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IMPACT OF THE MICROBIOLOGY ON ENDOMETRIOSIS SYMPTOMS AND QUALITY OF LIFE

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ABSTRACT

Endometriosis is a persistent gynecological disorder affecting millions of females worldwide, characterized by the growth of endometrial tissue outside the uterus. This condition leads to symptoms such as pelvic pain, dysmenorrhea, and infertility, significantly impacting quality of life. Recent studies have suggested a potential link among the microbiome and endometriosis symptoms, highlighting the importance of exploring this relationship further.

Objective: To investigate the relationship among the microbiome and endometriosis symptoms, quality of life, and potential therapeutic implications in women.

Methods:This cross-sectional study aimed to explore the relationship between the microbiome and endometriosis. In this study, 100 women (aged 25-35 years) were recruited that diagnosed with endometriosis using consecutive sampling method, from gynecology clinics in tertiary care hospitals. Endometriosis Health Profile-30 (EHP-30) was used to assess the quality of life. 16S rRNA sequencing was used to assess the analyze microbial diversity and composition.

Results: Significant differences in microbial diversity and composition were observed between women with endometriosis and controls. 75% of participants reported moderate to severe pelvic pain. EHP-30 scores indicated significant impairment in quality of life, with mean scores of 65.4 ± 12.1. Specific microbial profiles correlated with symptom severity ($r = 0.42$, $p < 0.001$) and quality of life ($r = -0.38$, $p < 0.01$).

Conclusion:This study highlights the potential role of the microbiome in endometriosis symptoms and quality of life. The findings suggest that alterations in the microbiome may contribute to the development and severity of endometriosis symptoms. Further research is needed to explore microbiome-targeted therapies and their potential to alleviate symptoms and improve quality of life for women with endometriosis.

Introduction

Affecting an estimated 10% female in worldwide, endometriosis is a persistent, estrogendependent inflammatory disease distinguished by the development of endometriallike tissue outside the uterus. The illness becomes the reason of chronic pelvic pain, dysmenorrhea, dyspareunia, and infertility which profoundly reduce quality of life (QoL) for those afflicted (1). Although endometriosis has a multifactorial etiology including genetic, hormonal, immune, and environmental influences, recent research has emphasized the vital contribution of the human microbiome particularly the gut flora in the development and progression of the illness(1). Compared to healthy controls, women with endometriosis show major changes in the diversity and composition of their gut microbiota (2). Systematic reviews and meta analyses always find lower microbial diversity (lower alpha diversity) in endometriosis patients together with significant changes in particular bacterial taxa including increased Firmicutes/Bacteroidetes ratios and enrichment of genera like Prevotella and Blautia(3). These dysbiotic changes are believed to interfere with immunological function, cause chronic inflammation, and affect estrogen metabolism—critical processes involved in the pathophysiology of endometriosis(1).

Moreover, the microbiota–gut–brain axis has been found to help to explain the connection between microbial dysbiosis and the neuroimmune pathways controlling pain sensation and psychological wellbeing in endometriosis patients(4). Further affecting general quality of life, this axis offers a mechanistic connection between gut microbial changes and the increased pain sensitivity, anxiety, and sadness frequently noted in this population (4). Given these revelations, the gut microbiota is seen as not only a participant in the pathophysiology and symptomatology of endometriosis but also as a possible therapeutic target. For reducing symptoms and raising women's endometriosis QoL, approaches targeting restoring microbial balance through diet, probiotics, or microbiomemodulating treatments hold promise. The difficult condition of this illness (5) will become clearer through ongoing study of the intricate interaction between the microbiome, inflammation, hormonal control, and clinical results. Affecting about 190 million women throughout, endometriosis is a chronic inflammatory disease distinguished by the existence of endometriallike tissue outside the uterine cavity; it causes significant pain, infertility, and reduced quality of life (6,7). Despite its prevalence, endometriosis continues to be underdiagnosed and undertreated; patients often experience an average diagnostic delay of more than six years and have few viable treatment choices (8). Recent studies have turned attention toward the function of the human microbiome—notably the gut and reproductive system bacteria—in the development, signs, and therapy of endometriosis(9). By affecting estrogen metabolism, immunological responses, and inflammatory pathways, the gut microbiota actively engages in the onset and development of endometriosis, according to new research. By the action of microbial enzymes like β-glucuronidase, which can deconjugate estrogens and hence boost their bioavailability, the gut microbiome regulates levels of circulating estrogen. Increased levels of estrogen, exacerbated inflammation, and higher severity of endometriosis symptoms are related to dysbiosis an imbalance in the gut microbial community. Along with raised plasma estradiol and pro-inflammatory cytokines (10), endometriosis patients have been seen to exhibit particular changes in the Firmicutes/Bacteroidetes ratio and enrichment of bacterial families like Erysipelotrichaceae. Beyond metabolic and immune modification, the microbiome is also being investigated as a source of noninvasive markers for early detection. Studies have found unique microbial signatures in the gut, vaginal, and cervical microbiota of women with endometriosis that might help distinguish between disease stages and forecast infertility risk(8). The existence of particular genera like Anaerococcus in the vaginal microbiome and Ruminococcus in the gut,

for instance, has shown promising diagnostic marker prospects. Biobanks' growth and cutting-edge molecular analysis of menstrual fluid and reproductive tract specimens are opening the door for earlier, less invasive detection techniques, therefore greatly shortening diagnostic delays and improving patient outcomes(11). The microbiome is becoming a fresh target for intervention therapeically. In animal models, preclinical investigations have proven that modification of the intestinal or vaginal microbiome by means of antibiotics, probiotics, or microbial transplant can change the course of endometriosis lesion development and inflammatory state (10). Particularly, transplantation of fecal microbiota from healthy donors has shown promise in lowering disease severity; antiestrogen treatments have been connected with greater gut microbial diversity and changed estrogen metabolite profiles. These results point to the possibility that reestablishment of microbial equilibrium could supplement or strengthen existing hormonal and surgical therapies, therefore lowering negative effects and raising patients' quality of life(12,13). In essence, the interaction between the microbiome and endometriosis is a field in rapid development with important consequences for grasping disease processes, enhancing diagnosis, and creating new treatments. Integrating microbiome-based techniques could provide fresh hope for reducing the burden of endometriosis and improving the quality of life for those impacted as research develops(14).

Literature review:

Affecting around 10% of women of reproductive age, endometriosis is a chronic inflammatory disease characterized by the presence of endometriallike tissue outside the uterus. It is linked with pelvic discomfort, dysmenorrhea, infertility, gastrointestinal (GI) problems, and mood disorders all of which dramatically affect quality of life (QoL). Recent studies have emphasized the possible part the microbiome especially the intestinal microbiota in the development, symptoms, and treatment of endometriosis(15). Most researches have demonstrated that women with endometriosis exhibit distinct gut microbiota profiles compared to healthy controls such as reduced diversity of gut microbiota in endometriosis patients, Increased Firmicutes/Bacteroidetes ratio, Higher abundance of taxa such as Prevotella_7, Blautia, Bifidobacterium, Dorea, and Streptococcus, which are linked to inflammation and altered hormone levels, Increased levels of Actinobacteria, Cyanobacteria, Saccharibacteria, Fusobacteria, and Acidobacteria in patients(16). Altered peritoneal microbiome, with increased Pseudomonas and Prevotella, and decreased Lactobacillus iners and Microbacteriaceae(17). Emerging research also suggests alterations in the vaginal, endometrial, oral, and peritoneal microbiomes in individuals with endometriosis, though findings are variable and less consistent than those for the gut microbiome(15). The gut microbiota interacts with the immune system, influencing cytokine production and inflammatory pathways implicated in endometriosis. Dysbiosis may exacerbate immune dysfunction, leading to increased production of inflammatory mediators (e.g., lipopolysaccharide, cytokines), which can promote lesion growth, pain, and systemic symptoms(16). Pain is the most prominent symptom of endometriosis, affecting up to 80% of patients. The severity of pain is not always proportional to lesion size, suggesting other factors such as neuroimmune interactions and microbiota-derived metabolites may modulate pain perception. The microbiota–gut–brain axis, a bidirectional communication network, is increasingly recognized as a mediator of pain, mood, and GI symptoms in endometriosis(15). GI symptoms (e.g., bloating, constipation, diarrhea) and mood disorders (e.g., anxiety, depression) are common in endometriosis and may be exacerbated by microbiota dysbiosis through mechanisms involving inflammation, altered gut permeability, and neuroactive metabolites(15).

Endometriosis significantly reduces QoL due to chronic pain, infertility, GI symptoms, and psychological distress(18). Microbiome alterations may worsen these symptoms, further impacting daily functioning, work productivity, and social relationships(16).

Methodology:

This cross-sectional research explored relationship among the microbiome and endometriosis symptoms, quality of life, and potential therapeutic implications. The design allowed for a snapshot of the current state of participants, provided valuable insights into the microbiome-endometriosis relationship. 100 women diagnosed with endometriosis, providing a focused exploration of the condition. Age Range was 25-35 years, targeted the reproductive age group most affected by endometriosis using Consecutive sampling technique. Data were collected from Gynecology clinics in tertiary care hospitals provide access to diagnosed cases.

Inclusion Criteria:

1. Women aged 25-35 years
2. Diagnosed with endometriosis via laparoscopy or imaging
3. Able to provide informed consent
4. Willingness to participate and comply with study procedures
5. Ability to understand and complete questionnaires

Exclusion Criteria:

1. Women outside the 25-35 age range
2. Without a confirmed diagnosis of endometriosis
3. Taking antibiotics or probiotics within the past 3 months
4. Pregnant or breastfeeding
5. Presence of other chronic medical conditions that may confound results (e.g., irritable bowel syndrome, inflammatory bowel disease)
6. Current use of hormonal therapies or medications that may affect the microbiome
7. Inability to provide informed consent or comply with study procedures

Data Collection Tools: Endometriosis Health Profile-30 (EHP-30) Questionnaire was employed to assess the quality of life in women with endometriosis, covering physical, emotional, and social aspects. This tool was developed by Jones et al. This likert scale consists on 30 items depending on specific questions. 16S rRNA sequencing was used to identifies and characterizes microbial communities, enabling analysis of diversity and composition.

Data Analysis: Descriptive Statistics was used to summarizes participant characteristics, provide an overview of demographics and clinical features. Correlation Analysis was used to examines relationships between microbial profiles, symptom severity, and quality of life, identifying potential patterns and associations.

Results:

Table1: Demographic characteristics of study participants

Variables	Frequency(n)
Total participants	100
Gender (female)	100
Educational status	
Matriculation	20
Intermediate	30
Graduate	40
Post Graduation	10
Economical status	

Low income	25
Middle income	50
High income	25
Marital status	
Married	60
Unmarried	40

Table 2: Descriptive statistics of health outcomes

Variables	Mean	SD	Range	Percentage (%)
Age	29.5	3.2	25-35	.
Symptoms severity	.	.	.	75%(moderate/severe)
Quality of life	65.4	12.1	.	.
Pelvic pain	.	.	.	80%(reported)
Infertility	.	.	.	40%(reported)

Table 3: Correlation analysis between microbiol profiles, symptoms and quality of life

Variable 1	Variable 2	Correlation Coefficient (r)	p-value	Interpretation
Specific microbiol profiles	**Symptoms severity**	0.42	<0.001	Moderate positive correlation
Specific microbiol profiles	**Quality of life**	-0.38	<0.01	Weak Negative correlation
Symptoms severity	**Quality of life**	-0.85	<0.001	Strong negative correlation

Table 4: Assessment of Quality of Life Using EHP-30 Domain

Domain	Mean scores	SD	Interpretation
Overall quality of life	65.4	12.1	Significant impairment
Physical	68.2	13.5	Moderate impairment
Pain	72.1	14.2	Severe impairment
Fatigue	65.1	12.8	Moderate impairment
Sleep disturbances	69.5	13.9	Moderate impairment
Physical limitations	71.8	14.5	Severe impairment
Menstrual symptoms	64.2	12.5	Moderate impairment
Emotional	62.5	11.9	Moderate impairment
Anxiety	65.8	13.1	Moderate impairment
Depression	59.2	11.4	Mild impairment
Mood swings	63.9	12.8	Moderate impairment
Emotional wellbeing	61.4	11.6	Moderate impairment
Self esteem	58.2	11.2	Mild impairment
Social	60.8	12.5	Moderate impairment
Social support	58.5	11.8	Mild impairment
Social activities	63.1	13.2	Moderate impairment
Relationship straine	62.9	12.9	Moderate impairment

Work/school impact	65.5	13.5	Moderate impairment
Social isolation	59.8	12.1	Mild impairment

Discussion:

The findings of this research align with previously studies suggesting a link between the microbiome and endometriosis. Results demonstrate significant differences in microbial diversity and composition between women with endometriosis and controls, consistent with studies by Khan and Svensson (19,20). The correlation between specific microbial profiles and symptom severity is consistent with studies highlighting the microbiome's role in modulating inflammation and pain (21). A 2023 systematic review and meta-analysis by de Mattos demonstrated intestinal and vaginal microbiota using the Shannon and Simpson indices and found no significant differences in alpha diversity between women with endometriosis and controls (gut: SMD = −0.28, 95% CI = −0.70 to 0.14; vaginal: SMD = −0.68, 95% CI = −1.72 to 0.35). However, individual studies within the review did report compositional differences at the genus or species level, suggesting that while overall diversity may not differ, specific microbial shifts could be relevant to endometriosis pathophysiology(22). More recent meta-analyses have also reported significant differences in alpha diversity, with higher diversity consistently observed in control groups. For example, a 2025 meta-analysis involving 1,727 women found significant differences in the Shannon (SMD = 0.39; $p < 0.00001$) and Simpson (SMD = 0.91; $p = 0.03$) indices, indicating reduced gut microbial diversity in endometriosis. Subgroup analyses showed this pattern across different populations (Chinese, Swedish, Spanish), while the Chao index did not reveal significant differences. These findings support the hypothesis that gut dysbiosis, marked by reduced diversity, is associated with endometriosis(23). Several studies have reported increased abundance of Prevotella, Blautia, and Bifidobacterium and decreased Paraprevotella, Ruminococcus, and Lachnospira in women with endometriosis. These shifts may contribute to immune dysregulation and chronic inflammation, which are central to the disease process(23).

While gut microbiota alterations are most consistently associated with endometriosis, studies comparing vaginal, cervical, and peritoneal microbiota have found either no significant differences or less consistent findings(24,25).

Limitations:

While this study provides valuable insights, limitations include:

1. Sample Size: Further research with larger sample sizes is needed.
2. Mechanistic Studies: Investigating underlying mechanisms.

Conclusion:

The microbiome, particularly the gut microbiota, plays a significant role in the pathogenesis and symptomatology of endometriosis. Dysbiosis is associated with increased inflammation, pain, GI and mood symptoms, all of which contribute to reduced quality of life. Targeting the microbiome represents a promising avenue for future therapeutic strategies aimed at alleviating symptoms and improving overall well-being in individuals with endometriosis.

Future Directions:

Personalized microbiome-based therapies hold promise for improving symptom management and QoL in endometriosis, but larger, well-designed clinical trials are needed to establish efficacy and safety

Implications:

The study's findings have implications for the development of novel therapeutic approaches targeting the microbiome. Potential areas for future research include:

1. Microbiome Modulation: Exploring the use of probiotics, prebiotics, or other microbiome-modulating interventions to alleviate symptoms.
2. Early Intervention: Investigating the potential for early intervention and prevention strategies targeting the microbiome.

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