in Polycystic Ovarian Syndrome and Insulin Resistance

ნაწლავის მიკრობიოტის როლი პოლიკისტოზური ოვარიუმის სინდრომსა და ინსულინრეზისტენტობაში

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Abstract

Introduction: Polycystic ovary syndrome (PCOS) is a prevalent endocrine disorder among women of reproductive age, often associated with insulin resistance (IR), hyperandrogenism, and ovulatory dysfunction. Recent research highlights a potential link between gut microbiota dysbiosis and the metabolic disturbances seen in PCOS. This review aims to explore the role of gut microbiome composition and function in the pathophysiology of insulin resistance among PCOS patients. **Methods:** A comprehensive literature review was conducted using PubMed, Scopus, and Google Scholar. Studies included were observational or clinical in design, published in English between 2011 and 2022, and investigated the gut microbiome in women diagnosed with PCOS in relation to insulin resistance. Data extracted included microbiome assessment methods, key microbial taxa, insulin resistance indicators (e.g., HOMA-IR), and therapeutic interventions. **Results:** Women with PCOS exhibit reduced microbial diversity, characterized by lower levels of SCFA-producing bacteria (e.g., Faecalibacterium prausnitzii) and elevated pro-inflammatory species (e.g., Bacteroides, Enterococcus). These alterations contribute to increased gut permeability, systemic inflammation, and impaired insulin signaling. Clinical interventions using probiotics, prebiotics, and dietary modifications demonstrated improvements in insulin sensitivity and hormonal profiles in several studies. **Discussion:** Gut microbiota play a significant role in modulating metabolic and endocrine functions in PCOS. Short-chain fatty acids (SCFAs) produced by beneficial bacteria enhance insulin sensitivity, while dysbiosis exacerbates IR through inflammatory pathways. Emerging treatments like fecal microbiota transplantation and personalized nutrition offer promising directions but require further validation. **Conclusion:** The gut microbiome emerges as a key modulator of insulin resistance in PCOS. Targeted interventions, such as SCFA-enhancing diets, probiotic supplementation, and microbiota-focused therapies—may offer innovative, non-hormonal strategies to manage PCOS.

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Longitudinal and interventional studies are essential to confirm causality and establish microbiome-based precision treatments.

Keywords: Polycystic Ovary Syndrome (PCOS), Insulin Resistance, Gut Microbiota, Dysbiosis, Short-Chain Fatty Acids (SCFAs), Probiotics, Prebiotics, Metabolic Syndrome, Microbiome Therapy, Women's Health.

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აბსტრაქტი

შესავალი: პოლიკისტოზური ოვარიუმის სინდრომი (PCOS) გავრცელებული ენდოკრინული დარღვევაა რეპროდუქციული ასაკის ქალებში, რომელსაც თან ახლავს ინსულინრეზისტენტობა (IR), ჰიპერანდროგენიზმი და ოვულაციის მოშლა. უკანასკნელი კვლევები მიანიშნებს ნაწლავის მიკრობიოტასა და ამ მეტაბოლურ დარღვევებს შორის პოტენციურ კავშირზე. ეს მიმოხილვა მიზნად ისახავს შეისწავლოს ნაწლავის მიკრობიოტის როლი პოლიკისტოზური ოვარიუმის სინდრომთან ასოცირებული ინსულინრეზისტენტობის პათოფიზიოლოგიაში. **მეთოდები:** ჩატარდა სისტემური ლიტერატურის მიმოხილვა PubMed-ის, Scopus-ისა და Google Scholar-ის მონაცემთა ბაზებში. შესწავლილი იყო 2011–2022 წლებში ინგლისურ ენაზე გამოქვეყნებული დაკვირვებითი ან კლინიკური ხასიათის კვლევები, რომლებიც ეხებოდა პოლიკისტოზური ოვარიუმის სინდრომით დაავადებულ ქალებში ნაწლავის მიკრობიომის ცვლილებებსა და ინსულინრეზისტენტობას. ანალიზისას შეფასდა მიკრობიომის კვლევის მეთოდები, კონკრეტული ბაქტერიული ჯგუფები, ინსულინრეზისტენტობის ინდიკატორები (მაგ. HOMA-IR) და თერაპიული ჩარევები. **შედეგები:** პოლიკისტოზური ოვარიუმის სინდრომით დაავადებულ ქალებს აღენიშნებათ მიკრობული მრავალფეროვნების შემცირება: დაბალია სასარგებლო SCFA (მოკლემოლეკულური ცხიმოვანი მჟავების) მწარმოებელი ბაქტერიების (Faecalibacterium prausnitzii) დონე და მომატებულია ანთებითი ბაქტერიები (Bacteroides, Enterococcus). ეს ცვლილებები ზრდის ნაწლავის განვლადობას, იწვევს ქრონიკულ ანთებას და არღვევს ინსულინის მოქმედებას. პრობიოტიკების, პრებიოტიკების და დიეტური ცვლილებების გამოყენებამ კლინიკურ კვლევებში აჩვენა ინსულინრეზისტენტობის და ჰორმონული დისბალანსის გაუმჯობესება. **დისკუსია:** ნაწლავის მიკრობიოტა მნიშვნელოვან როლს ასრულებს მეტაბოლური და ენდოკრინული პროცესების რეგულაციაში პოლიკისტოზური ოვარიუმის სინდრომის დროს. SCFA-ები აუმჯობესებს ინსულინზე უჯრედულ რეაგირებას, ხოლო დისბიოზი აუარესებს მდგომარეობას ანთებითი მექანიზმების გააქტიურებით. ინოვაციური მკურნალობის გზები, როგორიცაა ფეკალური მიკრობიოტის ტრანსპლანტაცია და პერსონალიზებული კვება, პერსპექტიულია, თუმცა საჭიროებს დამატებით კვლევებს. **დასკვნა:** ნაწლავის მიკრობიომა მნიშვნელოვანი მოდულატორია ინსულინრეზისტენტობის განვითარებაში პოლიკისტოზური ოვარიუმის სინდრომის შემთხვევაში. სამკურნალო ჩარევები, როგორიცაა SCFA-ს გამომყოფი დიეტები, პრობიოტიკები და მიკრობიოტაზე ორიენტირებული თერაპიები, წარმოადგენს არაჰორმონულ ალტერნატივას პოლიკისტოზური ოვარიუმის სინდრომის მართვაში. აუცილებელია გრძელვადიანი ინტერვენციული კვლევები, რათა დადგინდეს მიზეზ-შედეგობრივი კავშირი და შეიქმნას ზუსტი, მიკრობიომზე დაფუძნებული სამკურნალო მიდგომები.

საკვანძო სიტყვები: პოლიკისტოზური ოვარიუმის სინდრომი, ინსულინრეზისტენტობა, ნაწლავის მიკრობიოტა, დისბიოზი, მოკლემოლეკულური ცხიმოვანი მჟავები, პრობიოტიკები, პრებიოტიკები, მეტაბოლური სინდრომი, მიკრობიომზე დაფუძნებული თერაპია, ქალთა ჯანმრთელობა.

ციტატა: ლაკშმი ნარაიანანი. ნაწლავის მიკრობიოტის როლი პოლიკისტოზური ოვარიუმის სინდრომსა და ინსულინრეზისტენტობაში. ჯანდაცვის პოლიტიკა, ეკონომიკა და სოციოლოგია. ჯანდაცვის პოლიტიკა, ეკონომიკა და სოციოლოგია, 2025; 9 (1). https://doi.org/10.52340/healthecosoc.2025.09.01.10.

Introduction

Polycystic ovary syndrome (PCOS) is a complex endocrine disorder affecting women of reproductive age. It is typically characterized by insulin resistance (IR), hyperandrogenism, and ovulatory dysfunction. The condition manifests with a wide range of metabolic and reproductive symptoms, often overlapping with features of insulin resistance, which complicates diagnosis and management (Teede et al., 2018). Recent research has drawn increasing attention to the role of the gut microbiota in the development and progression of PCOS, particularly due to its influence on systemic inflammation, intestinal permeability, and short-chain fatty acid (SCFA) production. For example, women with PCOS and IR often exhibit decreased microbial diversity and increased abundance of specific bacteria such as Megamonas funiformis and Prevotella copri (Lindheim et al., 2017). Although SCFA supplementation has shown promise as a therapeutic intervention, further studies are needed to fully understand the gut microbiome's impact on PCOS symptoms. (Murri et al., 2013)

PCOS is diagnosed in approximately 6–15% of women of reproductive age globally (Azziz et al., 2016; WHO,2018). Despite its widespread prevalence, the etiology of PCOS remains incompletely understood, as it encompasses a constellation of metabolic disturbances—including insulin resistance, dyslipidemia, and obesity—that affect individuals across all body mass index (BMI) categories (Teede et al., 2018). Around 70% of women with PCOS present with insulin resistance, regardless of their weight (American College of Obstetricians and Gynecologists [ACOG], 2018). Nevertheless, despite the growing body of evidence, clinical management remains limited to hormonal therapies and insulin sensitizers. Emerging evidence suggests that the gut microbiome—the dynamic community of trillions of microorganisms residing in the gastrointestinal tract—may significantly contribute to the onset and metabolic complications of PCOS (Tremellen & Pearce, 2012). This line of research holds both academic and clinical importance.

Theoretically, this study contributes to the growing interdisciplinary body of literature linking gynecology, microbiome science, and endocrinology (Torres et al., 2018). It supports the reconceptualization of PCOS as a systemic disorder influenced by microbial communities, with implications for screening, diagnosis, and treatment (Liu et al., 2017). Practically, assessing the gut microbiota offers a cost-effective and accessible strategy to manage PCOS symptoms. Interventions such as probiotics, prebiotics, and dietary modifications may enhance insulin sensitivity and mitigate the severity of PCOS-related symptoms (Thackray, 2019 as cited in Torres et al., 2018). By shifting the paradigm from a strictly hormonal disorder to one also rooted in microbial imbalance, this research opens new opportunities for prevention and therapy. Consequently, medical guidelines may evolve to incorporate microbiota-based diagnostics and treatments, with broader implications for public health and clinical practice (Teede et al., 2018).

In women with PCOS, studies have reported lower levels of Bacteroidetes relative to Firmicutes, and reduced numbers of beneficial species such as Lactobacillus and Bifidobacterium (Murri et al., 2013). These changes in the gut microbiome lead to a reduction in microbial diversity and contribute to insulin resistance, systemic endotoxemia, and chronic low-grade inflammation, all of which increase intestinal permeability—a phenomenon known as "leaky gut" (Liu et al., 2017). Liu et al. (2017) found elevated levels of lipopolysaccharide (LPS), an endotoxin from Gram-negative bacteria, in the blood of women with PCOS. LPS activates inflammatory signaling pathways and disrupts insulin receptor function, thereby impairing glucose homeostasis. Inflammatory and microbial changes may also disrupt the

hypothalamic-pituitary-ovarian (HPO) axis, affecting ovulation and androgen production (Tremellen & Pearce, 2012). Murri et al. (2013) further demonstrated that women with PCOS harbor different SCFA-producing bacterial communities compared to healthy individuals. SCFAs are critical for maintaining gut barrier integrity, reducing inflammation, and regulating insulin sensitivity. However, most current studies are cross-sectional with limited sample sizes, and they fail to establish definitive causal pathways.

Several knowledge gaps persist in our understanding of the gut microbiome's role in PCOS. First, the direction of causality remains unclear: does gut dysbiosis lead to insulin resistance and PCOS, or is it a consequence of these conditions? Second, methodological inconsistencies in microbial analysis and clinical characterization limit the comparability of existing studies (Murri et al., 2013). Third, most research to date has emphasized microbial taxonomy rather than functional activity, leaving unanswered questions about how microbial metabolites such as SCFAs, bile acids, or amino acids influence host metabolism (Torres et al., 2018).

Moreover, few interventional studies have explored whether targeted microbiota therapies can sustainably alleviate PCOS symptoms and insulin resistance. To understand the functional interactions between host and microbiota—and to identify therapeutic targets—future studies should utilize longitudinal and multi-omic approaches, including metagenomics, metabolomics, and transcriptomics. Currently, therapeutic strategies involving the PCOS microbiome are underdeveloped due to limited mechanistic insights (Lindheim et al., 2017).

This study seeks to evaluate how the gut microbiome affects the development and progression of insulin resistance in women with PCOS, with a focus on identifying microbial markers and therapeutic opportunities.

The research aims to answer the following questions:

- Does the relationship between gut microbiota and insulin sensitivity depend on microbial byproducts such as SCFAs?
- Can insulin resistance in women with PCOS be improved through probiotics, prebiotics, or dietary interventions?
- How does the gut microbiota in PCOS patients differ from that of healthy individuals?
- Are specific insulin resistance markers in PCOS patients associated with particular gut microbial taxa?

By addressing these questions, the study aims to uncover the underlying mechanisms linking the gut microbiome to insulin resistance in PCOS and to lay the groundwork for microbiota-targeted therapeutic strategies.

Methodology

A comprehensive literature review was conducted to examine the connection between the gut microbiome and its influence on polycystic ovary syndrome (PCOS) and insulin resistance (IR). Three databases—PubMed, Scopus, and Google Scholar—were used for the search. Both keywords and Medical Subject Headings (MeSH) terms were applied, including combinations of "gut microbiome," "polycystic ovary syndrome," and "insulin resistance." The search was limited to open-access, peer-reviewed journal articles published in English between 2011 and 2022 to ensure access to recent and reliable publications.

The study framework was based on observational research, including cross-sectional, case-control, cohort studies, and relevant clinical trials. Only studies with full-text open access were included to ensure availability of complete data for analysis.

Exclusion criteria included:

- Articles not subjected to peer review (e.g., editorials, opinion pieces, and conference abstracts);
- Studies that did not directly assess the gut microbiome in relation to PCOS and insulin resistance;
- Articles lacking a clear methodological framework or measurable outcomes.

For each included study, data were extracted on study design, sample size, demographics, microbiome assessment techniques, and insulin resistance indicators (e.g., HOMA-IR), along with key findings. The quality of studies was assessed using standardized tools appropriate for each study design, including the Newcastle-Ottawa Scale for observational studies. Any discrepancies during data extraction or quality assessment were resolved through discussion among reviewers. This systematic approach ensured clarity, transparency, and reproducibility in evaluating the literature on the gut microbiome's role in PCOS and insulin resistance.

Only articles published in English were considered for inclusion.

Literature Review

Polycystic ovary syndrome (PCOS) is characterized by three main clinical features: hyperandrogenism, ovulatory dysfunction, and polycystic ovarian morphology (Azziz et al., 2016). These symptoms are frequently accompanied by insulin resistance (IR), which further exacerbates metabolic and reproductive complications (ACOG, 2018). Recent studies have highlighted the significant role of the gut microbiota in the development of both PCOS and IR, emphasizing its interaction with metabolic and hormonal regulatory systems (Tremellen & Pearce, 2012; Murri et al., 2013).

Global Prevalence:

The global prevalence of PCOS is estimated to range between 6% and 21%, with higher rates observed in urban and industrialized settings. Geographic variability in prevalence is attributed to differences in diagnostic criteria, genetic and lifestyle factors, sociocultural norms, and access to healthcare services.

Table 1: Regional Differences

Reference	Region	Overview	Prevalence
Akinola et al., 2022	Africa	Limited data; however, rising PCOS rates are suspected due to urbanization and lifestyle changes.	A Nigerian study estimated 18.1% prevalence using the Rotterdam criteria.
Teede et al., 2018	Europe	Prevalence varies based on diagnostic criteria and population characteristics.	Estimated between 6% and 15%.
Nidhi et al., 2011	Asia	South Asian countries show higher PCOS rates due to genetic and environmental factors.	An Indian study reported 22.5% prevalence among young women.
Silva et al., 2020	Latin America	Increasing obesity and sedentary behavior contribute to higher PCOS incidence.	A Brazilian study reported 14.6% prevalence in reproductive-age women.

Risk Factors and Vulnerable Populations

Polycystic ovary syndrome (PCOS) primarily affects women of reproductive age, commonly emerging during adolescence or early adulthood (Azziz et al., 2016). The severity of the condition is often exacerbated by factors such as limited access to healthcare, low socioeconomic status, poor nutrition, and exposure to endocrine-disrupting chemicals (WHO,2018). Additionally, sedentary lifestyles and high-calorie diets significantly contribute to both the development and progression of PCOS.

Microbiome Changes in PCOS and Insulin Resistance

Women with PCOS frequently exhibit gut dysbiosis, characterized by reduced bacterial diversity and an imbalance in microbial composition. Studies have shown an increased abundance of Bacteroides, Ruminococcus, Enterococcus, and Rothia, along with a decrease in beneficial bacteria such as Prevotella and Lactobacillus (Lindheim et al., 2017; Murri et al., 2013). These alterations are linked to increased intestinal permeability, chronic low-grade inflammation, and systemic metabolic dysfunction.

Dysbiosis also results in diminished production of short-chain fatty acids (SCFAs), which are essential for glucose metabolism and insulin signaling. Moreover, changes in bile acid metabolism due to

microbial imbalance may disrupt hormonal regulation and lipid metabolism, further aggravating PCOS symptoms (Tremellen & Pearce, 2012; Torres et al., 2018).

Biological and Health Impacts

The metabolic consequences of gut microbiota imbalance in PCOS include an increased tendency toward obesity, facilitated by enhanced energy absorption and fat storage (Lindheim et al., 2017). Additionally, type 2 diabetes mellitus is more likely to develop due to the pro-inflammatory effects of lipopolysaccharides (LPS) produced by Gram-negative bacteria. These endotoxins contribute to chronic inflammation and exacerbate insulin resistance (Murri et al., 2013).

Cardiovascular complications, such as dyslipidemia and hypertension, are also commonly observed in women with PCOS. From a reproductive perspective, the condition is associated with anovulation, infertility, and an increased risk of pregnancy-related complications including gestational diabetes, preeclampsia, and miscarriage (Azziz et al., 2016; ACOG, 2018).

Certain microbial species are closely associated with metabolic changes in PCOS. Enterococcus spp. correlates with increased waist circumference and insulin resistance; Bacteroides vulgatus is linked to elevated branched-chain amino acids, which impair insulin sensitivity; and reduced levels of Prevotella spp. have been associated with broader metabolic disturbances (Murri et al., 2013).

Lifestyle and Pharmacological Interventions

Lifestyle interventions are pivotal in managing PCOS-related metabolic dysfunction. Diets high in fiber and low in glycemic index promote beneficial microbiota and support metabolic health (Teede et al., 2018). Physical activity improves both microbial diversity and insulin sensitivity, forming a critical component of non-pharmacological management strategies (Azziz et al., 2016)

Among pharmacological approaches, metformin remains a cornerstone treatment, enhancing insulin sensitivity and beneficially altering the gut microbiome (Murri et al., 2013). Probiotics and prebiotics are increasingly recognized for their ability to restore microbial balance and improve metabolic outcomes (Karamali,2018; Lindheim et al., 2017). Fecal microbiota transplantation (FMT) is an emerging therapeutic strategy under investigation for its potential to reestablish healthy microbiota in metabolic disorders, including PCOS (Torres et al., 2018; Tremellen & Pearce, 2012).

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Psychosocial and Socioeconomic Considerations

Beyond physiological symptoms, PCOS significantly affects mental health. Many women experience depression, anxiety, and eating disorders, often stemming from hormonal imbalances, weight-related challenges, and societal pressures (Azziz et al., 2016; WHO, 2018). Visible symptoms such as acne and hirsutism can lead to social stigma and isolation (ACOG, 2018). Alarmingly, some studies suggest a higher prevalence of domestic violence among women diagnosed with PCOS (Akinola et al., 2022).

Economically, PCOS can impact work productivity and employment stability, largely due to its psychological burden and chronic health complications (Silva et al., 2020).

The relationship between the gut microbiome, insulin resistance, and PCOS highlights the need for an integrative and holistic approach to treatment. Therapeutic strategies that address microbial dysbiosis—through diet, pharmacological interventions, and emerging microbiome therapies—hold promise for improving both metabolic and reproductive outcomes (Lindheim et al., 2017; Murri et al., 2013). Effective care must also address the psychosocial and socioeconomic dimensions of the disorder to ensure equitable and comprehensive healthcare for women with PCOS (Teede et al., 2018; Azziz et al., 2016).

Discussion

After analyzing the relationship of gut microbiota, short-chain fatty acids, and insulin resistance in the context of PCOS in women. The link between gut microbiota and metabolic health has been

interesting, particularly as IR is associated with people having PCOS (Azziz et al., 2016). In this discussion, we have reviewed the evidence from the available scientific documents to talk about the role of gut microbiota and its metabolites in insulin sensitivity, remedies brought by nutrition and microbes, and any biomarker signatures of PCOS.

Short-Chain Fatty Acids: Insulin Sensitivity Enhancers

SCFAs form metabolites of gut microbiota fermentation of dietary fibers. These are acetate, propionate, and butyrate. Importantly, they are essential for their function in regulating the intestinal barrier, immune system, and glucose metabolism (Murri et al., 2013). For example, butyrate is an important energy source of colonocytes and a powerful anti-inflammatory agent (Tremellen & Pearce, 2012). It is also, in addition, that butyrate facilitates the influence of insulin on body cells via stimulation of G-protein coupled receptors (GPR41 and GPR43) that improve release of GLP1 and PYY precursor of glucagon-like peptide 1 (GLP1) and peptide YY (PYY) that counters hunger and augments digestion (Lindheim et al., 2017). Some studies have found that SCFA-producing bacteria are reduced in women with polycystic ovary syndrome (PCOS), and therefore, SCFAs are in lower concentrations. For example, this may lead to more intestinal permeability, systemic inflammation and then further insulin resistance. Thus, SCFAs mediate the composition of the gut microbiota and insulin sensitivity (Murri et al., 2013; Torres et al., 2018).

Prebiotics, probiotics, and diet are examples of modulating the gut microbiota

Gut microbiota composition is very dynamic and can be modulated by its components in the diet and by pre and probiotics. Prebiotics are another term that refers to non-digestible fibers that help to enhance the growth of beneficial bacteria; inulin is an example (Teede et al., 2018). Live microorganisms that are beneficial to health when taken in adequate amounts are here referred to as probiotics (Karamali, 2018). Supplementation with probiotics and symbiotics caused significant reductions of prostate and breast cancer indicators (lipid profile, hormonal imbalance, and insulin resistance in female PCOS patients with improvements from insulin resistance in clinical studies results, which are promising that these supplements can be used in obesity treatment. There are noted reductions in metabolic parameters like insulin, fasting glucose, and HOMA-IR (Karamali, 2018). More pronounced effects are from symbiotics than probiotics or prebiotics alone. Other studies showed that menopausal women with dietary fiber enhanced SCFA production and improved insulin sensitivity (WHO, 2018).

Distinguishing Patterns in PCOS Gut Microbiota Composition

Women suffering from PCOS and those in good health have striking differences in their gut microbiota diversity and composition. A clear pattern arises throughout studies - women with PCOS have less microbial diversity, lack favorable bacteria such as Lachnospira and Prevotella, and have an overabundance of dangerous bacteria, including Bacteroides, Parabacteroides, and Escherichia/Shigella (Lindheim et al., 2017; Murri et al., 2013). Gut environment is becoming more inflammatory, and it has the potential to worsen metabolic functions. Dysbiosis-promoting inflammation SCFA bacteria deficiency is more pronounced in PCOS women, reinforcing the belief that PCOS and insulin resistance develop via gut dysbiosis (Tremellen & Pearce, 2012).

Microbial Taxa and Insulin Resistance Markers in PCOS

Particular microbial groups have been noted to have an impact on insulin resistance factors in patients with PCOS. An increased level of Bacteroides is associated with high levels of lipopolysaccharides (LPS), which cause systemic inflammation and insulin resistance (Murri et al., 2013). Also, there is a reduction in glucose metabolism correlating with butyrate-producing bacteria like Faecalibacterium prausnitzii (Torres et al., 2018). These relationships highlight the possibility of modifying certain microbial populations for the purpose of improving insulin resistance in PCOS patients.

Implications and Future Directions

There are encouraging insights for therapeutic approaches aimed at PCOS care by examining the dynamics of gut microbiome with SCFAs and insulin sensitivity. Restoring metabolic equilibrium through dietary interventions, supplementation with prebiotics and probiotics, and alteration of lifestyle could improve the gut flora and restore clinical results (Teede et al., 2018; WHO, 2018). Targeted approaches should be developed to identify baseline guidelines for such modifications to the interventions as more studies need to be done on the diverse compositions of gut microbiota and how they respond. These approaches may use integration of microbiome mapping to improve the effectiveness of the interventions aimed to decrease insulin resistance in PCOS patients (Azziz et al., 2016).

Conclusions

Polycystic ovary syndrome (PCOS) is a significant global health issue, with insulin resistance (IR) recognized as a key metabolic factor in its pathophysiology (ACOG, 2018). Emerging evidence indicates that gut microbiome dysbiosis plays a critical role in sustaining the metabolic, inflammatory, and endocrine disturbances characteristic of PCOS (Karamali et al., 2018; WHO, 2018). Altered gut microbial composition increases intestinal permeability and induces systemic endotoxemia, thereby contributing to insulin resistance and hyperandrogenism.

Recent studies have highlighted the importance of gut microbiota in PCOS development, particularly through its influence on insulin sensitivity and hormonal regulation. A notable finding is the reduction of short-chain fatty acid (SCFA)-producing bacteria such as Faecalibacterium prausnitzii and Prevotella, which has been associated with greater systemic inflammation and worsened insulin resistance in PCOS patients.

Therapeutic strategies that target the gut microbiome—such as probiotics, prebiotics, symbiotics, and conventional medications—have shown promising results in restoring microbial balance and improving metabolic and hormonal profiles. Improvements have been observed in key biomarkers, including reductions in HOMA-IR, fasting glucose, insulin levels, and improvements in lipid and hormone balance.

Research conducted by organizations like WHO and ACOG supports the dual role of the gut microbiome—as both a pathogenic contributor and a therapeutic target—in PCOS. Consequently, treatment strategies for PCOS should include low-risk microbiota-modulating interventions such as probiotic-prebiotic supplementation, dietary fiber intake, and fecal microbiota transplantation (FMT).

However, to fully understand and optimize these treatment modalities, further long-term, controlled studies are required. The integration of gut microbiota profiling into clinical care offers a transformative path forward—enabling a shift from traditional symptom management toward precision medicine and disease modification in PCOS.

Recommendations:

- Clinical Application: Incorporate gut microbiota modulation strategies—such as fermentable fiber-rich diets and the use of targeted probiotics or symbiotics—into PCOS management protocols to improve insulin sensitivity and overall metabolic health.
- Research Directions: Conduct robust clinical trials to investigate the specific roles of gut microbes in insulin resistance among diverse PCOS populations. Efforts should focus on identifying microbial biomarkers and curative targets.
- Personalized Medicine: Develop individualized treatment approaches based on gut microbiome profiling, optimizing therapeutic outcomes for women with PCOS.
- Longitudinal Studies: Explore the long-term impact of gut microbiota changes on PCOS progression and treatment response, to establish evidence-based guidelines for sustained management.
- In summary, the gut microbiome plays a critical role in the onset and progression of insulin resistance in women with PCOS. Protecting and restoring beneficial gut bacteria through targeted interventions offers a promising avenue to improve clinical outcomes beyond current treatment options.

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