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Exploring the intersection of vaginal microbiome diversity and health outcomes in black women: a comprehensive analysis of infectious diseases, reproductive health, and gynecological conditions

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BOSTON UNIVERSITY

ARAM V. CHOBANIAN & EDWARD AVEDISIAN SCHOOL OF MEDICINE

Thesis

**EXPLORING THE INTERSECTION OF VAGINAL MICROBIOME
DIVERSITY AND HEALTH OUTCOMES IN BLACK WOMEN: A
COMPREHENSIVE ANALYSIS OF INFECTIOUS DISEASES,
REPRODUCTIVE HEALTH, AND GYNECOLOGICAL CONDITIONS**

by

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DEDICATION

I offer my deepest gratitude to the Most Gracious, the Most Merciful, whose boundless grace and unwavering guidance have illuminated every step of this academic journey. Your presence has been the steadfast beacon, illuminating the path through every challenge and triumph.

I owe an immeasurable gratitude to my beloved family, whose unwavering love, encouragement, and sacrifices have been the cornerstone of my strength and resilience. Thank you for your endless encouragement and understanding, bringing light to even the darkest moments. Your belief in my abilities propelled me forward when doubts loomed large. Your strong belief in me has been the driving force behind every milestone reached and every obstacle overcome.

To my cherished friends, your unwavering support and companionship have been invaluable.

This thesis is a testament to the love, support, and encouragement of those who have walked alongside me. I dedicate this work with profound gratitude and love to each of you. Your presence in my life has enriched this journey beyond measure, and I am eternally thankful for that.

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I am profoundly indebted to my family for their unwavering love, encouragement, and support throughout every stage of this academic pursuit. To my beloved parents, whose boundless love and sacrifices drive my ambitions, I owe an immeasurable debt of gratitude. Your unwavering belief in me has guided me through every challenge and triumph.

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This thesis reflects the collective love, support, and encouragement of those who have been my pillars of strength. To every one of you, I extend my deepest gratitude and love. Your unwavering presence in my life has made this journey infinitely more prosperous and more meaningful; I am eternally thankful for that.

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ABSTRACT

This thesis examines the correlation between vaginal microbiome diversity and health outcomes in Black women, focusing on infectious diseases, reproductive health, and gynecological conditions. Through a synthesis of existing research and empirical analysis, the study uncovers the intricate interplay between microbial composition and health status within this demographic. Highlighting the unique physiological and socioenvironmental factors influencing vaginal microbiota in Black women, the findings underscore the importance of tailored interventions to promote optimal reproductive and gynecological health in this population.

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LIST OF ABBREVIATIONS

BV.....	Bacterial Vaginosis
CSTs	Community State Types
HIV	Human Immunodeficiency Viruses
HMP	Human Microbiome Project
HIV	Human Immunodeficiency Viruses

CHAPTER ONE

Introduction

The vaginal microbiome plays a crucial role in maintaining women's reproductive health and overall well-being. It composes a complex ecosystem of microorganisms; the vaginal microbiome influences various physiological processes, including immune regulation, protection against pathogens, and the maintenance of pH balance (Ma et al., 2012). According to recent studies, synergistic relationships between microorganisms and hosts are found in nearly every niche of the human body, conditioning its physiology and physiopathology (Punzón-Jimenez & Labarta, 2021). Likewise, the female genital tract, vagina, cervix, endometrium, fallopian tubes, and ovaries harbor their microbiome, which accounts for 9% of the total bacterial amount in the female body (Punzón-Jimenez & Labarta, 2021). While the vaginal microbiome is composed of a complex ecosystem, its composition and diversity of the vaginal microbiome can vary significantly among individuals and populations, impacting susceptibility to infectious diseases and gynecological conditions (Kwon & Lee, 2022).

Black women, in particular, experience unique challenges concerning vaginal health. Socioeconomic disparities, cultural factors, and structural inequities intersect to create distinct patterns of health outcomes within this demographic group. Despite this, research on the vaginal microbiome and its implications for Black women's health remains relatively limited, with existing studies often lacking deep, comprehensive analyses of infectious diseases, reproductive health, and gynecological conditions specific to this population. Infectious diseases such as bacterial vaginosis (BV), candidiasis, and sexually transmitted infections (STIs) disproportionately affect Black

women, highlighting the urgent need for a deeper understanding of the underlying factors contributing to these disparities. BV, characterized by a shift in the vaginal microbiota from predominantly *Lactobacillus* species to diverse anaerobic bacteria, is especially prevalent among Black women and has been linked to adverse reproductive outcomes, including preterm birth and increased susceptibility to STIs such as HIV (Chen et al., 2021). Reproductive health issues such as infertility, menstrual irregularities, and pregnancy complications also disproportionately affect Black women, further underscoring the importance of investigating the role of the vaginal microbiome in these conditions. Gynecological conditions like fibroids, endometriosis, and cervical cancer exhibit disparities in prevalence and outcomes among Black women, suggesting potential links to vaginal microbiome composition and diversity.

Understanding the complex interplay between the vaginal microbiome, infectious diseases, reproductive health, and gynecological conditions is crucial for developing targeted interventions and improving health outcomes for Black women. By conducting a comprehensive analysis that considers the unique biological, social, and environmental factors shaping vaginal health in this population, researchers can pave the way for more personalized approaches to prevention, diagnosis, and treatment. This study aims to expose the existing gaps in knowledge by exploring the intersection of vaginal microbiome diversity and health outcomes in Black women. Additionally, it seeks to elucidate the complex dynamics influencing vaginal health within this population. Ultimately, the findings have the potential to inform policies, clinical practices, and

community-based interventions aimed at promoting vaginal health equity and reducing disparities among Black women.

The diversity of the vaginal microbiome in African American women represents a multifaceted aspect of their reproductive and overall health. Understanding how this diversity influences their risk and outcomes of various health issues compared to non-African American women requires a nuanced examination that considers biological, social, and environmental factors. This research question delves into the intricate interplay between vaginal microbiome diversity and health outcomes, with a focus on the unique experiences of African American women. Research suggests significant differences in the composition of the vaginal microbiome among women of different ancestral backgrounds. For instance, studies have shown that women of European ancestry are more likely to harbor a microbiome dominated by *Lactobacillus* species.

In contrast, African American women tend to exhibit a more diverse microbial profile (Fettweis et al., 2014). This diversity has important implications for health outcomes, as African American women are not only twice as likely to be diagnosed with bacterial vaginosis but also have double the risk of experiencing preterm births (Fettweis et al., 2014). These findings underscore the intricate relationship between microbial diversity, ancestral background, and reproductive health outcomes, highlighting the need for tailored approaches in healthcare interventions.

Firstly, it is important to acknowledge the complex nature of the vaginal microbiome. The vaginal ecosystem comprises a diverse array of microorganisms, predominantly bacteria, whose composition can vary considerably between individuals

and populations. 16s rRNA sequencing was done, and community state types were characterized. Community state types (CSTs) refer to distinct compositions of microbial communities within a particular ecological niche, such as the vaginal microbiome. These CSTs categorize the microbial diversity based on predominant bacterial species and their relative abundances in the context of the vaginal microbiome. Essentially, they help characterize variations in microbial populations, particularly noting the dominance and specificity of *Lactobacillus* species.

Within the HMP framework, researchers extensively explored the vaginal microbiome in healthy volunteers using techniques such as 16S rRNA gene sequencing and metagenomics. In their investigations, they have identified five distinct CSTs in the vagina of healthy women, each characterized by dominant bacterial species and associated pH values. These CSTs span a spectrum from those dominated by *Lactobacillus* species to those with higher proportions of strictly anaerobic genera, showcasing the diverse microbial compositions and pH regulation within the vaginal environment (Punzón-Jimenez & Labarta, 2021; Fettweis et al., 2014; Chen et al., 2021). Understanding CSTs is crucial as it sheds light on the diversity and stability of the vaginal microbiome, which in turn influences women's reproductive health outcomes, susceptibility to infections, and the development of conditions like BV or STIs.

Other factors, such as hormonal fluctuations, sexual behavior, hygiene practices, and microbial interactions, shape the diversity and stability of the vaginal microbiome. In African American women, distinct microbial profiles may emerge due to genetic predispositions, cultural practices, and socioeconomic disparities, contributing to

differential health outcomes compared to non-African American women (Kwon & Lee, 2022; Fettweis et al., 2014; Wright et al., 2022). To further contextualize this point, authors of a research article written at the Virginia Commonwealth University in Richmond, VA, while also using 16S rRNA gene sequencing, discovered that “Women of European ancestry are more likely to harbor a Lactobacillus-dominated microbiome, whereas African American women are more likely to exhibit a diverse microbial profile. African American women are also twice as likely to be diagnosed with bacterial vaginosis and are twice as likely to experience preterm birth” (Fettweis et al., 2014, p. 2272). This further supports the need for this research that suggests that African American women are highly likely to exhibit higher rates of BV compared to their non-African American counterparts, with implications for reproductive health and higher susceptibility to STIs such as HIV (Wright et al., 2022).

Reproductive health outcomes represent another dimension of inquiry. Infertility, menstrual irregularities, and adverse pregnancy outcomes disproportionately affect African American women, suggesting potential links to vaginal microbiome diversity. Moreover, gynecological conditions such as fibroids, endometriosis, and cervical cancer exhibit disparities in prevalence and outcomes among African American women. Biological factors do not solely determine the composition of the vaginal microbiome, but they are also influenced by social and economic determinants of health, as well as historical contexts. Socioeconomic factors such as income, education level, access to healthcare, and living conditions can significantly impact an individual’s microbiome through various pathways. For instance, disparities in access to healthcare among

marginalized communities, including Black women, have been well-documented, leading to differences in health-seeking behaviors, quality of care received, and exposure to environmental stressors (Kwon & Lee, 2022; Fettweis et al., 2014; Wright et al., 2022). Moreover, historical injustices and systemic inequalities, such as racial discrimination and intergenerational trauma, have enduring effects on health outcomes and microbiome composition. Studies have shown that experiences of discrimination and chronic stress can dysregulate the immune system and alter microbial communities, contributing to health disparities observed in minority populations.

Historically, research in this field has been marked by a need for more comprehensive data and analysis specific to the experiences of African American women. Throughout history, African American women have faced systemic barriers to healthcare access and quality, compounded by socioeconomic inequalities, structural racism, and cultural factors. Despite bearing a disproportionate burden of reproductive and gynecological health issues, including higher rates of BV, infertility, and adverse pregnancy outcomes, their experiences have often been marginalized or overlooked in research and clinical practice.

The lack of comprehensive data on the vaginal microbiome diversity and health outcomes of African American women not only perpetuates disparities but also hinders our ability to develop targeted interventions and address root causes of health inequities. This study represents a crucial step towards closing this gap by employing advanced sequencing techniques, interdisciplinary approaches, and community engagement strategies to generate robust evidence and insights into the underlying mechanisms

driving disparities. By elucidating the role of the vaginal microbiome in shaping health outcomes, particularly in marginalized communities, we can develop more inclusive and culturally sensitive approaches to healthcare delivery and research. Moreover, amplifying the voices and experiences of African American women can challenge existing paradigms and foster greater awareness of the intersecting social determinants of health that contribute to disparities.

The focus of this research will be on examining the intersection of vaginal microbiome diversity and health outcomes in African American women, addressing historical disparities and the scarcity of comprehensive data in this area. The introduction will provide an overview of the vaginal microbiome's significance in women's health, highlighting the historical neglect of African American women's experiences in research. It will underscore the importance of addressing health disparities and promoting health equity, setting the stage for the study's objectives and hypotheses.

The literature review will encompass an examination of the vaginal microbiome's composition, dynamics, and its implications for health outcomes. Special attention will be given to disparities in reproductive and gynecological health among African American women and existing evidence linking vaginal microbiome diversity to these outcomes. Methodologies in vaginal microbiome research will be explored, including advanced sequencing techniques and analytical approaches, with considerations for data collection, analysis, and interpretation.

The methodology section will detail the study design, using keywords such as participant recruitment, sampling methods, and data collection procedures. It will outline

the bioinformatics and statistical analyses used to analyze the data, ensuring robustness and reliability. An examination of methodologies employed in vaginal microbiome research will be undertaken, emphasizing the utilization of advanced sequencing techniques and analytical methodologies. The focus will be on elucidating the processes involved in data collection, analysis, and interpretation within the context of literary exploration rather than strict adherence to empirical research protocols.

Results will present descriptive analyses of vaginal microbiome diversity among African American women compared to non-African American women, as well as associations between microbial profiles and health outcomes. The discussion section will interpret findings concerning research objectives and hypotheses, discuss implications for health equity and offer recommendations for policy, practice, and future research. Limitations and potential biases will be critically assessed, with suggestions for addressing these in future studies.

In conclusion, the thesis will summarize key findings, highlight the study's contribution to knowledge, and emphasize the importance of its findings for advancing health equity. It will underscore the need for continued research to address remaining gaps and promote inclusive healthcare practices for all women. It also seeks to fill this critical gap in knowledge and catalyze efforts to dismantle health disparities by elucidating the complex interplay between vaginal microbiome diversity and health outcomes within this demographic group.

CHAPTER TWO

Literature Review and Discussion

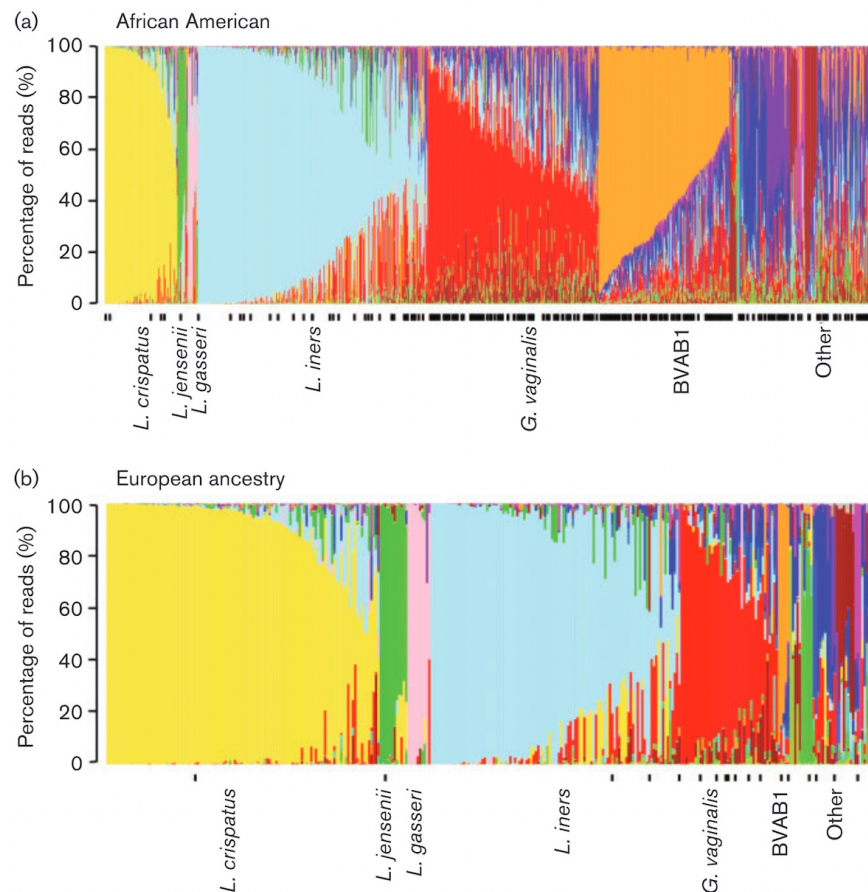
Community State Types

This research aims to delve deeper into the conventional understanding of a healthy vaginal microbiome, mainly focusing on its implications for Black women who exhibit heightened vulnerability to various illnesses. To be able to understand this complex relationship, it is essential first to understand how previous researchers have classified the vaginal microbiota in its healthy state. To classify the vaginal microbiota, a 16S rRNA gene sequence analysis was performed by the HMP at Virginia Commonwealth University (Punzón-Jimenez & Labarta, 2021; Fettweis et al., 2014; Chen et al., 2021). The 16S rRNA gene amplification sequencing uncovered five of the significant vaginal community state types that today identify a healthy vaginal microbiome. While doing so, the results of this extensive and precise gene sequencing showed significant variations in the vaginal microbiomes between women of European and African American descent. They highlighted several taxa associated with these changes.

As shown in Figure 1, these vaginal CSTs are a classification system used to categorize the microbial composition of the vaginal microbiome (Fettweis et al., 2014). These classifications help researchers and healthcare providers understand variations in vaginal health and how they relate to various conditions, such as BV or vaginal infections. These vaginal CSTs are a classification system used to categorize the microbial composition of the vaginal microbiome. These classifications help researchers and healthcare providers understand variations in vaginal health and how they relate to various conditions, such as bacterial vaginosis (BV) or vaginal infections. Recent

research in the field of vaginal microbiology has shed light on the significance of CSTs in determining women's reproductive health. Studies have elucidated the distinct microbial compositions characterizing CSTs I through V, each reflecting a different balance of bacterial species within the vaginal ecosystem. Notably, CSTs I and II, dominated by *Lactobacillus crispatus* and *Lactobacillus gasseri*, respectively, have been consistently associated with vaginal health due to their ability to maintain an acidic environment and inhibit pathogenic organisms (Fettweis et al., 2014).

Figure 1: Vaginal Community State Types (CSTs). CSTs serve as a classification system for categorizing the microbial composition of the vaginal microbiome (adapted from Fettweis et al., 2014).



Conversely, CSTs III through V, marked by a decrease in *Lactobacilli* and an increase in diverse anaerobic bacteria, have been linked to conditions such as BV and heightened susceptibility to STIs and particularly those associated with dysbiosis and vaginal infections and can be indicative of an imbalance in the vaginal microbiome (Zheng et al., 2021; Wright et al., 2022). Aligned with this point, Ma et al. explain that *Lactobacillus* species, identified as the hallmark of a healthy vagina since the late 19th century by Donderlein, are believed to play a crucial role in safeguarding the vaginal environment against foreign and potentially harmful microorganisms. (Ma et al., 2012). This classification system not only provides insights into the diversity of vaginal microbiomes but also offers valuable implications for personalized healthcare interventions aimed at restoring and maintaining vaginal health.

While these CSTs offer valuable insights into the microbial ecology of the vaginal microbiome, expounding on the significance of CSTs warrants a deeper analysis of specific bacterial species, particularly within the *Lactobacillus* genus a, is necessary. Throughout the research process, a significant trend emerged, highlighting the clear differentiation between the healthy state and dysbiosis of the vaginal microbiome. Mainly, this revolved around the abundance or absence of *Lactobacillus crispatus* and *Lactobacillus iners*, prompting a deeper investigation into these two species.

Among the diverse array of *Lactobacillus* species inhabiting the vaginal microbiota, *Lactobacillus crispatus* stands out for its profound implications on vaginal health and disease susceptibility. A closer examination of *Lactobacillus crispatus* reveals its pivotal role in maintaining vaginal homeostasis through various mechanisms,

including the production of lactic acid and bacteriocins, competitive exclusion of pathogens, and modulation of host immune responses. In support of this claim, Chee et al. study states that *Lactobacillus crispatus* dominated vaginal microbiota (CST I) is always associated with a healthy vagina (Chee et al., 2020). Studies have consistently shown that *L. crispatus*-dominated CSTs are associated with a lower risk of acquiring sexually transmitted infections (STIs), such as HIV, chlamydia, and gonorrhea, highlighting the protective effects conferred by this species.

Lactobacillus Crispatus

Furthermore, *L. crispatus* dominance is linked to decreased susceptibility to bacterial vaginosis (BV), a common dysbiosis condition characterized by an overgrowth of anaerobic bacteria and associated with adverse reproductive outcomes. Similarly, a study evaluating the modulatory activities of lactobacillus strains found that *L. crispatus* seems to play a role in preserving the balance of the vaginal environment by aiding the immune defenses of the vagina without provoking inflammation. Additionally, it decreases the levels of proinflammatory cytokines, which tend to rise during bacterial vaginosis. (Argentini et al., 2022). Moreover, recent research indicates that the presence of *L. crispatus* may influence the composition and stability of the vaginal microbiota, promoting a symbiotic environment conducive to women's health. Conversely, dysbiosis, characterized by the depletion of *L. crispatus* and the proliferation of pathogenic bacteria, is implicated in various gynecological conditions, including BV, preterm birth, and endometritis.

Within the intricate landscape of the vaginal microbiota, *Lactobacillus iners* also emerges as a significant yet enigmatic player, warranting a closer examination to unravel its roles in women's health and disease susceptibility. Despite its widespread presence in the vaginal microbiota, *L. iners* exhibits unique characteristics distinct from other *Lactobacillus* species, challenging the conventional paradigms of vaginal health and microbial ecology. Expounding on the significance of CSTs necessitates a deeper analysis of *L. iners* to elucidate its implications for vaginal homeostasis and disease pathogenesis.

Lactobacillus iners

A closer inspection of *Lactobacillus iners* reveals its versatile adaptation strategies and dynamic interactions within the vaginal ecosystem. Unlike *L. crispatus*, which is associated with stable and resilient vaginal communities, *L. iners* demonstrates a more transient and heterogeneous colonization pattern, often coexisting with diverse bacterial species in polymicrobial biofilms. This idea is supported by Chen et al., who writes, "Different from other *Lactobacillus* species, *L. iners* cannot generate D-lactic acid, which plays a more important role than L-lactic acid" (Chen et al., 2021, pg 3). The review by Zheng et al. titled "The Role of *Lactobacillus iners* in Vaginal Health and Diseases" emphasizes how *L. iners* differs from other common *Lactobacillus* species in the vagina by producing only L-lactic acid instead of both D- and L-lactic acid. This is because *L. iners* lacks the gene needed to produce D-lactic acid, unlike *L. crispatus*, *L. gasseri*, and *L. jensenii*, which can produce both types through glycogen fermentation (Zheng et al., 2021). Therefore, a higher L/D lactic acid ratio is observed in *L. iners*.

Research by Witkin et al. in 2013 showed that various forms of lactic acid affect the body's immune system differently. In the vagina, *L. iners* tend to increase the ratio of L to D lactic acid. This change can raise extracellular matrix metalloproteinase inducer (EMMPRIN) levels, which then activates another substance called matrix metalloproteinase-8 (MMP-8). Essentially, MMP-8 helps break down the tissue surrounding cells, which can help bacteria move through the cervix and potentially cause infections in the upper genital tract, as explained by Beghini et al. in 2015 (Zheng et al., 2021). Additionally, studies by Tachedjian et al. suggest that D-lactic acid exhibits a more substantial inhibitory effect on exogenous bacteria than L-lactic acid. Therefore, the predominant L-lactic acid production by *L. iners* may render it less effective in preventing pathogen invasion (Zheng et al., 2021). The basis of this review further highlights how *L. iners* differs from other vaginal *Lactobacillus* species by producing only L-lactic acid due to lacking the gene for D-lactic acid production. This unique feature may make *L. iners* less effective in inhibiting pathogen invasion compared to other *lactobacilli*, potentially affecting vaginal health. Furthermore, *L. iners* is often regarded as a transitional or intermediate species in vaginal microbiota dynamics, and its presence is associated with both protective and pathogenic outcomes, depending on contextual factors such as host genetics, hormonal fluctuations, and environmental exposures.

Lactobacillus crispatus & Lactobacillus iners

The comparison between the two bacterial species, *Lactobacillus crispatus* and *Lactobacillus iners*, reveals notable differences in their potential protective effects on reproductive health. *L. crispatus* appears to be more beneficial due to its association with greater stability in the vaginal microbiome, contrasting with *L. iners*, which is linked to transitions between different vaginal microbiome communities (Wright et al., 2022). Additionally, *L. iners*, particularly when dominant in the vaginal ecosystem (CST III), is more susceptible to vaginal dysbiosis, whereas *L. crispatus* dominance (CST I) is consistently associated with vaginal health (Chee et al., 2020). Studies also suggest that *L. crispatus* exhibits protective effects against STIs, BV, and vulvovaginal candidiasis through its ability to produce lactic acid and bacteriocin, unlike *L. iners*, thereby maintaining vaginal health (Chee et al., 2020; Muzny et al., 2020). In contrast, *L. iners* lacks the essential amino acid synthesis capabilities, relying heavily on host-derived nutrients, which renders it highly sensitive to environmental changes (Chee et al., 2020). Also affirming this similar relationship, Muzny et al. found that the crucial protective function of vaginal lactobacilli involves producing lactic acid by fermenting glycogen by-products.

This process helps acidify the cervicovaginal microenvironment, maintaining a pH below 4.5.(Muzny et al., 2020). This information underscores the importance of the distinct characteristics of these two bacterial species in modulating vaginal health. This information highlights the significance of the distinct characteristics of these two bacterial species in modulating vaginal health, showcasing the potential of *L. crispatus* as a more protective agent in maintaining reproductive health. Recent studies have delved

deeper into this aspect through comparative analyses of the vaginal microbiome across various demographic groups, with a primary focus on identifying differences between non-African American women and African American women.

Disparities in the prevalence and composition of CSTs have emerged as a focal point of the investigation, highlighting potential racial and ethnic differences in vaginal microbial profiles and their implications for women's health. Studies have indicated that African American women tend to exhibit a higher and more diverse prevalence of CSTs III, IV, and V, characterized by decreased levels of lactobacilli and increased microbial diversity, compared to non-African American women (Fettweis et al., 2014; Chen et al., 2021; Ma et al., 2012). These distinctions in CSTs distribution suggest a potential contributor to disparities in reproductive health outcomes, including elevated rates of BV and STIs observed in African American women. Understanding the underlying factors driving these disparities is crucial for developing targeted interventions aimed at promoting vaginal health equity across diverse populations.

Bacterial Vaginosis

BV, a common vaginal infection, presents a complex interplay between the vaginal microbiota and its disruption. The vaginal microbiota typically consists of a diverse array of microorganisms, predominantly *lactobacilli*, which overall plays a crucial role in maintaining vaginal health by producing lactic acid, maintaining an acidic pH, and preventing the overgrowth of harmful bacteria (Zheng et al., 2021; Wright et al., 2022). However, when this delicate balance is disturbed, often characterized by a decrease in *lactobacilli* and an increase in anaerobic bacteria such as *Gardnerella*

vaginalis, *Atopobium vaginae*, and *Prevotella species*, BV can occur. (Muzny et al., 2020). The disruption of the vaginal microbiota can stem from various factors, including sexual activity, hormonal fluctuations, antibiotic usage, douching, and other environmental influences. The repercussions of such disruption manifest in the form of clinical symptoms and signs. Women with BV commonly experience vaginal discharge with a characteristic fishy odor, which is particularly noticeable after sexual intercourse or during menstruation (Chen et al., 2021). Additionally, some may report vaginal itching, irritation, and discomfort. Moreover, BV increases the risk of adverse reproductive health outcomes, including preterm birth, pelvic inflammatory disease, and an enhanced susceptibility to sexually transmitted infections such as HIV, herpes simplex virus, Chlamydia trachomatis, and Neisseria gonorrhoeae (Chen et al., 2021).

The disruption of the vaginal microbiota in BV is not merely symptomatic, but it also involves intricate alterations at the microbial level, leading to dysbiosis. This dysbiosis is characterized by a decrease in the abundance and diversity of lactobacilli, coupled with an overgrowth of anaerobic bacteria, resulting in a shift towards a higher vaginal pH. Chen et al. further explains that in cases of dysbiosis and low stability, the vaginal microbiota is often dominated by *L. iners*. Conversely, the presence of *L. crispatus* typically correlates with vaginal health and high stability, as it produces both D- and L-lactic acids (Chen et al., 2021). The production of malodorous volatile amines, such as trimethylamine and putrescine, by anaerobes further exacerbates the clinical manifestations of BV (Chen et al., 2021). Moreover, when the absence of *lactobacilli*

diminishes the production of antimicrobial compounds, thereby compromising the vaginal epithelial barrier and allowing for the proliferation of pathogenic bacteria.

The relationship between BV and the vaginal microbiota extends beyond clinical manifestations to encompass epidemiological, immunological, and therapeutic dimensions. Figure 2 illustrates the complex interplay between BV and the vaginal microbiota, as well as the distinctions between healthy and unhealthy compositions, as described by Fettweis et al. 2014. Epidemiologically, BV demonstrates racial and ethnic disparities, with higher prevalence rates observed among Black and Hispanic women compared to white women, underscoring the influence of genetic and socioeconomic factors on vaginal health.

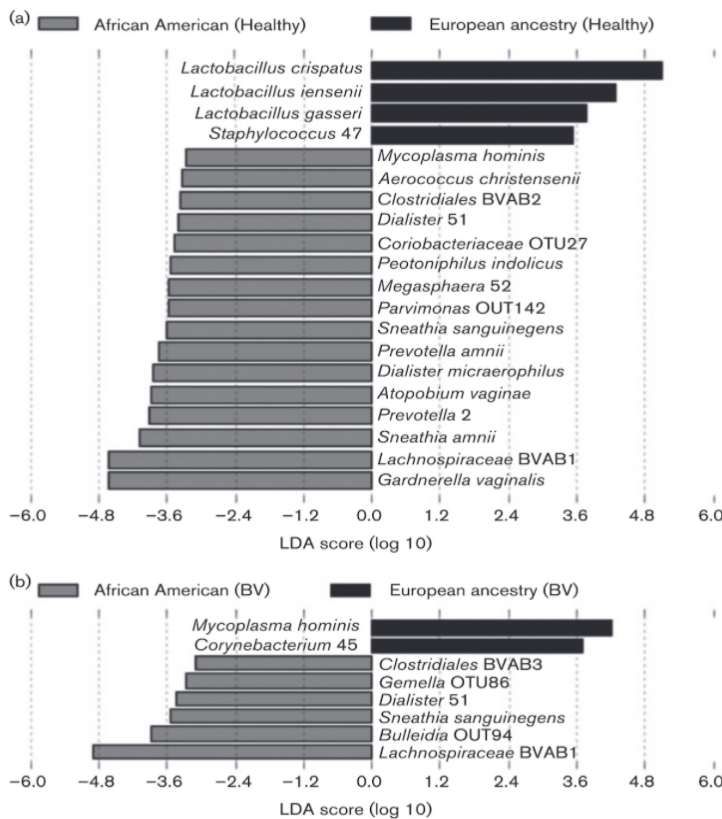


Figure 2: The Complex Interplay Between Bacterial Vaginosis (BV) and Vaginal Microbiota: Illustration depicting the intricate relationship between bacterial vaginosis (BV) and the vaginal microbiota, highlighting differences between healthy and unhealthy compositions between women of African American and European ancestry (adapted from Fettweis et al. 2014).

With the data collected today, what is known of a healthy vaginal microbiome significantly depends on its abundance of *Lactobacillus*. In a study by Michelle Wright in the Journal of Women's Health, the main objective was to explore the relationship of the protective bacteria in Black women's vaginal flora. To do so, Wright observed a group of pregnant African American women during their 8-14th week of pregnancy. It was concluded that sociodemographic significantly affected *Lactobacillus* abundance in African American women. Considering substance abuse, sexual practices, vaginal products and antibiotic exposure, results demonstrate that these factors contributed to the lack of *Lactobacillus* and, subsequently, the abundance and presence of more diverse non-lactobacillus vaginal microbiota (Wright et al., 2022).

A recent research article comparing the normalcy of the vaginal microbiome versus its dysbiosis published in 2021 also described the relationship of *Lactobacillus* in white women of European descent versus the lack of this bacteria in black women. The article states that the normal bacteria found in the vagina, mainly *lactobacilli*, are more common in women of European descent than in African American women. In comparison, the microbial composition in African Americans consists of a more *L. inner-*dominated *lactobacillus* species, while also more diverse, which negatively affects this group (Fettweis et al., 2014). A study by Donald J. Alcendor also supports this claim. He explains that African American women are disproportionately affected by BV due to the composition of their vaginal microbiome, which, as we now can say, is predominantly characterized by *Lactobacillus iners*, as opposed to white women whose vaginal

microflora is *L. crispatus* dominated (Alcendor, 2016). This difference is significant as high levels of *L. crispatus* are associated with a low vaginal pH.

In contrast, women with high levels of *L. iners* exhibit both high and low vaginal pH (Chen et al., 2021). Moreover, while a minority of women of African descent with *L. crispatus* predominance show low inflammatory states in the cervicovaginal mucosa, many of these women harbor diverse cervicovaginal bacterial communities with a low abundance of *lactobacilli*, which in turn potentially predisposes them to a higher inflammatory state (Alcendor, 2016). To further contextualize and support these findings, a 2018 article by Coleman and Gaydos also found that because this protective barrier bacteria (*L. crispatus*) is lacking in Black women's vaginal microbiome, they are more likely to develop bacterial vaginosis than white women (Coleman & Gaydos, 2018). Figure 2 illustrates the complex interplay between bacterial vaginosis (BV) and the vaginal microbiota, as described by (Fettweis et al., 2014).

Studies comparing women from developed and developing countries further underscore disparities, with a significantly lower proportion of *lactobacillus*-dominant cervicovaginal bacterial communities among African descent women from developing countries (Alcendor, 2016). Notably, a substantial majority of South African women with *lactobacillus*-dominant cervicovaginal communities (77%) are colonized with *Lactobacillus iners*. These findings highlight the complex interplay between race, microbial composition, and susceptibility to BV, emphasizing the need for tailored interventions addressing microbiome variations in this community.

Sexually transmitted infections (STIs) exert a significant influence on the delicate equilibrium of the vaginal microbiome, often resulting in microbial disruption. The vaginal microbiome, primarily composed of lactobacilli, is crucial for maintaining vaginal health through mechanisms such as lactic acid production and pH regulation. However, factors like sexual activity, hormonal fluctuations, and antibiotic usage can disrupt this balance, rendering the vaginal microbiome susceptible to dysbiosis.

Sexually Transmitted Illnesses

STIs like chlamydia, gonorrhea, syphilis, herpes simplex virus (HSV), human papillomavirus (HPV), and human immunodeficiency virus (HIV) not only pose health risks but also impact the vaginal microbiome (Alcendor, 2016). These infections can disturb the vaginal ecosystem through mechanisms like inflammation, pH alteration, and immune response modulation. For example, HPV infections can lead to local inflammation and epithelial damage, contributing to microbial dysbiosis (Gravitt et al., 2017). Furthermore, the immunosuppressive effects of HIV compromise the host's ability to maintain a healthy vaginal microbiome, facilitating the growth of pathogenic bacteria.

Like the relationship between BV, vaginal pH, and susceptibility to infections like HIV/AIDS, particularly in Black women, is intricate and multifaceted (Fettweis et al., 2017). As stated previously, Black women, especially those of African descent, often harbor diverse genital bacterial communities with low levels of *lactobacilli*, such as *Lactobacillus iners*, differing from the prevalence of *Lactobacillus crispatus* in other racial groups, which may contribute to variations in vaginal pH and susceptibility to infections. Black women face disproportionately high rates of HIV/AIDS, linked to

factors including the increased prevalence of herpes simplex virus type 2 (HSV-2) infection (Alcendor, 2016). As it is also known, *Lactobacilli* plays a crucial role in vaginal health by regulating pH levels and producing hydrogen peroxide, which inhibits HIV transmission.

Consequently, low levels of these lactobacilli increase the risk of HIV-1 infection. Genetic variations, particularly in cytokine genes, may influence cervical cytokine levels and inflammatory responses, affecting susceptibility to infections such as HIV/AIDS, especially in the presence of conditions like BV. BV can enhance HIV-1 replication, increase vaginal shedding of HIV, and induce HIV transcriptional activation and replication, potentially by affecting the structural integrity of the vaginal epithelium and heightening inflammation, thereby increasing the recruitment of cells susceptible to HIV infection (Alcendor, 2016). The relationship between STIs and vaginal microbiome disruption is not just associative; it involves a bidirectional interplay with significant clinical implications (Alcendor, 2016; Fettweis et al., 2014). On the one hand, alterations in the vaginal microbiome can increase susceptibility to STIs by weakening natural defense mechanisms against pathogens (Fettweis et al., 2014).

Conversely, STIs, like HIV, can exacerbate vaginal microbiome disruption. The consequences of STI-induced vaginal microbiome disruption are manifold, impacting reproductive health and beyond by promoting microbial dysbiosis through inflammation-mediated changes, epithelial barrier disruption, and immune modulation (Alcendor, 2016). Along with raising the risk of contracting STIs, microbial disruption can

predispose individuals to a multitude of gynecological conditions, such as adverse pregnancy outcomes like preterm birth and low birth weight (Price et al., 2022).

Gynecological Conditions

Preterm birth, a critical issue in obstetrics, continues to pose significant challenges in maternal and neonatal healthcare worldwide, especially in African American women. The mechanisms through which alterations in vaginal microbiota contribute to preterm birth are multifaceted. Firstly, dysbiosis can trigger inflammatory responses within the reproductive tract, producing pro-inflammatory cytokines and chemokines. These inflammatory mediators can weaken the fetal membranes and induce uterine contractions, ultimately culminating in preterm labor. The composition of vaginal microbiomes varies among asymptomatic women, with ethnicity playing a significant role. While women of European and Asian descent typically have a microbiome dominated by *Lactobacillus*, African, African American, and Hispanic women often have a more diverse microbiome not dominated by *Lactobacillus* (Florova et al., 2021; Fettweis et al., 2014; Zheng et al., 2021). Despite being asymptomatic, these women face a higher risk of pregnancy complications. During normal pregnancy, there is an increase in *Lactobacillus* dominance in the vaginal microbiome across ethnicities, but a diverse non-*Lactobacillus*-dominant microbiome may increase the risk of preterm birth, a leading cause of perinatal morbidity and mortality (Florova et al., 2021; Fettweis et al., 2014; Zheng et al., 2021).

During normal pregnancy, there is an increase in *Lactobacillus* dominance in the vaginal microbiome across ethnicities, but a diverse non-*Lactobacillus*-dominant

microbiome may increase the risk of preterm birth, a leading cause of perinatal morbidity and mortality (Florova et al., 2021; Fettweis et al., 2014; Zheng et al., 2021). Recent studies suggest a link between non-Lactobacillus vaginal bacteria and preterm birth, particularly in African American women, with specific bacterial taxa being more abundant in women delivering preterm. A study conducted by Tracy A. Manuck provides evidence to show that non-Hispanic Black women face twice the risk of preterm birth compared to non-Hispanic white women (Manuck, 2017). Her work is crucial to the study because she points out that the disparity in preterm birth rates among African American women compared to other racial and ethnic groups can be attributed to various factors.

Genetic studies have shown that differences in allele frequencies across the genome, particularly from the maternal side, can influence the likelihood of preterm birth, with higher proportions of black genes correlating with increased risk (Manuck, 2017). For instance, specific genotypes that offer protection against preterm birth in European-Americans may not have the same effect on African Americans, precisely the microbial vaginal composition of lactobacillus species (Fettweis et al., 2014). Expanding on this idea further, Fettweis et al. did a group study consisting of mainly African American women who looked at various factors to find signs of preterm birth. It was discovered that mothers who had preterm births had less of a specific bacterium, *Lactobacillus crispatus*, in their vagina (Fettweis et al., 2019).

Through a cohesive examination of the subject matter, a unified understanding emerges that the higher prevalence of BV during pregnancy among non-Hispanic Black

women, coupled with a greater likelihood of having a diverse vaginal microbiome rather than a *Lactobacillus*-dominant one, contributes to increased vulnerability to intra-amniotic infection and preterm birth (Manuck, 2017). These factors in their study collectively underline both genetic and environmental influences in addressing the disparities in preterm birth rates among different racial and ethnic populations, and more specifically in African American women.

CHAPTER THREE

Introduction to Methodology

The methodology employed in this thesis serves as a robust framework for investigating the complex interplay between vaginal microbiome diversity and various health outcomes experienced by Black women. A comprehensive analysis encompassing infectious diseases, reproductive health, and gynecological conditions is central to this exploration. This introduction delineates the research design, literature review process, data collection methods, and analytical procedures employed to understand this critical intersection.

At the heart of this study lies a qualitative research design, acknowledging the multifaceted nature of the phenomena under investigation. Qualitative methodologies afford a nuanced understanding of the lived experiences, perceptions, and socio-cultural contexts that shape the relationship between vaginal microbiome composition and health outcomes within the specific demographic of Black women. By privileging depth over breadth, this approach allows for exploring intricate patterns, narratives, and disparities that may otherwise remain obscured by quantitative methods alone.

The literature review process was guided by a systematic approach aimed at identifying, synthesizing, and critically evaluating existing research pertinent to the intersection of vaginal microbiome diversity and health outcomes among Black women. Leveraging electronic databases such as PubMed, and Web of Science, comprehensive searches were conducted using a combination of keywords including “vaginal microbiome,” “Black women,” “infectious diseases,” “reproductive health,” and “gynecological conditions.” Seminal texts, gray literature, and relevant policy documents were scrutinized to ensure a comprehensive field review.

Criteria for inclusion encompassed studies published in peer-reviewed journals, dissertations, and reports released within the last two decades. Preference was given to research conducted within diverse geographical contexts, acknowledging the influence of socio-economic, cultural, and environmental factors on vaginal microbiome composition and health outcomes among Black women. Articles were selected through a rigorous screening process based on their relevance, methodological rigor, and contribution to understanding the research problem.

Given the exploratory nature of this study and the absence of primary data collection, traditional methods such as surveys or interviews were not employed. Instead, data acquisition centered on the systematic retrieval and analysis of existing literature. This included peer-reviewed articles, observational studies, clinical trials, meta-analyses, and systematic reviews addressing the nexus of interest. By synthesizing findings across diverse disciplinary domains, this approach facilitated a comprehensive

examination of the subject matter while minimizing participant burden and ethical considerations associated with primary data collection.

The data analysis process involved a multifaceted approach characterized by thematic synthesis, content analysis, and critical interpretation of findings. Through iterative cycles of reading, coding, and categorizing literature, emergent themes, patterns, and discrepancies were identified. Upon principles of grounded theory, themes were systematically compared, contrasted, and organized to elucidate underlying relationships and conceptual frameworks. Additionally, theoretical frameworks such as the Social Ecological Model and Intersectionality Theory were employed to contextualize findings within broader socio-cultural, environmental, and structural determinants of health.

In summary, the methodology outlined herein underscores the rigor and comprehensiveness inherent in the investigation of the intersection of vaginal microbiome diversity and health outcomes in Black women. By adopting a qualitative research design, conducting a systematic literature review, and employing robust analytical procedures, this study endeavors to illuminate the complexities of this critical area of inquiry. Through synthesizing existing knowledge and identifying research gaps, this methodology lays the groundwork for advancing our understanding of the factors influencing health disparities among Black women and informing targeted interventions and policy initiatives.

Research Design

The research design adopted for this study is rooted in qualitative inquiry, aiming to provide a rich and nuanced understanding of the complex interplay between vaginal

microbiome diversity and health outcomes among Black women. Qualitative methodologies are used to offer a holistic approach that explores the subjective experiences, perceptions, and socio-cultural contexts shaping this relationship. By privileging depth over breadth, this design enables a comprehensive exploration of the diverse factors influencing health disparities within this demographic group.

The decision to employ a qualitative research design is grounded in several considerations. Firstly, qualitative methodologies are well-suited for investigating complex social phenomena, allowing researchers to delve into the intricacies of individual experiences and societal dynamics. Given the multifaceted nature of health outcomes influenced by vaginal microbiome diversity, a qualitative approach provides the flexibility to explore diverse perspectives, narratives, and contexts within the specific demographic of Black women.

Secondly, qualitative research is inherently participatory, centering the voices and lived experiences of research participants. In the context of this study, engaging with Black women through qualitative methods facilitates a deeper understanding of their perceptions, beliefs, and behaviors related to vaginal health. By foregrounding the perspectives of those directly affected, this approach enhances the relevance and applicability of research findings, ultimately contributing to more equitable and culturally responsive healthcare practices.

Scope and Objectives

This research undertakes a comprehensive investigation into infectious diseases, reproductive health, and gynecological conditions concerning the diversity of the vaginal

microbiome among Black women. The primary aim is to unravel the intricate interplay among microbial composition, host physiology, and socio-environmental factors, explicitly focusing on comprehending the mechanisms underlying health inequalities within this demographic. Specifically, the study endeavors to explore the spectrum of vaginal microbiota among Black women and its correlation with various health outcomes. It also aims to scrutinize the socio-cultural, environmental, and structural determinants influencing vaginal microbiome composition and the resultant health disparities. Furthermore, the research intends to identify gaps and limitations in the current body of knowledge on this subject and suggest pathways for future research and intervention.

In conclusion, the qualitative research design employed in this study offers a robust framework for exploring the intersection of vaginal microbiome diversity and health outcomes in Black women. By embracing the complexities of lived experiences and socio-cultural contexts, this approach aims to generate insights that transcend simplistic explanations and inform more nuanced understandings of health disparities within this population. Through purposive sampling and in-depth data collection, this research endeavors to amplify the voices of Black women and contribute to more equitable and inclusive approaches to healthcare research and practice.

Literature Review Process

The literature review process for this thesis involved a systematic and comprehensive exploration of published literature about the intersection of vaginal microbiome diversity and health outcomes in Black women. The following outlines the

methodology employed to conduct the literature review, including criteria for selection, databases utilized, and search strategies implemented. The literature review process was iterative, involving multiple rounds of searching, screening, and synthesis to identify, assess, and integrate relevant sources into the thesis. This rigorous approach synthesized a diverse body of literature to inform the theoretical framework, research questions, and analytical insights presented in the subsequent chapters.

The literature selection process adhered to specific criteria to ensure the relevance, quality, and recency of the sources incorporated into the review. Priority was placed on articles meeting key considerations:

1. Relevance was paramount, with a focus on studies directly addressing the relationship between vaginal microbiome composition and health outcomes among Black women, aligning with the research topic and objectives.
2. Quality was emphasized, with a preference for peer-reviewed articles from reputable academic journals known for their rigorous review processes. Studies employing robust methodologies, including experimental designs and longitudinal analyses, were prioritized to ensure the reliability and validity of findings.
3. Recency was considered crucial, with a preference for publications within the last decade due to the rapidly evolving nature of scientific research in this field.

However, seminal works and foundational studies published earlier were also included if they contributed significantly to establishing the topic's historical context and theoretical foundations.

The literature search was conducted using the scientific library provided by Boston University, which offers access to a comprehensive array of scholarly databases and electronic resources. Databases utilized for the literature review included but were not limited to:

1. PubMed
2. Web of Science

Search Strategies

Search strategies were developed iteratively, utilizing a combination of controlled vocabulary (e.g., Medical Subject Headings, MeSH terms) and keyword searches tailored to the specific focus of the study. Key search terms and phrases employed in the literature search included: "Vaginal microbiome", "Black women", "Infectious diseases", "Reproductive health", "Gynecological conditions", "Microbial diversity", "Health outcomes".

Boolean operators (e.g., AND, OR) were utilized to refine search results and capture relevant articles addressing the intersection of vaginal microbiome diversity and health outcomes among Black women.

Method of Analysis

The analysis of literature collected for this thesis involved a rigorous and systematic approach to distill key insights and identify patterns relevant to the research objectives. The following outlines the analytical techniques and frameworks employed to interpret the data and extract meaningful insights from the literature. Additionally, thematic synthesis was utilized as the primary analytical approach to identify the

literature's recurrent themes, patterns, and concepts. This method involved a systematic process of coding, categorizing, and synthesizing textual data to distill overarching themes and concepts relevant to the intersection of vaginal microbiome diversity and health outcomes in Black women. Through iterative cycles of coding and comparison, themes emerged organically, capturing the diverse range of factors influencing health disparities and outcomes within this demographic group. Framework analysis facilitated a structured and systematic literature examination within a predetermined conceptual framework. Drawing upon theoretical perspectives such as the Social Ecological Model and Intersectionality Theory, a conceptual framework was developed to organize and interpret findings within broader socio-cultural, environmental, and structural contexts. This approach enabled the exploration of multi-level determinants shaping vaginal microbiome composition, health behaviors, and health outcomes among Black women, fostering a nuanced understanding of the complex interplay between individual, interpersonal, community, and societal factors.

A comparative analysis approach was utilized to compare findings across studies, populations, and geographical contexts. By systematically examining similarities and differences in methodologies, sample characteristics, and key findings, this approach facilitated the identification of convergent themes and discrepancies within the literature. Comparative analysis enhanced the robustness of the synthesis process, enabling the identification of common patterns and outliers that may inform the formulation of research questions, hypotheses, and recommendations for future inquiry. The literature analysis was facilitated by using qualitative data analysis software, including but not

limited to Zotero, a reference management tool used for collecting, organizing, and citing sources. It allows users to save references from websites, library catalogs, and databases and to generate citations and bibliographies in various citation styles. Zotero facilitates collaboration and simplifies managing references, making it a valuable tool for literature review.

The findings from thematic synthesis, framework analysis, and comparative analysis were integrated to provide a holistic understanding of the intersection of vaginal microbiome diversity and health outcomes in Black women. Through triangulation of evidence from diverse sources and perspectives, a comprehensive analysis was achieved, elucidating the multifaceted nature of health disparities, and informing targeted interventions and policy initiatives to promote health equity among Black women.

Limitations and Methodological Constraints

The methodology employed in this thesis encountered several limitations that warrant acknowledgment. Foremost among these constraints is the challenge of accessing comprehensive and specific data about vaginal microbial illnesses among African American women. Throughout the research process, it became evident that existing literature predominantly focused on European or white women, thereby limiting the availability of tailored data relevant to the unique health needs and experiences of Black women. This disparity in data representation reflects broader socio-economic factors and historical disparities in healthcare access and research participation, contributing to gaps in knowledge and understanding of vaginal health outcomes in this demographic group.

The limited availability of specific data on vaginal microbiome diversity and health outcomes among African American women poses significant implications for the validity and generalizability of the findings presented in this thesis. By relying on generalized data, there is a risk of overlooking nuanced differences and disparities within the Black female population, potentially leading to inaccurate conclusions or incomplete understandings of the intersectional dynamics shaping vaginal health disparities. Moreover, the lack of representative data may hinder the applicability of findings to diverse subgroups within the Black community, limiting the generalizability of research findings and their relevance to real-world healthcare practices and interventions.

Motivation and Implications

Despite these methodological limitations, it is essential to acknowledge the underlying motivation driving this research endeavor. The lack of abundant tailored healthcare solutions for marginalized communities was a driving force behind the conception and execution of this thesis. The inherent passion and advocacy embedded within this research catalyze shedding light on underrepresented narratives and amplifying the voices of Black women in healthcare research and practice.

Implications for Tailored Medicine and Health Equity

While the limitations of methodology underscore the challenges inherent in researching vaginal health outcomes in Black women, they also highlight the urgent need for increased representation and inclusivity in healthcare research and policy. By advocating for the collection and analysis of more specific and comprehensive data on

diverse demographic groups, including African American women, opportunities arise to develop tailored medicine and interventions that address marginalized communities' unique needs and experiences. Through concerted efforts to prioritize inclusivity, representation, and community engagement, the potential for reducing health disparities and advancing health equity becomes more attainable, underscoring the critical importance of initiatives that center the voices and experiences of marginalized populations.

Strengths of the Methodology

The systematic literature review approach allowed for synthesizing a broad range of existing research, providing a comprehensive overview of the current state of knowledge in the field. By drawing from diverse sources and perspectives, the methodology facilitated a nuanced understanding of the complex interplay between vaginal microbiome diversity and health outcomes in Black women. Additionally, using qualitative data analysis techniques, such as thematic analysis and framework analysis, enabled the identification of recurrent themes and patterns within the literature. These analytical approaches allowed for the exploration of socio-cultural, environmental, and structural determinants shaping vaginal health disparities, highlighting the multi-level factors influencing health outcomes among Black women.

Weaknesses and Areas for Improvement

Despite its strengths, the methodology employed in this thesis has its limitations. One significant area for improvement is the reliance on existing literature rather than primary research data. While the systematic literature review approach provided valuable insights

into the current body of knowledge, it also constrained the depth of analysis. It precluded the exploration of new perspectives and insights that may have emerged from primary research on Black women. Moreover, the absence of personal experiences and perspectives from Black women, including the researcher herself, is a notable weakness of the methodology. While efforts were made to draw on existing literature and incorporate diverse viewpoints, the lack of direct engagement with Black women's lived experiences and voices represents a missed opportunity to capture the complexity and nuances of the research topic fully.

CHAPTER FOUR

Reflection

As a Black woman embarking on the journey of conducting a literature thesis on the intricate interplay between vaginal microbiome diversity and health outcomes in Black women, I find myself deeply immersed in the complexity of this endeavor. It is an exploration that resonates profoundly with my own lived experiences and identity, presenting challenges and opportunities that compel me to reflect on the inherent contradictions and nuances inherent in research of this nature.

The decision to pursue a literature-based approach was not made lightly but stemmed from various motivations. Foremost among these was the aspiration to contribute meaningfully to the existing body of knowledge, to carve out a space within academia where the voices and experiences of Black women are both recognized and validated. The landscape of research in this domain revealed glaring gaps and omissions,

particularly concerning the specificities of vaginal microbiome diversity and its implications for the health outcomes of Black women.

However, as I delved deeper into the research process, grappling with the vast expanse of literature and the myriad perspectives and methodologies presented therein, I found myself confronted with a profound realization. There existed within me a yearning, an ache almost, to bridge the chasm between academic inquiry and personal experience, to weave together the threads of empirical evidence with the fabric of lived reality. It became increasingly apparent that while literature can serve as a valuable foundation, a springboard for intellectual discourse, it is only complete with the infusion of personal narratives and voices.

This realization was challenging. It forced me to confront the limitations of traditional research paradigms to interrogate the privileging of objectivity over subjectivity and detachment over engagement. As a Black woman intimately familiar with the nuances of navigating spaces that often marginalize and erase our voices, I grappled with the tension between academic rigor and personal investment. It was a tension that demanded resolution, a dichotomy that demanded reconciliation.

In hindsight, I recognize the importance of centering personal experiences and voices in research endeavors, particularly when exploring topics as intimate and culturally sensitive as reproductive health and gynecological conditions. Our experiences and stories are not mere footnotes in the annals of academic discourse; they are the essence of our existence, imbued with wisdom and resilience that transcends the confines

of empirical inquiry. Dividing research from lived reality is to perpetuate a false dichotomy, to perpetuate the erasure of voices that have long been silenced.

As I navigate the final stages of this thesis, I am reminded of the imperative to bridge the gap between academia and activism, between theory and praxis. It is a journey that requires courage, vulnerability, and a willingness to challenge the status quo. And while the path ahead may be fraught with uncertainty and discomfort, I am encouraged by the conviction that my voice, our voices, matter. Audre Lorde said, “Your silence will not protect you.” Only by speaking our truths and reclaiming our narratives can we affect meaningful change in the world.

Areas for Future Research

Looking towards the horizon, having an acute awareness of the imperative to chart a course that acknowledges the limitations of existing research paradigms and actively seeks to transcend them. Considering the future trajectory of research in the field of vaginal microbiome diversity and health outcomes in Black women, there is a pronounced urgency in embracing more inclusive and participatory approaches that prioritize the voices and experiences of those most impacted by systemic inequities.

One avenue for future research lies in embracing community-based participatory research (CBPR) methods, offering a holistic framework for engaging communities as active partners in the research process. By co-creating knowledge with community members, researchers can ensure that the research agenda is driven by the needs and priorities of those directly impacted by the issues under investigation. CBPR holds the

potential to generate not only more culturally relevant and contextually sensitive findings but also to foster greater trust and collaboration between researchers and communities.

In addition to CBPR, qualitative interviews and focus groups represent valuable tools for capturing the rich tapestry of experiences within the Black female population. These methodologies provide a platform for amplifying voices that have historically been marginalized or silenced, allowing for a deeper exploration of the complexities of vaginal microbiome diversity and its implications for health outcomes. By centering the lived experiences of Black women in research, a more nuanced understanding of the intersecting factors that shape health disparities can be gained, informing targeted interventions.

However, pursuing more inclusive and equitable research practices must occur in collaboration with broader efforts to address the systemic barriers and disparities that hinder research participation and access to healthcare services among marginalized communities. Structural inequities, including racial discrimination, socioeconomic disparities, and healthcare access barriers, must be acknowledged, and actively dismantled through policy advocacy, community mobilization, and institutional reform.

Ultimately, the future of research in this field hinges on a collective commitment to centering the voices and experiences of Black women to confront the uncomfortable truths that lie at the intersection of race, gender, and health. It is a journey that demands humility, empathy, and a willingness to challenge existing power dynamics. But it's also a journey imbued with hope, promising a future where all voices are heard, all experiences are valued, and all bodies are respected.

CHAPTER FIVE

Conclusion

The exploration of the intersection between vaginal microbiome diversity and health outcomes in African American women represents a critical endeavor in understanding and addressing long-standing health disparities within this population. Throughout this thesis, an exploration has been conducted into the complexities of the vaginal microbiome, encompassing its composition, dynamics, and implications for reproductive and gynecological health outcomes. The comprehensive analysis underscores the urgent need to bridge existing knowledge gaps and promote health equity, particularly concerning African American women.

Historically, African American women have encountered systemic barriers to healthcare access and quality, compounded by socioeconomic disparities, structural racism, and cultural influences. Despite bearing a disproportionate burden of reproductive and gynecological health issues, their experiences have frequently been marginalized or disregarded in both research and clinical settings. This study centers African American women's voices and experiences, rectifying past neglect and empowering communities to advocate for equitable healthcare solutions.

Findings underscore significant differences in the composition of the vaginal microbiome among African American women compared to non-African American women. African American women tend to exhibit a more diverse microbial profile, with notable implications for health outcomes, including elevated rates of bacterial vaginosis, infertility, and adverse pregnancy outcomes. The study is a pivotal stride toward

narrowing the knowledge gap and promoting health equity by elucidating these disparities and comprehending the intricate interactions between microbial diversity, reproductive health, and gynecological conditions.

Furthermore, the research emphasizes the necessity of considering the multifaceted nature of health disparities, shaped by biological, social, and economic determinants, alongside historical contexts. Socioeconomic factors such as income, education level, access to healthcare, and living conditions profoundly influence an individual's microbiome through various pathways. Addressing these disparities necessitates a holistic approach that acknowledges the interconnectedness of social determinants of health and microbiome composition.

Looking ahead, it is imperative to advance research endeavors that prioritize the inclusion of diverse populations, amplify marginalized voices, and confront systemic inequities in healthcare. By integrating interdisciplinary methodologies, engaging communities, and implementing culturally sensitive interventions, we can cultivate more inclusive and equitable healthcare practices tailored to meet the needs of all women, particularly those from marginalized backgrounds.

This thesis proposes prioritizing health equity and justice in research, policy, and practice. By illuminating the intricate interplay between vaginal microbiome diversity and health outcomes among African American women, it is a step towards a significant stride toward dismantling health disparities and fostering reproductive and overall health equity for all women. Let us remain steadfast in our commitment to advancing inclusive

healthcare practices, envisioning a future where all women have access to the resources and support necessary for their well-being and flourishing.

The intricate relationship between vaginal microbiome diversity and health outcomes in Black women has been explored extensively in this comprehensive analysis. Through the lens of infectious diseases, reproductive health, and gynecological conditions, this research has shed light on the nuanced interplay between vaginal microbial composition and various health outcomes. By delving into the classification of the vaginal microbiota, mainly through the lens of CSTs, this study has elucidated the pivotal role of *Lactobacillus* species, notably *L. crispatus* and *L. iners*, in maintaining vaginal health and preventing dysbiosis-associated conditions such as BV, STIs, and preterm birth.

The findings underscore the significance of CSTs in characterizing the microbial diversity of the vaginal microbiome and their implications for women's reproductive health. CSTs I and II, dominated by *Lactobacillus crispatus* and *Lactobacillus gasseri*, respectively, are consistently associated with vaginal health. At the same time, CSTs III through V, marked by a decrease in lactobacilli and an increase in diverse anaerobic bacteria, are linked to dysbiosis and heightened susceptibility to infections and gynecological conditions. Within this context, the distinct characteristics of *L. crispatus* and *L. iners* have been highlighted, emphasizing their differential impacts on vaginal homeostasis and disease susceptibility in African American women.

Furthermore, racial, and ethnic disparities in vaginal microbiome composition have emerged as a focal point of the investigation, with African American women

exhibiting a higher prevalence of CSTs associated with dysbiosis and adverse health outcomes. Factors such as genetic predisposition, socioeconomic status, and environmental influences contribute to these disparities, underscoring the importance of tailored interventions to promote vaginal health equity across diverse populations. The influence of STIs on the vaginal microbiome and vice versa has been elucidated, highlighting the bidirectional interplay between microbial disruption and susceptibility to infections. Moreover, the association between dysbiosis and adverse pregnancy outcomes, particularly preterm birth, underscores the critical role of the vaginal microbiome in maternal and neonatal health.

In conclusion, the methodology employed in this thesis to investigate the intersection of vaginal microbiome diversity and health outcomes among Black women has encountered notable limitations, primarily stemming from the scarcity of specific data and representation within existing literature. This thesis proposes prioritizing health equity and justice in research, policy, and practice. By illuminating the intricate interplay between vaginal microbiome diversity and health outcomes among African American women, it is a stride toward dismantling health disparities and fostering reproductive and overall health equity for all women.

In the commitment to advancing inclusive healthcare practices, envisioning a future where all women have access to the resources and support necessary for their well-being and flourishing. By elucidating the complex interplay between microbial composition, infectious diseases, reproductive health, and gynecological conditions, this research contributes to a deeper understanding of the factors influencing vaginal health

disparities. It underscores the importance of tailored interventions to promote optimal health outcomes in diverse populations. Future investigations could delve deeper into elucidating the specific mechanisms through which variations in the vaginal microbiome composition influence the risk, severity, and recurrence of infections in Black women. Longitudinal studies tracking changes in the microbiome over time and in response to interventions could provide invaluable insights into the dynamics of vaginal health. Additionally, exploring the impact of socio-cultural factors, such as access to healthcare and experiences of discrimination, on vaginal microbiome diversity and health outcomes may further enrich our understanding. Furthermore, integrating microbiome analysis into routine gynecological care and developing personalized treatment approaches based on individual microbiome profiles represent promising avenues for future clinical practice.

In essence, this study underscores the imperative of understanding the intricate relationship between the vaginal microbiome, infectious diseases, reproductive health, and gynecological conditions among Black women. Embracing an approach that considers biological, social, and environmental factors, the aim is to illuminate the complexities influencing vaginal health within this population.

Through this research, the goal is to address existing knowledge gaps and pave the way for tailored interventions to promote health equity and reduce disparities. Moreover, the findings emphasize the critical need for targeted prevention and treatment strategies informed by an understanding of how variations in the vaginal microbiome composition impact health outcomes. By acknowledging the influence of socioeconomic

factors and historical contexts, efforts can be advanced to dismantle health inequities and foster reproductive health and well-being in Black women. This study represents a significant step toward achieving comprehensive, inclusive research in this field and lays the foundation for impactful policies, clinical practices, and community-based interventions.

Despite these challenges, the research remains motivated by a commitment to addressing healthcare disparities and amplifying the voices of marginalized communities. The findings underscore the urgent need for increased inclusivity and representation in healthcare research and policy to develop tailored interventions that address the unique needs of Black women. While the methodology has strengths in synthesizing existing knowledge and employing qualitative analysis techniques, such as thematic and framework analysis, there are opportunities for improvement, particularly in engaging directly with Black women's lived experiences and perspectives through primary research. Overall, this thesis contributes to a broader understanding of health disparities and underscores the importance of initiatives prioritizing inclusivity, representation, and community engagement in healthcare research and practice.

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