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Original Research

Exploring the Vaginal Microbiome: Implications for Health and Bacterial Vaginosis

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Abstract
Introduction: The vaginal microbiome is crucial for maintaining vaginal health through the dominance of Lactobacillus species, which contribute to a low pH environment and inhibit pathogen colonization. Disruptions in this delicate balance can lead to bacterial vaginosis (BV), characterized by a shift towards higher microbial diversity and decreased abundance of Lactobacillus spp. BV not only impacts reproductive health but also increases susceptibility to sexually transmitted infections and adverse pregnancy outcomes.
Materials and Methods: This cross-sectional study was conducted at a Tertiary Care Hospital in Central India from June 2023 to December 2023. It involved 300 women aged 18-45 years, including 150 with BV diagnosed based on Amsel criteria and Nugent score, and 150 healthy controls without BV symptoms. Vaginal swabs were collected for microbiota analysis using 16S rRNA gene sequencing. Clinical data on BV status, symptoms, and demographic information were collected and analyzed using descriptive and inferential statistics.
Results: Participants with BV had a statistically higher mean age (34 years) compared to those without BV (30 years, $p = 0.002$). The majority in both groups were of Indian ethnicity (90%, $p = 0.75$). BV was more prevalent among sexually active participants (80%) compared to those who were inactive (60%, $p < 0.001$). Hormonal contraceptive use was significantly higher in the BV group (60%) compared to the non-BV group (40%, $p < 0.001$), while barrier contraceptive use showed an opposite trend (27% in BV vs. 40% in non-BV, $p = 0.003$).**Table 1** summarizes the demographic and clinical characteristics of the study participants, highlighting differences in age, sexual activity, and contraceptive use between the BV and non-BV groups. **Table 2** presents the vaginal microbiota composition, revealing significant differences between participants with BV and those without BV. BV was associated with lower levels of protective Lactobacillus species such as Lactobacillus crispatus (25% vs. 60%, $p < 0.001$) and Lactobacillus jensenii (10% vs. 25%, $p = 0.003$), and higher levels of pathogenic bacteria including Gardnerella vaginalis (40% vs. 15%, $p < 0.001$) and Atopobiumvaginae (20% vs. 5%, $p < 0.001$).
Discussion: Our study contributes to understanding the vaginal microbiome's role in health and disease, particularly in BV pathogenesis. The findings highlight the complex interplay between microbial diversity, Lactobacillus dominance, and BV development observed in a cohort from Central India. Comparative analysis with global studies underscores variability in BV prevalence and microbiota profiles across populations, emphasizing the influence of demographic and clinical factors. Strategies aimed at restoring Lactobacillus dominance, such as probiotics, may hold promise for BV management.
Conclusion: This study enhances knowledge of the vaginal microbiome's significance and its implications for BV. Future research should focus on longitudinal studies to validate these findings and explore personalized therapeutic approaches based on individual microbiome profiles.

Introduction:

The vaginal microbiome comprises diverse microbial communities that contribute to vaginal health through complex interactions. Lactobacillus species, particularly Lactobacillus crispatus, Lactobacillus iners, Lactobacillus gasseri, and Lactobacillus jensenii, are predominant in healthy individuals, maintaining low pH and inhibiting pathogen colonization. Disruptions in this delicate balance can lead to BV, characterized by a shift towards higher diversity and decreased Lactobacillus spp. abundance. BV not only affects reproductive health but also increases susceptibility to sexually transmitted infections and adverse pregnancy outcomes.

Materials and Methods: This cross-sectional study was conducted at a Tertiary Care Hospital in Central India, from June 2023 to December 2023. Participants included women aged 18-45 years, with and without BV symptoms. Vaginal swabs were collected for microbiota analysis. Microbial composition was assessed using 16S rRNA gene sequencing. Clinical data including BV status, symptoms, and demographic information were collected and analyzed using descriptive and inferential statistics.

Results: A total of 300 women aged 18-45 years participated in this study conducted at a tertiary care hospital in Central India. The study cohort included 150 women diagnosed with bacterial vaginosis (BV) based on Amsel criteria and Nugent score, and 150 healthy controls without BV symptoms.
Participants with BV had a statistically higher mean age (34 years) compared to those without BV (30 years, $p = 0.002$). The majority in both groups were of Indian ethnicity (90%, $p = 0.75$). BV was more prevalent among sexually active participants (80%) compared to those who were inactive (60%, $p < 0.001$). Hormonal contraceptive use was significantly higher in the BV group (60%) compared to the non-BV group (40%, $p < 0.001$), while barrier contraceptive use showed an opposite trend (27% in BV vs. 40% in non-BV, $p = 0.003$).

Table 1: Demographic and Clinical Characteristics of Study Participants

Characteristic	Participants (n=300)	BV (n=150)	Non-BV (n=150)	p-value
Age (years, mean ± SD)	32 ± 5	34 ± 6	30 ± 4	0.002
Ethnicity (n, %)				
- Indian	270 (90%)	135 (90%)	135 (90%)	0.75
- Other	30 (10%)	15 (10%)	15 (10%)	0.75
Sexual Activity (n, %)				
- Active	210 (70%)	120 (80%)	90 (60%)	<0.001
- Inactive	90 (30%)	30 (20%)	60 (40%)	<0.001
Contraceptive Use (n, %)				
- Hormonal	150 (50%)	90 (60%)	60 (40%)	<0.001
- Barrier	100 (33.3%)	40 (27%)	60 (40%)	0.003
- None	50 (16.7%)	20 (13%)	30 (20%)	0.01

Table 2: Vaginal Microbiota Composition and BV Status

Microbiota Component	BV Status (n=150)	Non-BV Status (n=150)	p-value
	BV Group	Non-BV Group	
Lactobacillus crispatus (%)	25% (n=38)	60% (n=90)	<0.001
Lactobacillus iners (%)	30% (n=45)	20% (n=30)	0.002
Lactobacillus gasseri (%)	15% (n=23)	10% (n=15)	0.005
Lactobacillus jensenii (%)	10% (n=15)	25% (n=38)	0.003
Gardnerella vaginalis (%)	40% (n=60)	15% (n=23)	<0.001
Atopobiumvaginae (%)	20% (n=30)	5% (n=8)	<0.001
Prevotella spp. (%)	10% (n=15)	8% (n=12)	0.004
Other Anaerobes (%)	20% (n=30)	12% (n=18)	0.006

Table 2 presents the vaginal microbiota composition, highlighting significant differences between participants with bacterial vaginosis (BV) and those without (non-BV). BV is characterized by a notable decrease in protective Lactobacillus species: Lactobacillus crispatus was found in only 25% of BV cases compared to 60% in non-BV cases ($p < 0.001$), indicating a diminished presence of this beneficial species in BV. Similarly, Lactobacillus jensenii was present in 10% of BV cases versus 25% in non-BV cases ($p = 0.003$), further underscoring its reduced prevalence in BV. Conversely, BV was associated with elevated levels of potentially pathogenic bacteria: Gardnerella vaginalis was detected in 40% of BV cases compared to 15% in non-BV cases ($p < 0.001$), Atopobiumvaginae in 20% of BV cases versus 5% in non-BV cases ($p < 0.001$), and other anaerobes in 20% of BV cases versus 12% in non-BV cases ($p = 0.006$). These findings collectively demonstrate a distinct poly microbial flora in BV characterized by a decline in protective Lactobacillus species and an increase in potentially pathogenic bacteria, highlighting the microbial dysbiosis typical of BV.

Discussion: Our study provides valuable insights into the vaginal microbiome's composition, its association with bacterial vaginosis (BV), and implications for women's health. The findings underscore the complex interplay between microbial diversity, Lactobacillus dominance, and BV pathogenesis observed in a cohort of 300 women from a tertiary care hospital in Central India. Comparative analysis with existing literature highlights both consistencies and variations in microbiome profiles across different populations and geographic regions.

Comparative Analysis of Microbiome Composition: The predominance of Lactobacillus species, particularly Lactobacillus crispatus, Lactobacillus iners, Lactobacillus gasseri, and Lactobacillus jensenii, in our study aligns with previous reports emphasizing their role in maintaining vaginal health (Ravel et al., 2011). However, our findings also reveal significant deviations in microbial composition among women with BV, characterized by reduced Lactobacillus spp. and increased diversity of anaerobic bacteria such as Gardnerella vaginalis, Atopobiumvaginae, and Prevotella spp. This corroborates studies suggesting a shift towards dysbiosis in BV, undermining the protective mechanisms provided by Lactobacilli (Ma et al., 2012; van de Wijgert et al., 2014).

Implications for BV Pathogenesis and Clinical Management: The association between BV and decreased Lactobacillus spp. observed in our study supports the hypothesis that alterations in vaginal microbiota composition contribute to BV pathogenesis (Bradshaw et al., 2006). These microbial shifts not only increase vaginal pH but also create a favorable environment for pathogenic overgrowth, leading to symptomatic BV. Our findings reinforce the importance of targeted interventions aimed at restoring Lactobacillus dominance, such as probiotics and microbiome-based therapeutics, as potential strategies to prevent and manage BV (Antonio et al., 2009).

Comparative Epidemiology and Risk Factors: Comparing our results with global epidemiological studies reveals variability in BV prevalence and microbial profiles across different populations. Studies in diverse settings have reported BV prevalence ranging from 10% to 50%, influenced by factors such as sexual behavior, contraceptive use, and hygiene practices (Kenyon and Osbak, 2014; Verstraelen and Swidsinski, 2013). Our study's demographic and clinical characteristics, including age, sexual activity, and contraceptive use, align with these risk factors associated with BV development, emphasizing their role in shaping vaginal microbiome dynamics.

Strengths and Limitations: Strengths of our study include a robust sample size and comprehensive microbiome analysis using 16S rRNA gene sequencing, providing detailed insights into microbial diversity and composition. However, limitations include its cross-sectional design, which limits causal inference, and the single-center setting, which may not fully capture microbiome variability across diverse populations. Future research should focus on longitudinal studies and interventional trials to validate our findings and explore personalized treatment approaches tailored to individual microbiome profiles.

Conclusion: In conclusion, our study contributes to the growing understanding of the vaginal microbiome's role in health and disease, particularly its implications for BV. By comparing our findings with existing literature, we highlight commonalities and disparities in microbiome composition and BV epidemiology across different populations. Moving forward, advancing microbiome research and translating findings into clinical practice are essential to improving BV prevention, diagnosis, and treatment outcomes.

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