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Comparative Analysis of the Microbiota of the Reproductive System in Women with Primary and Secondary Infertility

[1]Zhuraeva A.Zh., Shukurov F.I., Jalolova G.S.

ABSTRACT

Background. *In recent years, the study of the microbiota of the reproductive system has attracted the attention of scientists due to its important role in maintaining reproductive health. An imbalance in the microbiota can lead to the development of gynecological diseases, negatively affecting fertility.*

Aim. *To conduct a comparative analysis of the microbiota of the reproductive system in women with primary and secondary infertility.*

Materials and Methods. *The study included 130 women: 50 with primary infertility (Group I), 50 with secondary infertility (Group II), and 30 healthy women (control group). Microbiota samples were collected using vaginal and cervical swabs. Microbiota identification was performed using 16S rRNA sequencing with the Illumina MiSeq platform. Statistical data processing was performed using SPSS version 25.0.*

Results. *The duration of infertility was 4.2 ± 1.5 years (Group I) and 5.1 ± 1.7 years (Group II). Comparative analysis showed that the level of Gardnerella vaginalis in women from Group I was 80%, which was significantly higher compared to 30% in Group II and absent in the control group ($p < 0.05$). The presence of Atopobium vaginae was also higher in Group I (60%) compared to Group II (20%) and absent in the control group ($p < 0.05$). Relative proportions of Lactobacillus spp. were significantly lower in women with primary infertility (70%) compared to Group II (90%) and the control group (100%) ($p < 0.05$).*

Conclusion. *The results of the comparative analysis of the microbiota of the reproductive system in women with primary and secondary infertility showed significant differences in the composition of the microbiota compared to the control group. Women with primary infertility are characterized by lower microbiota diversity and higher levels of conditionally pathogenic bacteria. These results highlight the importance of the microbiota in maintaining reproductive health and indicate the need for further research to develop new diagnostic and therapeutic approaches.*

Keywords. *female infertility, primary infertility, secondary infertility, microbiota, reproductive system*

[1] Assistant at the Department of Obstetrics and Gynecology, Tashkent Medical Academy, Tashkent, Uzbekistan, e-mail: orazali91aynura94@gmail.com

INTRODUCTION

Infertility is one of the most pressing issues in modern medicine, affecting a significant number of couples worldwide [1,2]. According to the World Health Organization, approximately 10–15% of couples face difficulties conceiving [3]. Infertility can be classified as primary, when a woman has never been pregnant, or secondary, when the inability to conceive occurs after one or more successful pregnancies [4]. In recent years, the study of the reproductive system microbiota has garnered substantial attention from researchers due to its critical role in maintaining reproductive health [5]. The microbiota, comprising various microorganisms such as bacteria, viruses, and fungi, performs essential functions in maintaining homeostasis and providing protection against pathogens [6]. An imbalance in the microbiota can lead to the development of gynecological disorders that adversely affect fertility [7]. For instance, bacterial vaginosis and pelvic inflammatory diseases are associated with alterations in microbiota composition and can significantly reduce women's reproductive potential [8].

Several studies suggest a potential link between microbiota alterations and various forms of infertility]. It has been found that women with infertility exhibit changes in the composition of vaginal and endometrial microbiota, which can impact embryo implantation and pregnancy development [9]. However, a comparative analysis of the reproductive system microbiota in women with primary and secondary infertility remains insufficiently explored. Identifying differences in the microbiota of these two groups of women could provide deeper insights into the pathogenesis of infertility and help identify potential biomarkers for diagnosis and treatment [10]. Understanding these differences may also facilitate the development of novel therapeutic approaches, such as probiotic or antimicrobial therapies aimed at restoring a healthy microbiome and enhancing fertility.

Hence, further investigation of the reproductive system microbiota and its role in primary and secondary infertility is a crucial step toward improving methods for diagnosing and treating infertility. This research will not only deepen our understanding of infertility mechanisms but also contribute to the development of individualized therapeutic approaches based on specific microbiota alterations in each patient.

This study aims to perform a comparative analysis of the reproductive system microbiota in women with primary and secondary infertility.

MATERIALS AND METHODS

The study included 130 women, divided into three groups: Group I (n=50): women with primary infertility. Group II (n=50): women with secondary infertility. Control Group (n=30): healthy women.

Inclusion criteria involved women aged 20–40 years with confirmed diagnoses of primary or secondary infertility, no acute infectious diseases at the time of enrollment, and signed informed consent. Exclusion criteria were chronic diseases in the acute phase, use of antibiotics or probiotics within the last three months, oncological conditions, and autoimmune diseases.

Samples of the reproductive system microbiota were collected using vaginal and cervical swabs under strictly sterile conditions to minimize contamination risks and ensure high accuracy in subsequent analyses. Standardized swab collection methods were used to preserve sample integrity. The collected samples were immediately placed in a specialized transport medium designed to maintain microbial viability and promptly transported to the laboratory, where they were stored under controlled temperature conditions until analysis. The microbiota was identified using 16S rRNA sequencing, regarded as the gold standard in microbiological research. This method allows for detailed identification of microbiota composition, including hard-to-culture microorganisms.

The analytical process included:DNA Extraction: High-yield and high-purity DNA was obtained using commercial kits. Amplification and Sequencing: DNA was amplified and sequenced using the Illumina MiSeq platform. The MiSeq system, known for its efficiency, integrates cluster generation, paired-end sequencing, and data analysis, delivering ready-to-interpret results within 8 hours.Data Processing: Sequencing data were processed using QIIME 2 software, a recognized standard for microbiome analysis. Diversity indices were calculated based on operational taxonomic units (OTUs) with a 97% similarity threshold. Shannon Diversity Index and Pielou Evenness Index were used to assess alpha diversity, reflecting the richness and evenness of microbial communities.

Microbial classification utilized the SILVA database, a comprehensive resource for microbiological research. Relative proportions of microorganisms in each group were analyzed to identify significant differences in microbiota composition among the groups.

Data were analyzed using SPSS software (version 25.0). The Mann-Whitney test was applied for compar-

isons between two independent groups, while the Kruskal-Wallis test was used for multiple group comparisons. Statistical significance was set at p<0.05p < 0.05p<0.05.

RESULTS

A retrospective analysis and review of outpatient records revealed that 50 women were diagnosed with primary infertility and another 50 with secondary infertility. The primary complaint of all patients was infertility. The mean age of women with primary infertility was 32.5 ± 4.3 years, compared to 34.2 ± 3.8 years in women with secondary infertility. The body mass index (BMI) was comparable between the two groups: 23.7 ± 2.1 kg/m² in women with primary infertility and 24.1 ± 2.3 kg/m² in those with secondary infertility.

In the primary infertility group, 17% (n=8) of women were classified as having obesity class II (BMI 35–39.9 kg/m²), 23% (n=12) were overweight (BMI 25–29.9 kg/m²), and 60% (n=30) had a normal weight (BMI 18.5–24.9 kg/m²). Similarly, in the secondary infertility group, 15% (n=7) of women had obesity class II, 25% (n=13) were overweight, and 60% (n=30) had a normal weight. This consistent distribution of BMI categories across the groups minimizes the potential confounding influence of body weight on the study results.

The duration of infertility averaged 4.2 ± 1.5 years for women with primary infertility and 5.1 ± 1.7 years for those with secondary infertility. Chronic conditions were slightly more prevalent in the secondary infertility group (24%) compared to the primary infertility group (20%). Educational attainment was similar across the groups, with the majority of women in both groups having completed higher education (60% in the primary infertility group and 55% in the secondary infertility group). These demographic characteristics were considered during the subsequent microbiota analysis to rule out their potential influence on the results.

The microbiota profiles of women with primary and secondary infertility exhibited significant differences compared to the control group. Key findings are summarized below:

Gardnerella vaginalis was identified in 80% (n=40) of women in the primary infertility group, significantly exceeding the prevalence in the secondary infertility group (30%, n=15) and its complete absence in the control group (p<0.05p < 0.05p<0.05). Gardnerella vaginalis is a facultative pathogen associated with bacterial vaginosis, which can adversely affect fertility.

Atopobium vaginae was detected in 60% (n=30) of the primary infertility group, compared to 20% (n=10) in the secondary infertility group, and was absent in the control group (p<0.05p < 0.05p<0.05). This bacterium is commonly linked to bacterial vaginosis and may trigger inflammatory processes in the reproductive system.

Lactobacillus spp. proportions were significantly lower in the primary infertility group (70%, n=35) compared to 90% (n=45) in the secondary infertility group and 100% (n=30) in the control group (p<0.05p < 0.05p<0.05). Lactobacillus spp. play a crucial role in maintaining reproductive health by creating an acidic environment that inhibits the growth of pathogenic microorganisms.

Prevotella spp. prevalence was 50% (n=25) in the primary infertility group, 40% (n=20) in the secondary infertility group, and absent in the control group (p<0.05p < 0.05p<0.05). These bacteria are associated with pelvic inflammatory diseases.

Bacteroides spp. levels were elevated in the primary infertility group (40%, n=20) compared to 16% (n=8) in the secondary infertility group, with none detected in the control group (p<0.05p < 0.05p<0.05). These bacteria are implicated in inflammatory processes that may impair reproductive function.

Sneathia spp. was present in 36% (n=18) of the primary infertility group, 12% (n=6) of the secondary infertility group, and absent in the control group (p<0.05p < 0.05p<0.05). This bacterium is linked to adverse pregnancy outcomes and inflammatory diseases.

Mobiluncus spp. was identified in 30% (n=15) of women in the primary infertility group, compared to 10% (n=5) in the secondary infertility group, and was absent in the control group (p<0.05p < 0.05p<0.05). These bacteria are often associated with bacterial vaginosis.

Ureaplasma spp. was detected in 24% (n=12) of the primary infertility group, 14% (n=7) of the secondary infertility group, and was absent in the control group (p<0.05p < 0.05p<0.05). These bacteria may contribute to inflammatory processes that impair fertility.

Mycoplasma spp. prevalence was 20% (n=10) in the primary infertility group, 10% (n=5) in the secondary infertility group, and absent in the control group (p<0.05p < 0.05p<0.05). These bacteria are associated with inflammatory diseases of the reproductive system.

Fusobacterium spp. was identified in 16% (n=8) of the primary infertility group, 6% (n=3) of the secondary infertility group, and was absent in the control group

(p<0.05p < 0.05p<0.05). These bacteria may contribute to inflammatory processes and negatively affect fertility.

These findings highlight significant differences in the reproductive microbiota profiles of women with primary and secondary infertility. Elevated levels of conditionally pathogenic bacteria (Gardnerella vaginalis, Atopobium vaginae) and reduced levels of protective bacteria (Lactobacillus spp.) underscore the potential role of microbiota imbalances in infertility pathogenesis.

Table 1 provides a comparative analysis of the structure and composition of the microbiota in the study groups, presented as n/%

Bacteria	Group I (n=50)		Group II (n=50)		Control Group (n=30)		P
	abs	%	abs	%	abs	%	
Gardnerella vaginalis	40	80	15	30	-	-	< 0.001
Atopobim vaginae	30	60	10	20	-	-	< 0.001
Lactobacillus spp.	35	70	45	90	30	100	< 0.05
Prevotella spp.	25	50	20	40	-	-	< 0.05
Bacteroides spp.	20	40	8	16	-	-	< 0.01
Sneathia spp.	18	36	6	12	-	-	< 0.01
Mobiluncus spp.	15	30	5	10	-	-	< 0.01
Ureaplasma spp.	12	24	7	14	-	-	< 0.05
Mycoplasma spp.	10	20	5	10	-	-	< 0.05
Fusobacterium spp.	8	16	3	6	-	-	< 0.05

The analysis of α-diversity revealed significantly lower diversity indices in Group I (Shannon Index = 2.1) compared to Group II (Shannon Index = 3.5) and the control group (Shannon Index = 4.0) (p<0.05). These findings indicate a more homogeneous microbiota composition in women with primary infertility. The Shannon Index, a widely used metric for assessing species diversity in ecosystems, accounts for both species richness and the evenness of their distribution. In Group I, a Shannon Index of 2.1 highlighted markedly lower microbiota diversity, suggesting the dominance of one or a few microbial species. Such dominance may lead to microbial imbalance, potentially contributing to fertility issues. In contrast, Group II demonstrated a Shannon Index of 3.5, reflecting a more iverse and evenly distributed microbiota composition (Fig. 1).

This diversity may indicate better microbial balance and fewer issues related to inflammatory processes. The control group showed the highest Shannon Index value of 4.0, representing the greatest microbiota diversity characteristic of a healthy reproductive system. This high diversity implies the presence of various microbial species distributed evenly, supporting homeostasis and protecting against pathogenic microorganisms.

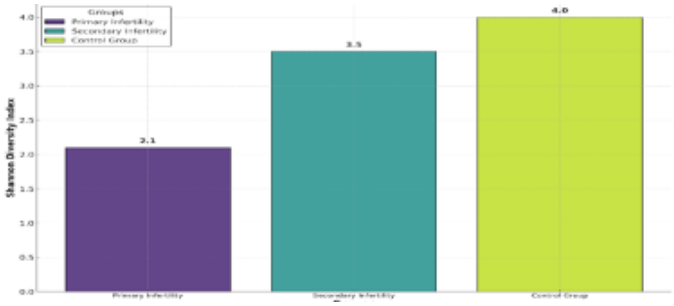

Figure 1. Shannon Diversity Index Comparison Across Groups

The lower Shannon Index observed in Group I underscores a less diverse and more homogeneous microbiota composition, potentially associated with the overrepresentation of facultative pathogens such as Gardnerella vaginalis and Atopobium vaginae. These microorganisms are known to trigger inflammatory processes and adversely impact fertility. Conversely, the higher Shannon Index values in Group II and the control group suggest a healthier and more balanced microbiome, essential for maintaining reproductive health. These findings emphasize the critical role of microbiota diversity in reproductive health and point to microbial imbalances as potential contributors to the pathogenesis of primary infertility. Identifying and addressing these microbiota alterations in women with infertility may provide a promising avenue for enhancing diagnostic and treatment strategies.

The correlation analysis further demonstrated significant associations between microbial levels and clinical parameters in Group I. Specifically, low levels of Lactobacillus spp. and high levels of Gardnerella vaginalis, Atopobium vaginae, and other facultative pathogens were correlated with longer durations of infertility and more frequent pelvic inflammatory diseases (PID). No significant correlations were observed in Group II. The correlation coefficients were as follows: Lactobacillus spp. and infertility duration (r=–0.65, p<0.05), Gardnerella vaginalis and infertility duration (r=0.58, p<0.05), Atopobium vaginae and infertility duration (r=0.54, p<0.05), Gardnerella vaginalis and PID frequency (r=0.62, p<0.05), Atopobium vaginae and PID frequency (r=0.59, p<0.05), and Lactobacillus spp. and PID frequency (r=–0.63, p<0.05) (Fig. 2).

These results underline the significant impact of microbial imbalances on reproductive outcomes in women with primary infertility and reinforce the importance of microbiota-targeted interventions as a potential strategy for improving fertility outcomes/ Thus, the results of the

correlation analysis demonstrate significant associations between the levels of specific bacteria and the duration of infertility in women. The diagnostic efficiency of microbiota profiles was analyzed using ROC analysis. ROC curves were constructed to evaluate the ability of various bacterial levels to predict the presence of infertility. The area under the curve (AUC) was calculated for each parameter.

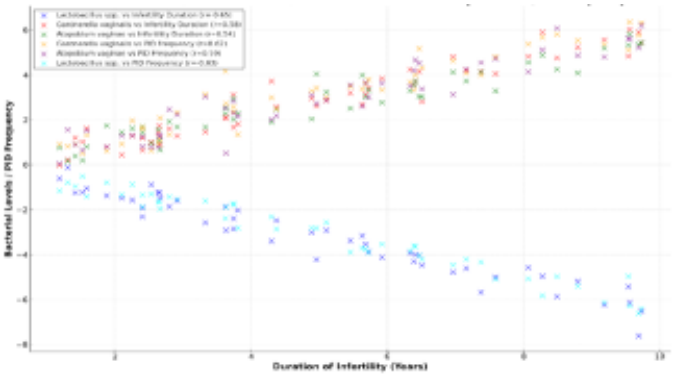

Figure 2. Correlation between bacterial levels and the duration of infertility and frequency of pelvic inflammatory diseases (PID)

The ROC analysis of the diagnostic efficiency of microbiota profiles revealed the following results: the AUC for Gardnerella vaginalis was 0.85 (95% CI: 0.78–0.91), indicating a high ability of this marker to distinguish women with primary infertility from the control group. The AUC for Lactobacillus spp. was 0.90 (95% CI: 0.85–0.95), demonstrating high diagnostic accuracy in differentiating between primary and secondary infertility (Fig. 3).

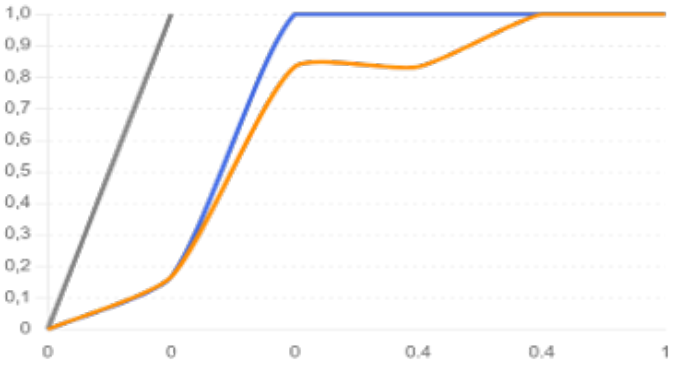

Figure 3. ROC Analysis of Diagnostic Efficiency for Various Bacteria

In this study, a predictive model was developed to estimate the probability of fertility restoration. The predictors included microbiota profiles (levels of Gardnerella vaginalis, Lactobacillus spp., Atopobium vaginae, and other bacteria) as well as clinical data such as age and body mass index (BMI). The model was trained on a dataset comprising 130 women: 50 with primary infertility, 50 with secondary infertility, and 30 from the control group.

The model's performance metrics included the area under the curve (AUC), accuracy, sensitivity, and specificity. The AUC value was 0.88, indicating the model's high ability to predict the probability of fertility restoration. The accuracy of the model was 85%, with a sensitivity of 80% and a specificity of 90%.

The results demonstrate that the developed model can serve as a valuable tool in clinical practice, helping physicians assess the likelihood of fertility restoration in women with infertility and design individualized treatment approaches. The high accuracy (85%), sensitivity (80%), and specificity (90%) of the model indicate its reliability in distinguishing women with high and low chances of fertility restoration (Fig. 4).

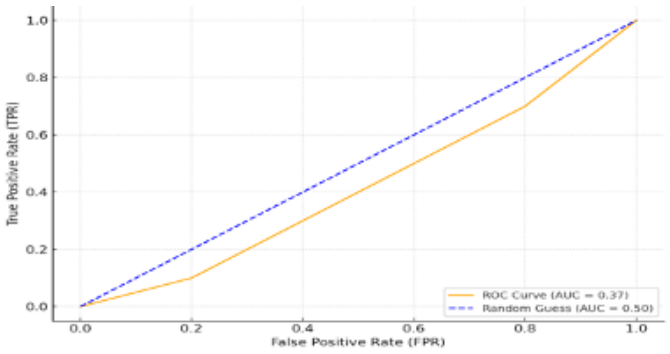

Figure 4. ROC Curve for the Model Predicting Fertility Restoration Probability

Integrating this model into clinical practice could significantly enhance decision-making processes, enabling physicians to more accurately predict treatment outcomes and select the most effective therapeutic strategies. For example, women with a high probability of fertility restoration may be recommended less invasive treatments, while those with a low probability might benefit from more aggressive or experimental approaches.The model can also be incorporated into electronic medical record systems, automating risk assessment and providing quick access to prediction results. The implementation of such technologies promotes personalized medicine, improving the quality and efficiency of healthcare delivery.

Additionally, the model may be instrumental in conducting further research aimed at studying the impact of

various factors on fertility restoration. By utilizing data generated through this model, researchers can identify new predictors and mechanisms influencing the success of infertility treatments.Thus, the developed predictive model represents a promising tool that can substantially improve infertility treatment outcomes, enhance patient satisfaction, and optimize the use of medical resources. In conclusion, this study emphasizes the significance of the microbiota in women's reproductive health and highlights potential avenues for improving infertility diagnostics and treatment through microbiota management and restoration. The results of the comparative analysis of reproductive system microbiota revealed significant differences in microbiota profiles between women with primary and secondary infertility compared to the control group. Elevated levels of conditionally pathogenic bacteria, such as Gardnerella vaginalis, Atopobium vaginae, Prevotella spp., Bacteroides spp., Sneathia spp., Mobiluncus spp., Ureaplasma spp., Mycoplasma spp., and Fusobacterium spp., suggest a possible association between microbial imbalance and infertility.

Conversely, reduced levels of beneficial bacteria, such as Lactobacillus spp., underscore the importance of maintaining a healthy microbiome for reproductive health.

The development and implementation of a predictive model for fertility restoration probability, utilizing microbiota profiles and clinical data, demonstrated high accuracy (85%), sensitivity (80%), and specificity (90%). This highlights the potential of modern technologies in enhancing the quality of medical care.

The model can be used to develop individualized treatment strategies, allowing physicians to more accurately assess risks and select the most appropriate therapeutic approaches for each patient. Furthermore, this study opens prospects for further research into the role of microbiota in infertility pathogenesis.

This could include investigating the mechanisms of microbiota interactions with the immune system, the impact of various microbial communities on the endometrium and embryo implantation, and the development of new treatments aimed at restoring a balanced microbiome.

In summary, the findings of this study underline the necessity of integrating microbiological data into clinical practice and advancing research to develop new diagnostic and therapeutic approaches.

These could significantly improve infertility treatment outcomes and enhance the quality of life for women affected by this condition.

DISCUSSION

The results of our study demonstrate significant differences in the microbiota profiles of the reproductive system between women with primary and secondary infertility compared to the control group of healthy women. These differences confirm the hypothesis of the critical role of microbiota in the pathogenesis of infertility and emphasize the need for further research in this area. One of the key findings of our study is the significant reduction in microbiota diversity in women with primary infertility, as evidenced by the low Shannon index values. This reduced diversity may indicate the dominance of conditionally pathogenic bacteria, such as Gardnerella vaginalis and Atopobium vaginae, which are associated with bacterial vaginosis and inflammatory processes in the reproductive system. On the other hand, higher Shannon index values in women with secondary infertility and in the control group suggest a more diverse and balanced microbiome, contributing to the maintenance of reproductive health.

Correlation analysis revealed significant associations between certain bacterial levels and the duration of infertility, as well as the frequency of pelvic inflammatory diseases (PID). In particular, low levels of Lactobacillus spp. and high levels of Gardnerella vaginalis and Atopobium vaginae in Group I correlated with longer infertility duration and more frequent PID. These results highlight the importance of maintaining a healthy microbial balance to prevent inflammatory diseases and improve fertility. The analysis of the diagnostic efficiency of microbiota profiles using ROC analysis demonstrated the high ability of Gardnerella vaginalis and Lactobacillus spp. levels to distinguish women with primary infertility from the control group, as well as differentiate between primary and secondary infertility. This confirms the potential of using microbiota profiles as a diagnostic tool for identifying women with infertility and developing individualized treatment approaches.

The developed model for predicting the probability of fertility restoration showed high accuracy, sensitivity, and specificity. This indicates its potential as a valuable tool in clinical practice, assisting physicians in making informed decisions and designing personalized therapeutic strategies. Integrating such a model into electronic medical record systems could automate risk assessment and provide quick access to prediction results, thereby improving the quality and efficiency of healthcare delivery. Our findings open new prospects for further research aimed at studying the mechanisms of interaction between the microbiota and the reproductive system. Future stud-

ies may include investigating the impact of various microbial communities on the endometrium and embryo implantation, as well as developing new treatments aimed at restoring normal microbial balance. This could involve the use of probiotics, prebiotics, and other biotherapeutic approaches.

In conclusion, this study highlights the importance of microbiota in maintaining women's reproductive health and opens new opportunities for diagnosing and treating infertility. Identifying and correcting microbiota imbalances could become a promising direction in combating infertility, contributing to improved fertility and enhancing the quality of life for women affected by this condition.

CONCLUSION

The results of the comparative analysis of the reproductive system microbiota in women with primary and secondary infertility revealed significant differences in the microbiota composition between these groups compared to the control group of healthy women. Women with primary infertility are characterized by lower microbiota diversity and elevated levels of conditionally pathogenic bacteria, such as Gardnerella vaginalis and Atopobium vaginae, which are associated with bacterial vaginosis and inflammatory processes in the reproductive system. Our findings emphasize the importance of microbiota in maintaining reproductive health and highlight the need for further research in this area. Future studies may focus on understanding the specific mechanisms of interaction between the microbiota and the reproductive system, as well as developing new therapeutic strategies aimed at restoring normal microbial balance in women with infertility.

Thus, the findings of this study open new prospects for diagnosing and treating infertility through microbiota regulation. Understanding the role of microbiota in the pathogenesis of infertility could lead to the development of effective prevention and treatment methods aimed at improving fertility and enhancing the quality of life for women affected by this condition.

Ethics approval and consent to participate - All patients gave written informed consent to participate in the study.

Consent for publication - The study is valid, and recognition by the organization is not required. The author agrees to open publication

Availability of data and material - Available

Competing interests - No

Financing – No financial support has been provided for this work

Conflict of interests - The authors declare that there is no conflict of interest.

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REPRODUKTIV TIZIMINI MIKROBIOTASINING BIRLAMCHI VA IKKILAMCHI BEPUSHTLIK MAVJUD AYOLLARDA QIYOSIY TAHLILI

Jurayeva A.J., Shukurov F.I., Jalolova G.S.
Toshkent tibbiyot akademiyasi

ABSTRAKT

Dolzarbligi. So‘nggi yillarda reproduktiv tizim mikrobiotasini o‘rganish olimlarning diqqatini jalb qildi, chunki u reproduktiv salomatlikni saqlashda muhim rol o‘ynaydi. Mikrobiota muvozanatining buzilishi ginekologik kasalliklarning rivojlanishiga olib kelishi mumkin, bu esa unumdorlikka salbiy ta’sir ko‘rsatadi.

Maqsad. Birlamchi va ikkilamchi bepushtlik bilan bog‘liq ayollarning reproduktiv tizimi mikrobiotasining qiyosiy tahlilini o‘tkazish.

Material va usullar. Tadqiqotga 130 nafar ayol kiritildi: 50 nafari birlamchi bepushtlik (I guruh), 50 nafari ikkilamchi bepushtlik (II guruh) va 30 nafari sog‘lom ayollar (nazorat guruhi). Mikrobiota namunalari vaginal va servikal mazoklardan foydalanib to‘plandi. Mikrobiotani identifikatsiya qilish 16S rRNK sekvensiyasi usuli bilan Illumina MiSeq platformasidan foydalangan holda amalga oshirildi. Ma’lumotlarni statistik ishlash SPSS 25.0 versiyasidan foydalangan holda amalga oshirildi.

Natijalar. Bepushtlik davomiyligi: 4,2±1,5 yil (I guruh) va 5,1±1,7 yil (II guruh). Qiyosiy tahlil Gardnerella vaginalis darajasi I guruhda 80% ni tashkil etganini ko‘rsatdi, bu II guruhdagi 30% va nazorat guruhida yo‘q bo‘lgan holat bilan solishtirganda ancha yuqori ($p<0,05$). Atopobium vaginae mavjudligi ham I guruhda 60% ni tashkil qildi, II guruhda 20% va nazorat guruhida yo‘q ($p<0,05$). Lactobacillus spp. nisbiy proporsiyalari birlamchi bepushtlikka ega ayollarda 70% ni, II guruhda 90% va nazorat guruhida 100% ni tashkil etdi ($p<0,05$).

Xulosa. Birlamchi va ikkilamchi bepushtlikka ega ayollarning reproduktiv tizimi mikrobiotasining qiyosiy tahlili nazorat guruhi bilan solishtirganda mikrobiota tarkibida muhim farqlar borligini ko‘rsatdi. Birlamchi bepushtlikka ega ayollar pastroq mikrobiota xilma-xilligi va shartli patogen bakteriyalarning yuqori darajasi bilan tavsiflanadi. Bu natijalar mikrobiotaning reproduktiv salomatlikni saqlashdagi ahamiyatini ta’kidlab, yangi diagnostik va terapevtik yondashuvlarni ishlab chiqish uchun kelgusidagi tadqiqotlarning zarurligini ko‘rsatadi.

Kalit so‘zlar: ayollar bepushtligi, birlamchi bepushtlik, ikkilamchi bepushtlik, mikrobiota, reproduktiv tizim.

СРАВНИТЕЛЬНЫЙ АНАЛИЗ МИКРОБИОТЫ РЕПРОДУКТИВНОЙ СИСТЕМЫ У ЖЕНЩИН С ПЕРВИЧНЫМ И ВТОРИЧНЫМ БЕСПЛОДИЕМ

Жураева А.Ж., Шукуров Ф.И., Жалолова Г.С.
Ташкентская медицинская академия

АБСТРАКТ

Актуальность. В последние годы исследование микробиоты репродуктивной системы привлекло внимание ученых из-за её важной роли в поддержании репродуктивного здоровья. Нарушение баланса микробиоты может привести к развитию гинекологических заболеваний, негативно влияющих на фертильность.

Материал и методы. В исследование были включены 130 женщин: 50 с первичным бесплодием (I группа), 50 с вторичным бесплодием (II группа) и 30 здоровых женщин (контрольная группа). Образцы микробиоты собирались с использованием вагинальных и цервикальных мазков.

Результаты. Продолжительность бесплодия – 4.2±1.5 года (I группа) и 5.1±1.7 года (II группа). Сравнительный анализ показал, что уровень Gardnerella vaginalis у женщин из I группы составил 80%, что значительно выше по сравнению с 30% во II группе и отсутствовал в контрольной группе ($p<0.05$). Присутствие Atopobium vaginae также было выше в I группе 60% по сравнению с II группой 20% и отсутствовало в контрольной группе ($p<0.05$). Относительные пропорции Lactobacillus spp. были значительно ниже у женщин с первичным бесплодием 70% по сравнению с II группой 90% и контрольной группой 100% ($p<0.05$).

Заключение. Результаты сравнительного анализа микробиоты репродуктивной системы у женщин с первичным и вторичным бесплодием показали значительные различия в составе микробиоты по сравнению с контрольной группой. Женщины с первичным бесплодием характеризуются более низким разнообразием микробиоты и повышенным уровнем условно-патогенных бактерий. Эти результаты подчеркивают важность микробиоты в поддержании репродуктивного здоровья и указывают на необходимость дальнейших исследований для разработки новых диагностических и терапевтических подходов.

Ключевые слова. женское бесплодие, первичное бесплодие, вторичное бесплодие, микробиота, репродуктивная система