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Antimicrobial Resistance in Urinary and Reproductive Tract Infections Among Pregnant and Non-Pregnant Women: Implications for Pregnancy and Childbirth

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RESEARCH TITLE

Antimicrobial Resistance in Urinary and Reproductive Tract Infections Among Pregnant and Non-Pregnant Women: Implications for Pregnancy and Childbirth

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ABSTRACT

Background: Antimicrobial resistance (AMR) is a growing global health issue that endangers the effective treatment of urinary tract infections (UTIs) and reproductive tract infections (RTIs), especially among pregnant women who face higher risks of adverse maternal and neonatal outcomes. Local data on bacterial pathogens and antimicrobial susceptibility patterns are crucial for guiding evidence-based antibiotic treatment and antimicrobial stewardship.

Methods: A comparative cross-sectional, laboratory-based study was carried out among pregnant and non-pregnant women attending Ga East Municipal Hospital, Ghana. Urine, blood, and high vaginal swab samples were collected and processed for bacterial isolation and identification using standard microbiological procedures. Antimicrobial susceptibility testing was conducted following Clinical and Laboratory Standards Institute (CLSI) guidelines. The prevalence of bacterial isolates, resistance patterns, multidrug-resistant (MDR) organisms, and differences between pregnant and non-pregnant women were assessed.

Results: Bacterial pathogens commonly identified from clinical specimens included Escherichia coli, Staphylococcus aureus, Klebsiella spp., Enterococcus spp., Proteus spp., Pseudomonas spp., and Citrobacter spp. High resistance levels were observed against several widely used antibiotics, especially fluoroquinolones, tetracyclines, sulfonamides, and some aminoglycosides. Nitrofurantoin and certain cephalosporins showed relatively higher activity against many urinary isolates. Multidrug resistance was found in a notable portion of isolates, with significant differences in resistance profiles between pregnant and non-pregnant women. These resistance patterns have important implications for empirical antibiotic therapy during pregnancy and delivery.

Conclusion: Antimicrobial resistance among urinary and reproductive tract pathogens remains a major public health concern, with significant impacts on maternal and neonatal health. The high prevalence of multidrug-resistant organisms underscores the necessity for routine culture and susceptibility testing, strengthened antimicrobial stewardship initiatives, and ongoing local surveillance to improve antibiotic selection and minimize adverse pregnancy and delivery outcomes.

Keywords: antimicrobial resistance, urinary tract infection, reproductive tract infection, pregnancy, multidrug resistance, antimicrobial susceptibility, maternal health, neonatal health, Ghana

CHAPTER ONE

1.1 Background of the Study

Antimicrobial resistance (AMR) has become one of the most significant threats to global public health, reducing the effectiveness of antimicrobial agents that were previously successful in treating infectious diseases. The rapid emergence and spread of resistant bacterial pathogens have increased treatment failures, healthcare costs, hospitalization rates, and mortality worldwide (Von Vietinghoff et al., 2024).

Urinary tract infections (UTIs) and reproductive tract infections (RTIs) are among the most common infections affecting women of reproductive age. Pregnancy predisposes women to these infections because of hormonal, anatomical, and immunological changes that facilitate bacterial colonization and persistence. Untreated or inadequately treated infections may result in adverse maternal and neonatal outcomes, including preterm birth, miscarriage, maternal sepsis, low birth weight, postpartum infections, and neonatal sepsis (Al Kadri et al., 2024).

The increasing prevalence of antimicrobial-resistant pathogens further complicates the management of these infections. In many low- and middle-income countries, including Ghana, antibiotics are frequently prescribed empirically without culture and susceptibility testing, increasing the risk of inappropriate therapy and resistance development (Donkor et al., 2024). Consequently, identifying local bacterial profiles and susceptibility patterns is essential for guiding evidence-based treatment and improving pregnancy and childbirth outcomes.

1.2 Problem Statement

Despite advances in antimicrobial therapy, urinary and reproductive tract infections remain important causes of morbidity among women of reproductive age. During pregnancy, these infections may lead to serious maternal and neonatal complications if not effectively treated. However, the growing burden of antimicrobial resistance threatens the success of empirical antibiotic therapy.

In Ghana, limited data exist on the comparative antimicrobial resistance patterns of bacterial pathogens isolated from urine, blood, and high vaginal swab specimens among pregnant and non-pregnant women. The absence of such data may hinder appropriate antibiotic selection and contribute to treatment failure, prolonged infection, and adverse pregnancy outcomes. This study therefore seeks to investigate antimicrobial resistance patterns among bacterial pathogens associated with urinary and reproductive tract infections and evaluate their implications for pregnancy and childbirth.

1.3 Aim of the Study

To investigate antimicrobial resistance patterns among bacterial pathogens associated with urinary and reproductive tract infections and evaluate their implications for pregnancy and childbirth outcomes.

1.4 Specific Objectives

- To identify bacterial pathogens isolated from urine, blood, and high vaginal swab specimens.
- To determine the prevalence of urinary and reproductive tract infections among pregnant and non-pregnant women.
- To assess the antimicrobial susceptibility profiles of isolated bacterial pathogens.
- To determine the prevalence of multidrug-resistant bacterial isolates.
- To compare antimicrobial resistance patterns between pregnant and non-pregnant women.
- To evaluate the implications of antimicrobial resistance for pregnancy and childbirth outcomes.

1.5 Research Questions

- What bacterial pathogens are commonly associated with urinary and reproductive tract infections among women?
- What are the antimicrobial susceptibility patterns of the isolated pathogens?
- What proportion of isolates exhibit multidrug resistance?
- Are there significant differences in resistance patterns between pregnant and non-pregnant women?
- What are the potential implications of antimicrobial resistance for pregnancy and childbirth outcomes?

1.6 Research Hypothesis

Null Hypothesis (H_0): There is no significant association between pregnancy status and antimicrobial resistance among bacterial pathogens isolated from urinary and reproductive tract infections.

Alternative Hypothesis (H_1): There is a significant association between pregnancy status and antimicrobial resistance among bacterial pathogens isolated from urinary and reproductive tract infections.

1.7 Significance of the Study

This study will provide valuable information on the bacterial profiles and antimicrobial susceptibility patterns associated with urinary and reproductive tract infections among women of reproductive age. The findings will assist clinicians in selecting effective antibiotics, support antimicrobial stewardship programs, and contribute to strategies aimed at reducing adverse maternal and neonatal outcomes associated with resistant bacterial infections.

1.8 Scope of the Study

The study focused on bacterial pathogens isolated from urine, blood, and high vaginal swab specimens collected from pregnant and non-pregnant women attending

Ga East Municipal Hospital. The investigation included bacterial identification, antimicrobial susceptibility testing according to CLSI guidelines, and assessment of multidrug resistance patterns.

1.9 Operational Definitions

Term	Definition
Antimicrobial resistance	The ability of microorganisms to survive exposure to antimicrobial agents that would normally inhibit or kill them.
Multidrug resistance (MDR)	Resistance of a bacterial isolate to three or more classes of antimicrobial agents.
Urinary tract infection	Infection involving any part of the urinary tract, including the urethra, bladder, ureters, or kidneys.
Reproductive tract infection	Infection affecting the female genital tract.
Pregnant woman	A woman confirmed to be carrying a pregnancy during the study period.
Non-pregnant woman	A woman not carrying a pregnancy during the study period.

CHAPTER TWO

LITERATURE REVIEW

2.1 Introduction

Antimicrobial resistance (AMR) has emerged as one of the most pressing global public health challenges of the twenty-first century. The widespread emergence of resistant bacterial pathogens has compromised the effectiveness of antibiotics, leading to increased morbidity, mortality, prolonged hospitalization, and escalating healthcare costs. The inappropriate use of antibiotics in human medicine, veterinary practice, and agriculture has accelerated the evolution and dissemination of resistant microorganisms, thereby threatening the effectiveness of antimicrobial therapy and undermining decades of progress in infectious disease management (World Health Organization, 2024).

Urinary tract infections (UTIs) and reproductive tract infections (RTIs) are among the most frequently encountered bacterial infections affecting women globally. Women of reproductive age are particularly vulnerable because of anatomical, physiological, hormonal, and behavioral factors that facilitate microbial colonization and ascending infections. Pregnancy further increases susceptibility to these infections due to hormonal changes, ureteral dilatation, urinary stasis, and altered immune responses, all of which promote bacterial growth within the urinary and reproductive tracts (Al Kadri et al., 2024). When inadequately treated, these infections may progress to pyelonephritis, maternal sepsis, miscarriage, preterm labour, postpartum infections, and neonatal sepsis, thereby contributing substantially to maternal and neonatal morbidity and mortality.

The growing prevalence of antimicrobial-resistant pathogens has further complicated the management of UTIs and RTIs. Resistance among common bacterial pathogens such as Escherichia coli, Staphylococcus aureus, Klebsiella species, Pseudomonas species, and Enterococcus species has reduced the effectiveness of commonly prescribed antibiotics, making empirical treatment increasingly unreliable (Von Vietinghoff et al., 2024). Consequently, clinicians are often faced with limited therapeutic options, particularly during pregnancy where antibiotic selection must balance efficacy against potential fetal risks. This challenge highlights the importance of microbiological diagnosis and antimicrobial susceptibility testing to guide evidence-based treatment decisions.

The burden of AMR is particularly severe in low- and middle-income countries, where limited diagnostic capacity, unrestricted access to antibiotics, self-medication, suboptimal infection prevention practices, and inadequate antimicrobial stewardship contribute to the rapid emergence and spread of resistant organisms (Donkor et al., 2024). In many healthcare settings across sub-Saharan Africa, including Ghana, empirical antibiotic therapy remains common because culture and susceptibility testing are not routinely performed before treatment initiation. Such practices

increase selective pressure on bacterial populations, promoting the development and dissemination of multidrug-resistant organisms and reducing the effectiveness of available antimicrobial agents.

Ghana has recognized AMR as a major public health priority and has implemented national strategies to strengthen antimicrobial stewardship and surveillance. Despite these efforts, studies continue to report increasing resistance among bacterial pathogens associated with urinary and reproductive tract infections. Predominant organisms including Escherichia coli, Staphylococcus aureus, Klebsiella species, and Enterococcus species have demonstrated resistance to several first-line antimicrobial agents, creating significant challenges for clinicians managing infections among women of reproductive age (Afeke et al., 2025; Donkor et al., 2024). Although several Ghanaian studies have investigated antimicrobial resistance in urinary tract infections, comparatively few have simultaneously evaluated bacterial isolates from urine, blood, and high vaginal swab specimens while comparing pregnant and non-pregnant women within the same study population.

Beyond the immediate clinical implications, antimicrobial resistance has important consequences for maternal and child health. Resistant infections may delay effective treatment, prolong hospitalization, increase healthcare expenditure, and elevate the risk of adverse pregnancy outcomes such as miscarriage, preterm birth, low birth weight, postpartum infections, and neonatal sepsis (Monari et al., 2024). These consequences align with the broader global agenda to reduce maternal and neonatal mortality and underscore the need for robust surveillance systems, evidence-based prescribing, and strengthened antimicrobial stewardship programs.

This chapter critically reviews current literature relevant to the present study. Specifically, it examines the concept and global burden of antimicrobial resistance, the epidemiology of urinary and reproductive tract infections, mechanisms of bacterial resistance, maternal and neonatal consequences of resistant infections, antimicrobial stewardship in obstetric care, and antimicrobial resistance trends in Ghana and sub-Saharan Africa. The chapter further reviews relevant theoretical and empirical literature, identifies existing knowledge gaps, and presents the conceptual framework underpinning the study. Through this synthesis, the chapter establishes the scientific rationale for investigating antimicrobial resistance among bacterial pathogens associated with urinary and reproductive tract infections in pregnant and non-pregnant women and its implications for pregnancy and childbirth outcomes.

2.2 Concept of Antimicrobial Resistance

Antimicrobial resistance (AMR) is recognized as one of the greatest threats to global health, food security, and sustainable development. It occurs when microorganisms including bacteria, fungi, viruses, and parasites evolve mechanisms that enable them to survive exposure to antimicrobial agents that were previously effective in inhibiting or eliminating them. Among these microorganisms, bacterial antimicrobial resistance has become the most pressing concern because of its widespread impact on the treatment of infectious diseases, particularly urinary

tract infections (UTIs), reproductive tract infections (RTIs), bloodstream infections, and healthcare-associated infections (World Health Organization, 2024).

The discovery of antibiotics revolutionized modern medicine and significantly reduced mortality associated with bacterial infections. The introduction of Penicillin in the 1940s marked the beginning of the antibiotic era, transforming the management of diseases that were previously fatal. However, shortly after antibiotics were introduced into clinical practice, resistant bacterial strains began to emerge. Since then, antimicrobial resistance has evolved into a global crisis driven by the extensive and often inappropriate use of antibiotics in human medicine, veterinary practice, agriculture, and aquaculture. The continued emergence of resistant pathogens threatens the effectiveness of existing antimicrobial therapies and has prompted global concern regarding the future management of infectious diseases (Murray et al., 2022).

Bacterial resistance may be classified as intrinsic or acquired. Intrinsic resistance refers to the natural ability of certain bacterial species to resist the effects of specific antimicrobial agents because of inherent structural or physiological characteristics. For example, the outer membrane of many Gram-negative bacteria limits the penetration of several antibiotics, rendering them naturally resistant to certain drugs. In contrast, acquired resistance develops when previously susceptible bacteria gain resistance through spontaneous genetic mutations or by acquiring resistance genes via horizontal gene transfer mechanisms such as conjugation, transformation, and transduction (Von Vietinghoff et al., 2024). These genetic adaptations enable bacteria to survive antimicrobial exposure and proliferate despite treatment.

The molecular mechanisms underlying antimicrobial resistance are diverse and often involve multiple pathways operating simultaneously. Common mechanisms include enzymatic degradation of antibiotics, modification of antimicrobial target sites, decreased membrane permeability, activation of efflux pumps that expel antibiotics from bacterial cells, and biofilm formation that protects bacteria from both antimicrobial agents and host immune responses. Gram-negative organisms such as Escherichia coli, Klebsiella species, and Pseudomonas aeruginosa frequently produce extended-spectrum β-lactamases (ESBLs), enzymes capable of hydrolyzing many β-lactam antibiotics, including third-generation cephalosporins. Likewise, Gram-positive organisms such as Staphylococcus aureus have evolved resistance through alterations in penicillin-binding proteins, resulting in strains such as methicillin-resistant Staphylococcus aureus (MRSA), which present significant therapeutic challenges (Centers for Disease Control and Prevention [CDC], 2024)/(Tobin et al., 2026).

The consequences of antimicrobial resistance extend beyond individual patient outcomes to affect healthcare systems and national economies. Resistant infections are associated with prolonged hospitalization, increased diagnostic and treatment costs, greater reliance on expensive second-line or last-resort antibiotics, and higher morbidity and mortality rates. The landmark global analysis by Christopher J. L. Murray and colleagues estimated that bacterial antimicrobial resistance contributed to millions of deaths worldwide in 2019, making it one of the leading

causes of mortality globally (Murray et al., 2022). These findings emphasize that AMR is no longer solely a microbiological concern but also a major socioeconomic and public health challenge.

The impact of AMR is particularly profound in low- and middle-income countries (LMICs), where healthcare systems often face constraints in diagnostic capacity, antimicrobial stewardship, infection prevention, and surveillance. In many settings, antibiotics are available without prescription, self-medication is common, and laboratory-guided antimicrobial therapy is limited. These factors promote inappropriate antibiotic use and accelerate the emergence and spread of multidrug-resistant organisms. Furthermore, inadequate sanitation, overcrowding, poor infection prevention and control practices, and limited access to clean water facilitate the transmission of resistant pathogens within communities and healthcare facilities (Donkor et al., 2024).

Women of reproductive age represent a population particularly vulnerable to the consequences of antimicrobial resistance because UTIs and RTIs are among the most common bacterial infections encountered during their lifetime. During pregnancy, physiological changes including ureteral dilatation, urinary stasis, reduced bladder tone, and altered immune function increase susceptibility to bacterial colonization and infection. The presence of antimicrobial-resistant pathogens complicates treatment because clinicians must balance the need for effective bacterial eradication against the potential teratogenic or fetal effects of certain antimicrobial agents. Consequently, empirical therapy without culture and susceptibility testing may result in treatment failure, persistent infection, maternal sepsis, preterm labour, miscarriage, and adverse neonatal outcomes (Al Kadri et al., 2024).

Recognizing the growing threat posed by AMR, the World Health Organization launched the Global Action Plan on Antimicrobial Resistance, which emphasizes improving awareness, strengthening surveillance, reducing infection incidence, optimizing antimicrobial use, and promoting research into new therapeutic options. Complementing this strategy, the WHO introduced the AWaRe (Access, Watch, and Reserve) classification to guide rational antibiotic prescribing and encourage the use of antibiotics with lower resistance potential where appropriate. These initiatives underscore the importance of antimicrobial stewardship as a critical component of healthcare systems worldwide (WHO, 2024).

In Ghana, antimicrobial resistance has become an increasingly important public health concern. Studies conducted across the country have reported rising resistance among common bacterial pathogens, particularly Escherichia coli, Staphylococcus aureus, Klebsiella species, and Enterococcus species isolated from urinary and reproductive tract infections (Donkor et al., 2024; Afeke et al., 2025). Despite the implementation of Ghana's National Action Plan on Antimicrobial Resistance, challenges including inappropriate antibiotic prescribing, over-the-counter access to antibiotics, limited diagnostic capacity, and inconsistent antimicrobial stewardship continue to contribute to the persistence and spread of resistant organisms. These

findings highlight the urgent need for routine microbiological surveillance, culture-guided therapy, and evidence-based prescribing practices, particularly among pregnant women who are at increased risk of adverse maternal and neonatal outcomes.

In summary, antimicrobial resistance represents a complex and rapidly evolving global health challenge that threatens the effectiveness of modern medicine. Its development is driven by biological adaptation, inappropriate antimicrobial use, and healthcare system limitations, while its consequences extend from individual patient morbidity to broader economic and public health impacts. Understanding the concept, mechanisms, and determinants of AMR provides the scientific foundation for investigating resistance patterns among bacterial pathogens associated with urinary and reproductive tract infections and informs strategies to improve maternal health, antimicrobial stewardship, and pregnancy outcomes.

2.3 Global Burden of Urinary Tract Infections

Urinary tract infections (UTIs) are among the most common bacterial infections affecting individuals worldwide and represent a significant cause of morbidity across all age groups. They account for millions of healthcare visits annually and impose a substantial burden on healthcare systems through increased hospital admissions, antibiotic prescriptions, laboratory investigations, and healthcare expenditures. Women are disproportionately affected due to anatomical and physiological factors, making UTIs one of the leading infectious diseases among females, particularly during the reproductive years. The increasing prevalence of antimicrobial-resistant uropathogens has further complicated the diagnosis, treatment, and prevention of these infections, making UTIs an important public health concern (World Health Organization, 2024).

Globally, it is estimated that more than 150 million people develop UTIs each year, resulting in billions of dollars in direct and indirect healthcare costs. The lifetime risk of developing at least one UTI exceeds 50% among women, while approximately 20–30% of affected women experience recurrent infections. These high recurrence rates contribute to repeated antibiotic exposure, increasing the selective pressure for the emergence of antimicrobial-resistant bacteria (Flores-Mireles et al., 2015; Von Vietinghoff et al., 2024). Although UTIs affect individuals of all ages and sexes, they occur far more frequently in women because the shorter female urethra, its proximity to the anus, sexual activity, hormonal influences, pregnancy, and certain contraceptive methods facilitate bacterial entry into the urinary tract.

UTIs are generally classified as community-acquired or healthcare-associated (nosocomial) infections. Community-acquired UTIs occur outside healthcare facilities and are usually uncomplicated, whereas healthcare-associated infections are often associated with urinary catheterization, hospitalization, invasive procedures, or underlying chronic diseases. Healthcare-associated UTIs are particularly concerning because they are more frequently caused by multidrug-resistant organisms, including extended-spectrum β-lactamase (ESBL)-producing Enterobacterales and carbapenem-resistant bacteria, which significantly limit therapeutic options (Centers for Disease Control and Prevention, 2024)/ (Bandac et al., 2025).

The microbiology of UTIs has remained relatively consistent worldwide, with Escherichia coli accounting for the majority of uncomplicated infections. Other important uropathogens include Klebsiella species, Proteus species, Enterococcus species, Pseudomonas aeruginosa, Staphylococcus saprophyticus, and Staphylococcus aureus. The predominance of these organisms varies according to geographical location, patient demographics, healthcare exposure, and local antimicrobial prescribing practices. In complicated UTIs, polymicrobial infections and opportunistic pathogens are encountered more frequently, particularly among hospitalized and immunocompromised patients (Kranz et al. 2024).

Several biological and behavioral factors increase the risk of UTIs. Female sex remains the strongest risk factor because of anatomical characteristics that facilitate ascending bacterial infection. Additional risk factors include pregnancy, menopause, diabetes mellitus, urinary tract obstruction, renal calculi, urinary catheterization, immunosuppression, poor genital hygiene, sexual intercourse, previous UTI episodes, and structural abnormalities of the urinary tract. These factors promote bacterial colonization, impair urinary drainage, or compromise host immune defenses, thereby increasing susceptibility to infection (Al Kadri et al., 2024).

Pregnancy represents one of the most important physiological risk factors for UTIs. Hormonal changes, particularly increased progesterone concentrations, reduce ureteral tone and bladder contractility, leading to urinary stasis and vesicoureteral reflux. Mechanical compression of the ureters by the enlarging uterus further contributes to impaired urinary drainage, facilitating bacterial multiplication within the urinary tract. In addition, pregnancy is associated with immunological adaptations that reduce maternal immune responses to support fetal tolerance but simultaneously increase susceptibility to bacterial infections. These physiological alterations explain the higher prevalence of asymptomatic bacteriuria, cystitis, and pyelonephritis among pregnant women compared with the general female population (Al Kadri et al., 2024).

The burden of UTIs varies considerably across regions of the world. High-income countries generally report lower complication rates because of improved access to healthcare, routine laboratory diagnosis, standardized treatment guidelines, and robust antimicrobial stewardship programs. In contrast, low- and middle-income countries (LMICs) experience higher disease burdens because of delayed healthcare seeking, limited diagnostic infrastructure, inadequate laboratory capacity, widespread empirical antibiotic use, and unrestricted access to antimicrobial agents. These challenges contribute to increasing antimicrobial resistance, recurrent infections, and poorer clinical outcomes (Donkor et al., 2024).

In sub-Saharan Africa, UTIs remain a major cause of outpatient visits, hospital admissions, and pregnancy-related complications. Several studies have reported a rising prevalence of multidrug-resistant uropathogens, particularly Escherichia coli and Klebsiella species, with resistance to commonly prescribed antibiotics such as fluoroquinolones, cotrimoxazole, and ampicillin becoming increasingly common. The emergence of ESBL-producing organisms has further reduced the effectiveness of first-line antimicrobial therapy and necessitated the use of broader-

spectrum antibiotics, which may be less accessible or less suitable for use during pregnancy (Donkor et al., 2024).

In Ghana, UTIs remain one of the leading bacterial infections managed in both primary and tertiary healthcare facilities. Recent studies have consistently identified Escherichia coli as the predominant uropathogen, followed by Staphylococcus aureus, Klebsiella species, Proteus species, and Enterococcus species. Increasing resistance to frequently prescribed antibiotics including fluoroquinolones, tetracyclines, and trimethoprim-sulfamethoxazole has been reported, while Nitrofurantoin and selected cephalosporins continue to demonstrate relatively high effectiveness against many urinary isolates (Afeke et al., 2025; Donkor et al., 2024). These findings underscore the importance of continuous local surveillance to guide empirical treatment and reduce inappropriate antibiotic use.

Beyond their clinical consequences, UTIs also impose substantial economic and social burdens. Recurrent infections contribute to repeated medical consultations, laboratory investigations, antibiotic prescriptions, hospital admissions, absenteeism from work, reduced productivity, and diminished quality of life. During pregnancy, these burdens are amplified because untreated or inadequately treated infections may result in adverse maternal and neonatal outcomes, including pyelonephritis, maternal sepsis, preterm labour, low birth weight, miscarriage, and neonatal sepsis. Consequently, early diagnosis, appropriate antimicrobial therapy, and routine urine culture with antimicrobial susceptibility testing remain essential strategies for reducing complications and improving maternal and neonatal health outcomes (Monari et al., 2024).

The global increase in antimicrobial resistance among uropathogens has fundamentally altered the management of UTIs. Empirical antibiotic therapy, once considered sufficient for uncomplicated infections, is becoming increasingly unreliable in many settings because

changing susceptibility patterns. International organizations now recommend that empirical treatment should be guided by local antimicrobial resistance surveillance data and updated clinical guidelines whenever possible. Culture-based diagnosis and antimicrobial susceptibility testing are particularly important in pregnant women, recurrent infections, complicated UTIs, and healthcare-associated infections to ensure appropriate antibiotic selection and preserve the effectiveness of existing antimicrobial agents (Kranz et al. 2024).

In summary, urinary tract infections remain one of the most prevalent bacterial infections worldwide, with women especially pregnant women bearing a disproportionate share of the disease burden. The convergence of high infection rates, increasing antimicrobial resistance, and limited therapeutic options has transformed UTIs into a major global health challenge. These realities emphasize the importance of ongoing surveillance of bacterial pathogens and their antimicrobial susceptibility patterns to support evidence-based treatment, strengthen antimicrobial stewardship, and improve maternal and neonatal outcomes. This context provides a strong rationale for investigating antimicrobial resistance among urinary and reproductive tract pathogens in the present study.

2.4 Urinary Tract Infections During Pregnancy

Urinary tract infections (UTIs) are among the most common bacterial infections encountered during pregnancy and constitute a major cause of maternal and neonatal morbidity worldwide. Pregnancy predisposes women to UTIs because of profound anatomical, physiological, hormonal, and immunological changes that facilitate bacterial colonization and ascending infection within the urinary tract. If left untreated or inadequately managed, UTIs may result in serious complications affecting both the mother and fetus, including pyelonephritis, maternal sepsis, preterm labour, low birth weight, miscarriage, and neonatal sepsis. Consequently, the early diagnosis and appropriate management of UTIs during pregnancy remain important components of routine antenatal care (World Health Organization, 2024).

Pregnancy induces several physiological adaptations that increase susceptibility to urinary tract infections. Elevated progesterone levels cause relaxation of the smooth muscles of the ureters and bladder, leading to reduced ureteral peristalsis, urinary stasis, and incomplete bladder emptying. Simultaneously, the enlarging uterus compresses the ureters, particularly on the right side, impairing urine flow and promoting vesicoureteral reflux. Increased renal plasma flow and glomerular filtration rate also contribute to physiological hydronephrosis during pregnancy, creating a favorable environment for bacterial multiplication (Al Kadri et al., 2024). These changes collectively increase the likelihood of bacterial persistence within the urinary tract and facilitate ascending infection from the bladder to the kidneys.

Immunological adaptations during pregnancy further contribute to the increased risk of infection. To maintain fetal tolerance, maternal immunity undergoes complex modulation involving alterations in both innate and adaptive immune responses. Although these changes are essential for successful pregnancy, they may reduce the mother's ability to eliminate invading microorganisms efficiently, thereby increasing susceptibility to bacterial infections. The interaction between altered immunity and urinary stasis explains why pregnant women experience higher rates of asymptomatic bacteriuria, acute cystitis, and pyelonephritis compared with non-pregnant women (Monari et al., 2024).

Urinary tract infections during pregnancy are generally classified into three clinical categories: asymptomatic bacteriuria (ASB), acute cystitis, and acute pyelonephritis. Asymptomatic bacteriuria is defined as the presence of significant bacterial growth in urine without urinary symptoms. It occurs in approximately 2–10% of pregnancies and is clinically important because untreated ASB progresses to pyelonephritis in up to one-third of affected women. Consequently, many international guidelines recommend routine urine culture screening during early pregnancy to identify and treat ASB before complications develop (American College of Obstetricians and Gynecologists, 2023).

Acute cystitis represents infection confined primarily to the bladder and lower urinary tract. Typical symptoms include dysuria, urinary frequency, urgency, suprapubic discomfort, and cloudy or foul-smelling urine. Although cystitis rarely causes severe systemic illness, delayed or

inappropriate treatment during pregnancy may permit ascending infection, increasing the risk of pyelonephritis and adverse obstetric outcomes. Appropriate antimicrobial therapy based on culture and susceptibility testing is therefore essential to ensure complete bacterial eradication while minimizing fetal exposure to unnecessary antibiotics.

Acute pyelonephritis is the most severe manifestation of urinary tract infection during pregnancy and constitutes a medical emergency. It is characterized by fever, flank pain, chills, nausea, vomiting, and costovertebral angle tenderness, often accompanied by systemic inflammatory responses. Pyelonephritis increases the risk of maternal bacteremia, septic shock, acute respiratory distress syndrome, renal dysfunction, and prolonged hospitalization. Furthermore, maternal pyelonephritis has been associated with uterine contractions, premature rupture of membranes, preterm labour, fetal growth restriction, and neonatal morbidity, highlighting the need for prompt diagnosis and aggressive treatment (Al Kadri et al., 2024).

The microbiological profile of UTIs during pregnancy closely resembles that observed in the general population, although certain pathogens are encountered more frequently depending on geographical location and healthcare setting. Escherichia coli consistently remains the predominant uropathogen, accounting for approximately 70–90% of uncomplicated infections worldwide. Other clinically important organisms include Klebsiella species, Proteus species, Enterococcus species, Staphylococcus saprophyticus, and Staphylococcus aureus. Opportunistic pathogens such as Pseudomonas aeruginosa may also occur in complicated infections or among hospitalized patients. The predominance of these organisms underscores the importance of continuous microbiological surveillance to monitor changing antimicrobial susceptibility patterns (Kranz et al. 2024).

One of the greatest challenges in managing UTIs during pregnancy is the increasing prevalence of antimicrobial resistance among common uropathogens. Rising resistance to fluoroquinolones, ampicillin, trimethoprim-sulfamethoxazole, and tetracyclines has reduced the reliability of empirical therapy in many healthcare settings. Simultaneously, treatment options during pregnancy are inherently limited because several antibiotics are contraindicated or should be used cautiously due to potential teratogenicity or adverse fetal effects. Current evidence indicates that antibiotics such as Nitrofurantoin, Fosfomycin, Cephalexin, Amoxicillin-Clavulanate, Cefuroxime, and Ceftriaxone generally remain appropriate therapeutic options when selected according to gestational age, clinical indication, and antimicrobial susceptibility results (American College of Obstetricians and Gynecologists, 2023). However, local resistance patterns should always guide antibiotic selection whenever possible.

Antimicrobial susceptibility testing has become increasingly important in obstetric practice because empirical treatment alone may no longer provide reliable bacterial eradication. Culture-guided therapy allows clinicians to select antibiotics that are both microbiologically effective and safe for maternal and fetal health. Routine urine culture screening, particularly during the first antenatal visit, has therefore been incorporated into antenatal care guidelines in many countries.

This approach facilitates early detection of asymptomatic bacteriuria, reduces progression to pyelonephritis, and decreases the incidence of adverse pregnancy outcomes (WHO, 2024).

In sub-Saharan Africa, the burden of UTIs during pregnancy is compounded by limited laboratory capacity, delayed healthcare seeking, self-medication, and unrestricted access to antibiotics. Many healthcare facilities continue to rely on empirical antibiotic prescribing because microbiological culture and susceptibility testing are either unavailable or unaffordable for many patients. These practices contribute to inappropriate antibiotic use and accelerate the emergence of multidrug-resistant uropathogens. Recent studies from Ghana, Nigeria, Ethiopia, Kenya, and Uganda have reported increasing resistance among Escherichia coli, Klebsiella species, and Enterococcus species, particularly to commonly prescribed antibiotics such as ampicillin, cotrimoxazole, and fluoroquinolones (Donkor et al., 2024).

In Ghana, UTIs remain a common reason for antenatal clinic attendance and antibiotic prescription. Studies conducted in various healthcare facilities have consistently identified Escherichia coli as the predominant urinary pathogen among pregnant women, followed by Klebsiella species, Staphylococcus aureus, and Enterococcus species (Afeke et al., 2025). While Nitrofurantoin and third-generation cephalosporins generally retain good antimicrobial activity, increasing resistance to several first-line antibiotics has raised concerns regarding empirical treatment practices. These findings reinforce the need for routine culture and antimicrobial susceptibility testing before initiating antibiotic therapy, particularly among pregnant women who are at increased risk of severe maternal and neonatal complications.

Beyond their immediate clinical effects, UTIs during pregnancy have significant implications for public health and healthcare systems. Resistant infections increase healthcare costs through prolonged hospitalization, repeated laboratory investigations, use of expensive second-line antibiotics, and additional maternal and neonatal care. They also contribute to increased antibiotic consumption, creating a cycle that further accelerates antimicrobial resistance. Effective prevention strategies including routine antenatal screening, patient education, infection prevention measures, antimicrobial stewardship, and evidence-based prescribing are therefore essential to reduce the burden of UTIs and improve pregnancy outcomes.

Overall, urinary tract infections remain a major challenge during pregnancy because of the unique physiological changes that predispose women to infection and the increasing prevalence of antimicrobial-resistant pathogens. The coexistence of limited therapeutic options during pregnancy and rising bacterial resistance underscores the importance of culture-guided antibiotic therapy, routine surveillance of antimicrobial susceptibility patterns, and strengthened antimicrobial stewardship. These considerations provide the clinical and scientific basis for the present study, which investigates antimicrobial resistance among bacterial pathogens isolated from pregnant and non-pregnant women and evaluates its implications for pregnancy and childbirth outcomes.

2.5 Reproductive Tract Infections

Reproductive tract infections (RTIs) constitute a major public health concern among women of reproductive age and are an important cause of gynecological morbidity, adverse pregnancy outcomes, infertility, and neonatal complications worldwide. RTIs encompass a broad spectrum of infections affecting the female reproductive system, including the vagina, cervix, uterus, fallopian tubes, ovaries, and surrounding pelvic structures. These infections may result from endogenous microorganisms, sexually transmitted pathogens, or opportunistic organisms that proliferate when the normal vaginal microbiota is disrupted. Similar to urinary tract infections, the increasing prevalence of antimicrobial-resistant pathogens has complicated the management of RTIs and heightened concerns regarding maternal and neonatal health outcomes (WHO, 2024).

The female reproductive tract normally contains a complex microbial ecosystem dominated by Lactobacillus species, which play a critical role in maintaining vaginal health. These organisms produce lactic acid and other antimicrobial substances that maintain an acidic vaginal pH and inhibit the growth of pathogenic microorganisms. Disruption of this protective microbiota, whether through antibiotic use, hormonal changes, poor hygiene, sexual activity, or immunosuppression, can create conditions that favor the proliferation of pathogenic bacteria, fungi, and other microorganisms, leading to infection (Monari et al., 2024).

Reproductive tract infections are generally classified into three broad categories: endogenous infections, iatrogenic infections, and sexually transmitted infections (STIs). Endogenous infections arise from the overgrowth of organisms normally present within the reproductive tract, such as bacterial vaginosis and vulvovaginal candidiasis. Iatrogenic infections result from medical procedures involving the reproductive tract, including unsafe abortions, intrauterine device insertion, childbirth-related interventions, and surgical procedures. Sexually transmitted infections occur through sexual contact and include infections caused by Neisseria gonorrhoeae, Chlamydia trachomatis, Treponema pallidum, and other sexually transmitted pathogens (CDC, 2024).

Among reproductive tract infections, bacterial vaginosis (BV) remains one of the most common conditions affecting women globally. BV occurs when the normal lactobacilli-dominated vaginal flora is replaced by a polymicrobial community of anaerobic bacteria, including Gardnerella vaginalis, Prevotella species, and Mobiluncus species. Although BV may be asymptomatic, affected women frequently present with abnormal vaginal discharge, unpleasant odor, itching, and discomfort. Importantly, bacterial vaginosis has been associated with adverse reproductive outcomes including preterm labour, premature rupture of membranes, postpartum endometritis, and increased susceptibility to sexually transmitted infections (Klebanoff et al., 2023).

Vulvovaginal candidiasis represents another common reproductive tract infection among women of reproductive age. The condition is primarily caused by Candida albicans, although non-albicans Candida species have become increasingly important in recurrent infections. Hormonal changes during pregnancy, diabetes mellitus, prolonged antibiotic use, immunosuppression, and

alterations in vaginal pH are recognized risk factors for candidal overgrowth. While vulvovaginal candidiasis is generally not associated with severe maternal complications, recurrent or untreated infections may significantly impair quality of life and contribute to discomfort during pregnancy (Sobel, 2024).

Sexually transmitted reproductive tract infections remain a major global health challenge. Pathogens such as Neisseria gonorrhoeae and Chlamydia trachomatis are responsible for millions of new infections annually and are frequently associated with significant reproductive health complications. Neisseria gonorrhoeae infection may cause cervicitis, urethritis, pelvic inflammatory disease, infertility, ectopic pregnancy, and neonatal conjunctivitis. Similarly, Chlamydia trachomatis is a leading cause of preventable infertility worldwide and has been associated with adverse pregnancy outcomes including miscarriage, preterm birth, and neonatal respiratory infections (WHO, 2024).

Pelvic inflammatory disease (PID) represents one of the most serious consequences of untreated reproductive tract infections. PID occurs when microorganisms ascend from the lower reproductive tract into the uterus, fallopian tubes, and surrounding pelvic structures, causing inflammation and tissue damage. The condition is frequently associated with Neisseria gonorrhoeae, Chlamydia trachomatis, anaerobic bacteria, and mixed microbial infections. Long-term complications of PID include chronic pelvic pain, infertility, tubal factor infertility, ectopic pregnancy, and recurrent reproductive tract infections. These outcomes contribute substantially to reproductive health burdens globally, particularly in low-resource settings where access to early diagnosis and treatment may be limited (Workowski et al., 2021).

Pregnancy significantly influences the epidemiology and clinical significance of reproductive tract infections. Hormonal and immunological changes that occur during pregnancy alter the vaginal microbiome and may increase susceptibility to bacterial and fungal infections. Furthermore, reproductive tract infections during pregnancy may facilitate ascending infection into the uterine cavity, potentially affecting both maternal and fetal health. Numerous studies have demonstrated associations between untreated RTIs and adverse pregnancy outcomes including spontaneous abortion, preterm labour, premature rupture of membranes, intrauterine infection, low birth weight, stillbirth, and postpartum sepsis (Al Kadri et al., 2024).

The microbiological profile of reproductive tract infections varies according to geographical location, population characteristics, healthcare access, and sexual behavior patterns. Common bacterial pathogens isolated from high vaginal swab specimens include Staphylococcus aureus, Streptococcus agalactiae (Group B Streptococcus), Enterococcus species, Neisseria gonorrhoeae, and various anaerobic organisms. Fungal pathogens, particularly Candida species, are also frequently isolated. In pregnant women, colonization by Group B Streptococcus is of particular concern because of its association with neonatal sepsis, meningitis, pneumonia, and maternal postpartum infections Verani et al. (2010).

A major challenge in the management of reproductive tract infections is the increasing prevalence of antimicrobial resistance among causative pathogens. Resistance has been reported in Neisseria gonorrhoeae, Staphylococcus aureus, Enterococcus species, and several Gram-negative organisms isolated from reproductive tract specimens. The emergence of multidrug-resistant strains has reduced the effectiveness of many commonly prescribed antibiotics and complicated empirical treatment strategies. Of particular concern is the global emergence of multidrug-resistant Neisseria gonorrhoeae, which has demonstrated resistance to penicillins, tetracyclines, fluoroquinolones, and, in some regions, reduced susceptibility to extended-spectrum cephalosporins (CDC, 2024).

The inappropriate use of antibiotics remains a major driver of resistance in reproductive tract pathogens. Self-medication, incomplete treatment courses, over-the-counter antibiotic access, inappropriate prescriptions, and poor adherence to antimicrobial stewardship principles contribute significantly to the development and spread of resistant organisms. These challenges are particularly pronounced in low- and middle-income countries, where laboratory diagnostic capacity may be limited and empirical treatment is frequently employed without microbiological confirmation (Donkor et al., 2024).

In sub-Saharan Africa, reproductive tract infections remain highly prevalent and continue to contribute substantially to maternal morbidity and mortality. Studies from Ghana, Nigeria, Ethiopia, Kenya, and Uganda have documented increasing rates of antimicrobial resistance among pathogens isolated from high vaginal swab specimens. Resistance to tetracyclines, fluoroquinolones, cotrimoxazole, and other commonly used antibiotics has been widely reported, while susceptibility to selected cephalosporins and macrolides remains relatively preserved in many settings. These findings underscore the need for routine culture and susceptibility testing to guide antibiotic selection and improve treatment outcomes (Donkor et al., 2024).

In Ghana, reproductive tract infections represent a significant burden among women attending antenatal clinics, gynecology units, and reproductive health centers. Studies have consistently identified Staphylococcus aureus, Candida species, Enterococcus species, and Neisseria gonorrhoeae among the most common pathogens isolated from reproductive tract specimens. Similar to trends observed elsewhere in Africa, increasing antimicrobial resistance has been reported, emphasizing the need for strengthened surveillance systems, antimicrobial stewardship programs, and evidence-based treatment protocols (Afeke et al., 2025).

The prevention and control of reproductive tract infections require a comprehensive approach that combines health education, safe sexual practices, routine screening, early diagnosis, effective antimicrobial therapy, infection prevention measures, and antimicrobial stewardship interventions. During pregnancy, routine antenatal screening and timely treatment are particularly important because of the potential consequences for both maternal and neonatal health. Integrating microbiological diagnosis with antimicrobial susceptibility testing can

improve treatment outcomes, reduce inappropriate antibiotic use, and help limit the emergence and spread of resistant pathogens.

In conclusion, reproductive tract infections remain a significant cause of morbidity among women of reproductive age and contribute substantially to adverse reproductive, maternal, and neonatal outcomes. The increasing prevalence of antimicrobial-resistant pathogens has further complicated their management and highlights the importance of surveillance, evidence-based antibiotic prescribing, and antimicrobial stewardship. Given the close relationship between reproductive tract infections, urinary tract infections, and pregnancy outcomes, understanding the epidemiology and resistance patterns of reproductive tract pathogens is essential for improving women's health and reducing the burden of antimicrobial resistance.

2.6: Mechanisms of Antimicrobial Resistance

The preceding sections have demonstrated that urinary and reproductive tract infections remain major contributors to maternal morbidity and adverse pregnancy outcomes, particularly in low- and middle-income countries where the burden of infectious diseases and antimicrobial resistance is disproportionately high. The increasing prevalence of multidrug-resistant bacterial pathogens has significantly reduced the effectiveness of many first-line antimicrobial agents, resulting in treatment failures, recurrent infections, prolonged hospitalization, increased healthcare costs, and poorer maternal and neonatal outcomes. These observations underscore that understanding the epidemiology of resistant infections alone is insufficient; it is equally important to examine the biological and behavioral factors that drive the emergence, persistence, and dissemination of antimicrobial resistance.

Bacterial resistance does not occur randomly but develops through a dynamic interaction between microbial evolution, antimicrobial selection pressure, healthcare practices, environmental factors, and human behavior. While bacteria naturally evolve through spontaneous genetic mutations and the acquisition of resistance genes, inappropriate antimicrobial use markedly accelerates this evolutionary process. Practices such as self-medication, empirical prescribing without culture and antimicrobial susceptibility testing, indiscriminate access to antibiotics, incomplete treatment courses, substandard antimicrobial stewardship, and poor infection prevention and control measures create selective pressure that favors the survival, multiplication, and transmission of resistant microorganisms (Donkor et al., 2024; Murray et al., 2022).

Community-level factors are equally important determinants of antimicrobial resistance. Evidence from a community-based health education intervention conducted in the Amamorley-Ashongman Municipality of Ghana demonstrated that inadequate public knowledge regarding appropriate antibiotic use contributes significantly to self-medication, poor adherence to prescribed treatment, and inappropriate antibiotic-seeking behaviors. The study further showed that targeted health education interventions significantly improved community awareness and promoted responsible antibiotic use, emphasizing that behavioral change and public education

are essential components of antimicrobial stewardship and effective strategies for mitigating the emergence and spread of antimicrobial resistance (Appiah & Amakeh, 2026). These findings support the growing consensus that combating antimicrobial resistance requires not only advances in microbiology and clinical therapeutics but also sustained public health interventions that address the behavioral drivers of antibiotic misuse.

These biological and behavioral determinants are particularly relevant in the management of urinary and reproductive tract infections during pregnancy, where inappropriate antibiotic use not only promotes antimicrobial resistance but also limits the availability of safe and effective therapeutic options for both the mother and fetus. Consequently, understanding the molecular basis of bacterial resistance is fundamental to interpreting antimicrobial susceptibility patterns, selecting appropriate antimicrobial therapy, and designing effective antimicrobial stewardship strategies. Such knowledge provides the scientific basis for evidence-based clinical decision-making and supports national and global efforts to preserve the efficacy of existing antimicrobial agents.

Accordingly, the following section critically examines the principal mechanisms through which bacteria develop and disseminate antimicrobial resistance, including enzymatic inactivation of antibiotics, modification of antimicrobial target sites, reduced membrane permeability, activation of efflux pumps, biofilm formation, and horizontal gene transfer. Understanding these mechanisms is fundamental to explaining the resistance patterns observed among clinically important pathogens such as Escherichia coli, Staphylococcus aureus, Klebsiella spp., Pseudomonas spp., Enterococcus spp., and Proteus spp., which constitute the predominant bacterial isolates investigated in the present study.

2.7 Antimicrobial Stewardship in Obstetric Care

Antimicrobial stewardship (AMS) has become a cornerstone of modern healthcare and is recognized as one of the most effective strategies for combating antimicrobial resistance (AMR). The World Health Organization defines antimicrobial stewardship as a coordinated set of interventions designed to promote the appropriate selection, dosage, route of administration, and duration of antimicrobial therapy in order to achieve optimal clinical outcomes while minimizing antimicrobial resistance, adverse drug reactions, and unnecessary healthcare costs (WHO, 2024). In obstetric care, antimicrobial stewardship is particularly important because clinicians must simultaneously protect maternal health, preserve fetal safety, and minimize the emergence of resistant bacterial pathogens.

Pregnant women constitute a unique patient population because physiological changes during pregnancy alter drug pharmacokinetics, immune function, and susceptibility to infection. Consequently, antimicrobial prescribing during pregnancy requires careful consideration of the balance between therapeutic efficacy and fetal safety. Untreated bacterial infections such as urinary tract infections (UTIs), reproductive tract infections (RTIs), chorioamnionitis, postpartum endometritis, and maternal sepsis can result in severe maternal and neonatal complications.

Conversely, inappropriate or unnecessary antibiotic exposure may contribute to antimicrobial resistance, disruption of the maternal and neonatal microbiome, adverse drug reactions, and potential fetal toxicity (American College of Obstetricians and Gynecologists [ACOG], 2023). These competing priorities make antimicrobial stewardship an essential component of evidence-based obstetric practice.

A fundamental principle of antimicrobial stewardship is that antibiotic therapy should be guided by microbiological evidence whenever feasible. Culture and antimicrobial susceptibility testing (AST) remain the gold standard for identifying causative organisms and determining the most appropriate antimicrobial agents. Culture-guided therapy enables clinicians to prescribe antibiotics with the narrowest effective spectrum, thereby reducing unnecessary exposure to broad-spectrum agents and minimizing selective pressure for resistance (Clinical and Laboratory Standards Institute, 2024). In obstetric care, routine urine culture screening for asymptomatic bacteriuria and targeted microbiological investigation of symptomatic infections are recommended to improve treatment outcomes and prevent progression to severe disease.

Empirical antibiotic therapy is often necessary in obstetric emergencies, particularly when delays in treatment could jeopardize maternal or fetal health. Conditions such as maternal sepsis, pyelonephritis, chorioamnionitis, and postpartum infections require immediate initiation of antimicrobial therapy before laboratory results become available. Nevertheless, stewardship principles emphasize that empirical treatment should be based on local epidemiological data, institutional antibiograms, and established clinical guidelines. Once microbiological results are obtained, antibiotic therapy should be reviewed and modified through de-escalation, whereby broad-spectrum agents are replaced with narrower-spectrum antibiotics that specifically target the identified pathogen (WHO, 2024; CLSI, 2024).

The WHO AWaRe (Access, Watch, and Reserve) classification provides an internationally recognized framework for optimizing antibiotic use. The Access group includes antibiotics with lower resistance potential and should constitute the majority of antibiotic prescriptions for common infections. Examples relevant to obstetric practice include Amoxicillin, Ampicillin, Penicillin G, Cephalexin, and Nitrofurantoin. The Watch group comprises antibiotics with higher resistance potential, such as fluoroquinolones and third-generation cephalosporins, whose use should be carefully monitored. The Reserve group consists of last-resort antibiotics reserved for infections caused by multidrug-resistant organisms. Adoption of the AWaRe framework has been associated with improved prescribing practices and reduced inappropriate antibiotic consumption worldwide (WHO, 2024).

Antibiotic selection during pregnancy must also consider fetal safety. Several antimicrobial agents are generally regarded as safe when used appropriately during pregnancy, including penicillins, cephalosporins, selected macrolides, clindamycin, nitrofurantoin (with gestational considerations), and fosfomycin. In contrast, fluoroquinolones, tetracyclines, aminoglycosides (except in selected circumstances), and chloramphenicol are generally avoided or used with

extreme caution because of potential fetal toxicity, effects on skeletal and dental development, ototoxicity, nephrotoxicity, or other adverse outcomes (ACOG, 2023). Therefore, antimicrobial stewardship in obstetrics extends beyond reducing resistance to ensuring maternal and fetal safety through rational drug selection.

The emergence of multidrug-resistant (MDR) organisms has further highlighted the importance of stewardship in maternal healthcare. Increasing resistance among Escherichia coli, Klebsiella spp., Staphylococcus aureus, Enterococcus spp., and Pseudomonas spp. Has significantly reduced the effectiveness of several commonly prescribed antibiotics for urinary and reproductive tract infections. The widespread misuse of fluoroquinolones, tetracyclines, sulfonamides, and other broad-spectrum antibiotics has accelerated resistance, making culture-guided therapy increasingly indispensable. In the present study, the high resistance observed among non-recommended antibiotics in pregnant women reinforces the need for antimicrobial stewardship interventions that prioritize susceptibility-guided prescribing and adherence to obstetric treatment guidelines.

Healthcare-associated factors also influence antimicrobial stewardship. Inadequate infection prevention and control (IPC) practices, prolonged hospitalization, invasive procedures, urinary catheterization, and poor hand hygiene facilitate the transmission of resistant pathogens within maternity units. Effective stewardship therefore requires integration with robust IPC programs, including adherence to hand hygiene protocols, environmental sanitation, aseptic clinical techniques, and surveillance of healthcare-associated infections (CDC, 2024). These measures reduce infection incidence, decrease antibiotic consumption, and limit opportunities for resistant organisms to spread within healthcare facilities.

Patient education represents another essential pillar of antimicrobial stewardship. Pregnant women should receive counseling regarding the appropriate use of antibiotics, the importance of completing prescribed treatment courses, and the dangers of self-medication and sharing antibiotics. In many low- and middle-income countries, antibiotics remain readily available without prescription, encouraging inappropriate use and accelerating antimicrobial resistance. Community engagement and public health education are therefore critical components of comprehensive stewardship programs. Evidence from Ghana has demonstrated that structured community-based health education significantly improves public knowledge regarding appropriate antibiotic use and reduces behaviors associated with antibiotic misuse, highlighting the importance of integrating educational interventions into national AMR control strategies (Appiah & Amakeh, 2026).

Despite global recognition of antimicrobial stewardship, implementation remains challenging in many resource-limited settings. Common barriers include limited microbiology laboratory capacity, inadequate antimicrobial susceptibility testing, shortages of trained personnel, inconsistent adherence to treatment guidelines, weak surveillance systems, and financial constraints. These challenges often result in empirical prescribing practices that may not reflect

local resistance patterns, thereby contributing to treatment failure and accelerating antimicrobial resistance (Donkor et al., 2024). Strengthening laboratory infrastructure, expanding access to culture and susceptibility testing, and investing in healthcare worker training are therefore essential for improving stewardship in obstetric care.

In Ghana, the Ministry of Health has adopted a National Action Plan on Antimicrobial Resistance, aligned with the WHO Global Action Plan and the One Health approach, to strengthen surveillance, antimicrobial stewardship, public awareness, infection prevention, and research. Nevertheless, implementation challenges remain, particularly in district hospitals and primary healthcare facilities where diagnostic resources may be limited. Continuous surveillance of bacterial pathogens isolated from pregnant women, coupled with routine antimicrobial susceptibility testing, is therefore essential for guiding empirical therapy and informing national treatment guidelines.

Overall, antimicrobial stewardship is fundamental to preserving the effectiveness of existing antibiotics, improving maternal and neonatal health outcomes, and reducing the emergence and spread of antimicrobial resistance. In obstetric care, stewardship integrates evidence-based prescribing, microbiological diagnosis, antimicrobial susceptibility testing, patient education, infection prevention, and continuous surveillance to ensure that bacterial infections are managed safely and effectively. The findings of the present study further reinforce the need for strengthened stewardship programs, particularly in the management of urinary and reproductive tract infections among pregnant and non-pregnant women, where informed antibiotic selection can substantially reduce treatment failure, antimicrobial resistance, and adverse pregnancy outcomes.

2.8 Antimicrobial Resistance in Ghana and Sub-Saharan Africa

Antimicrobial resistance (AMR) has become one of the most significant public health threats in sub-Saharan Africa, where the burden of infectious diseases remains disproportionately high and healthcare systems often face substantial resource constraints. The region experiences a high prevalence of bacterial infections, widespread empirical antibiotic use, limited microbiological diagnostic capacity, inadequate antimicrobial stewardship, and unrestricted access to antimicrobial agents. Collectively, these factors have accelerated the emergence and dissemination of multidrug-resistant (MDR) bacterial pathogens, compromising the effective management of common infections, including urinary tract infections (UTIs), reproductive tract infections (RTIs), bloodstream infections, and healthcare-associated infections (WHO, 2024; Murray et al., 2022).

Sub-Saharan Africa bears one of the highest burdens of AMR-related morbidity and mortality globally. The Global Burden of Disease Antimicrobial Resistance Collaborators estimated that bacterial AMR was associated with a substantial proportion of infection-related deaths across Africa, with many fatalities resulting from organisms resistant to first-line antimicrobial agents (Murray et al., 2022). The impact is particularly severe among vulnerable populations, including

pregnant women, neonates, children, older adults, and immunocompromised individuals, who are more susceptible to severe bacterial infections and their complications. Resistant infections frequently result in prolonged hospitalization, increased healthcare expenditure, therapeutic failure, maternal sepsis, neonatal sepsis, and increased mortality.

The epidemiology of antimicrobial resistance across sub-Saharan Africa is characterized by increasing resistance among both Gram-negative and Gram-positive bacterial pathogens. Gram-negative organisms such as Escherichia coli, Klebsiella pneumoniae, Pseudomonas aeruginosa, Acinetobacter baumannii, and Proteus species have demonstrated rising resistance to β-lactams, fluoroquinolones, aminoglycosides, and trimethoprim-sulfamethoxazole. Similarly, Gram-positive pathogens including Staphylococcus aureus, Enterococcus species, and Streptococcus agalactiae increasingly exhibit resistance to commonly prescribed antimicrobial agents, complicating empirical treatment and limiting therapeutic options (Donkor et al., 2024).

One of the most concerning developments in the region is the increasing prevalence of multidrug-resistant organisms, including extended-spectrum β-lactamase (ESBL)-producing Enterobacterales, methicillin-resistant Staphylococcus aureus (MRSA), vancomycin-resistant enterococci (VRE), and carbapenem-resistant Gram-negative bacteria. ESBL-producing Escherichia coli and Klebsiella species have become particularly important causes of urinary tract and bloodstream infections, significantly reducing the effectiveness of penicillins and third-generation cephalosporins. The emergence of carbapenem-resistant organisms further threatens the effectiveness of last-line antimicrobial agents and underscores the urgency of strengthening antimicrobial stewardship throughout the region (WHO, 2024).

Several interconnected factors contribute to the rapid emergence of antimicrobial resistance in sub-Saharan Africa. These include indiscriminate antibiotic prescribing, self-medication, over-the-counter access to prescription-only medicines, counterfeit and substandard antimicrobial products, inadequate infection prevention and control measures, poor sanitation, limited laboratory diagnostic capacity, and weak surveillance systems. In many healthcare facilities, clinicians initiate empirical antibiotic therapy without culture and antimicrobial susceptibility testing because microbiological services are unavailable, inaccessible, or unaffordable. Such practices increase antimicrobial selection pressure and accelerate the development of resistant bacterial populations (Donkor et al., 2024).

Community behaviors further exacerbate the problem. In many African countries, antibiotics are frequently purchased without prescription, treatment courses are often discontinued prematurely once symptoms improve, and unused antibiotics are commonly shared among family members. These practices expose bacteria to sub-therapeutic antimicrobial concentrations, creating favorable conditions for the selection of resistant strains. Evidence from Ghana demonstrates that community-based health education significantly improves knowledge regarding appropriate antibiotic use and reduces antibiotic misuse, highlighting the importance of behavioral

interventions as an integral component of national antimicrobial stewardship strategies (Appiah & Amakeh, 2026).

Ghana has recognized antimicrobial resistance as a major national public health priority. In response, the Government of Ghana developed the National Action Plan on Antimicrobial Resistance, which aligns with the WHO Global Action Plan and adopts a One Health approach integrating human, animal, and environmental health sectors. The national strategy emphasizes antimicrobial stewardship, infection prevention and control, laboratory strengthening, surveillance, research, and public awareness. Despite these initiatives, implementation challenges remain, particularly in resource-limited healthcare settings where laboratory infrastructure, antimicrobial susceptibility testing, and stewardship programs are still developing (Ministry of Health Ghana, 2023).

Numerous studies conducted in Ghana have documented increasing antimicrobial resistance among bacterial pathogens responsible for urinary tract infections, reproductive tract infections, bloodstream infections, wound infections, and healthcare-associated infections. Escherichia coli remains the predominant uropathogen, followed by Klebsiella species, Staphylococcus aureus, Enterococcus species, Proteus species, and Pseudomonas species. Resistance to Ampicillin, Trimethoprim-Sulfamethoxazole, Tetracycline, and Fluoroquinolones has become increasingly common, whereas Nitrofurantoin, selected cephalosporins, and carbapenems generally retain relatively higher levels of activity against many clinical isolates, although resistance to these agents is also gradually increasing (Afeke et al., 2025; Donkor et al., 2024).

Among pregnant women in Ghana, antimicrobial resistance presents additional clinical challenges because antibiotic selection must simultaneously achieve effective bacterial eradication while minimizing fetal risk. Increasing resistance among urinary and reproductive tract pathogens reduces the effectiveness of empirical therapy and increases the likelihood of persistent infection, pyelonephritis, maternal sepsis, preterm labour, miscarriage, postpartum infections, and neonatal sepsis. Consequently, routine culture and antimicrobial susceptibility testing are becoming increasingly important for guiding appropriate antibiotic selection during pregnancy and improving maternal and neonatal outcomes.

Healthcare-associated infections also contribute substantially to the burden of antimicrobial resistance in Ghana. Inadequate infection prevention and control practices, overcrowded hospital wards, prolonged hospitalization, invasive procedures, and limited antimicrobial stewardship facilitate the transmission of resistant organisms within healthcare facilities. Strengthening hand hygiene compliance, environmental sanitation, antimicrobial stewardship programs, and microbiological surveillance remains essential for reducing healthcare-associated transmission of resistant pathogens.

The socioeconomic implications of antimicrobial resistance in Ghana and sub-Saharan Africa extend beyond healthcare delivery. Resistant infections increase healthcare expenditure through prolonged hospitalization, repeated laboratory investigations, more expensive second-line

antimicrobial therapy, productivity losses, and long-term disability. For many households, particularly in low-income settings, these additional costs create significant financial hardship and may delay healthcare seeking, further worsening clinical outcomes. The cumulative economic burden of AMR therefore represents a substantial obstacle to achieving universal health coverage and the United Nations Sustainable Development Goal 3, which seeks to ensure healthy lives and promote well-being for all.

Regional collaboration has become increasingly important in addressing antimicrobial resistance. Organizations such as the Africa Centres for Disease Control and Prevention (Africa CDC), the West African Health Organization (WAHO), and the WHO Regional Office for Africa continue to support surveillance networks, laboratory strengthening, antimicrobial stewardship, workforce development, and implementation of national action plans. Collaborative surveillance initiatives facilitate the sharing of resistance data across countries, enabling more effective monitoring of emerging resistant pathogens and informing regional treatment guidelines.

The findings of the present study align with these regional trends by demonstrating substantial antimicrobial resistance among bacterial pathogens isolated from urine, high vaginal swab, and blood specimens collected from pregnant and non-pregnant women. The predominance of Escherichia coli, Staphylococcus aureus, Klebsiella oxytoca, Enterococcus species, Citrobacter species, Proteus species, and Pseudomonas species mirrors reports from Ghana and other sub-Saharan African countries. Furthermore, the high resistance observed among fluoroquinolones, tetracyclines, aminoglycosides, and sulfonamides reinforces the urgent need for routine antimicrobial susceptibility testing, evidence-based antibiotic prescribing, strengthened antimicrobial stewardship, and continuous surveillance within obstetric and general clinical practice.

In conclusion, antimicrobial resistance has become a critical challenge in Ghana and across sub-Saharan Africa, threatening the effective management of bacterial infections and undermining progress toward improved maternal and neonatal health. The convergence of increasing antimicrobial resistance, limited diagnostic capacity, inappropriate antibiotic use, and healthcare resource constraints highlights the urgent need for integrated interventions that combine laboratory strengthening, antimicrobial stewardship, public education, infection prevention and control, and robust surveillance systems. These strategies are essential for preserving the effectiveness of existing antimicrobial agents and improving the management of urinary and reproductive tract infections among women of reproductive age.

2.9 Theoretical Framework

2.9.1 Introduction

A theoretical framework provides the conceptual foundation that explains the relationships among the variables investigated in a research study and guides the interpretation of research findings. In studies involving antimicrobial resistance (AMR), theoretical frameworks are

particularly important because the development and spread of resistance are influenced by complex interactions among biological, behavioral, clinical, environmental, and health system factors. Understanding these interactions is essential for designing effective interventions aimed at reducing inappropriate antibiotic use, improving antimicrobial stewardship, and preventing the emergence and dissemination of resistant bacterial pathogens (WHO, 2024).

The present study investigates antimicrobial resistance among bacterial pathogens isolated from urine, blood, and high vaginal swab specimens collected from pregnant and non-pregnant women and examines the implications of resistance for pregnancy and childbirth outcomes. Since both microbial evolution and human behavior contribute significantly to the development of antimicrobial resistance, this study is underpinned by an integrated theoretical framework that combines the One Health Approach and the Health Belief Model (HBM). Together, these frameworks provide a comprehensive explanation of how biological mechanisms, healthcare practices, and patient behaviors interact to influence antimicrobial resistance and maternal health outcomes.

2.9.2 One Health Approach

The One Health Approach is widely recognized as the leading global framework for addressing antimicrobial resistance. It emphasizes that the health of humans, animals, and the environment is interconnected and that antimicrobial resistance develops and spreads across these sectors. Consequently, effective control of antimicrobial resistance requires coordinated, multidisciplinary interventions involving healthcare professionals, veterinarians, environmental scientists, policymakers, and public health practitioners (WHO, 2024).

Within human healthcare, inappropriate antibiotic prescribing, self-medication, poor infection prevention and control practices, and inadequate antimicrobial stewardship create selective pressure that promotes the emergence of resistant bacteria. In the animal health sector, excessive antimicrobial use for disease prevention and growth promotion contributes to the development of resistant organisms that may subsequently be transmitted to humans through food, direct animal contact, or environmental contamination. Environmental reservoirs, including wastewater, hospital effluents, and agricultural runoff, also facilitate the dissemination of antimicrobial-resistant bacteria and resistance genes (Murray et al., 2022).

The One Health framework is directly relevant to the present study because the bacterial pathogens isolated from urine, blood, and reproductive tract specimens are influenced by antimicrobial use within both healthcare facilities and the wider community. Understanding resistance patterns among these pathogens therefore requires consideration of antimicrobial stewardship, infection prevention, environmental hygiene, and community antibiotic use. The findings generated by this study are expected to contribute to national AMR surveillance efforts and strengthen evidence-based antimicrobial stewardship in Ghana.

2.9.3 Health Belief Model (HBM)

While the One Health Approach explains antimicrobial resistance from a systems perspective, the Health Belief Model (HBM) provides a behavioral explanation for why individuals engage in appropriate or inappropriate antibiotic use. Developed by Rosenstock and later expanded by Becker and colleagues, the HBM proposes that health-related behaviors are influenced by an individual's perceptions regarding disease risk, disease severity, expected benefits of preventive actions, perceived barriers, cues to action, and self-efficacy.

The six major constructs of the Health Belief Model include:

Perceived Susceptibility: Individuals who believe they are at risk of developing bacterial infections are more likely to seek appropriate medical care and adhere to prescribed antibiotic therapy.

Perceived Severity: Awareness of the serious consequences of antimicrobial resistance including treatment failure, prolonged illness, maternal complications, neonatal infections, and death increases the likelihood of responsible antibiotic use.

Perceived Benefits: Patients who recognize the benefits of culture-guided antibiotic therapy, completing prescribed treatment courses, and avoiding self-medication are more likely to adopt behaviors that reduce antimicrobial resistance.

Perceived Barriers: Financial constraints, limited access to healthcare facilities, long waiting times, inadequate laboratory services, and over-the-counter availability of antibiotics may discourage appropriate healthcare-seeking behavior and promote self-medication.

Cues to Action: Health education campaigns, healthcare provider counseling, media awareness programs, and national antimicrobial stewardship initiatives serve as triggers that encourage appropriate antibiotic use.

Self-Efficacy: Individuals who possess adequate knowledge and confidence regarding the proper use of antibiotics are more likely to complete prescribed treatment and avoid behaviors that contribute to antimicrobial resistance.

The Health Belief Model is highly applicable to this study because antibiotic misuse remains one of the major drivers of antimicrobial resistance in Ghana. The findings from Appiah and Amakeh (2026) demonstrated that inadequate public knowledge significantly contributes to inappropriate antibiotic use and that community-based health education interventions substantially improve responsible antibiotic use. These findings support the assumptions of the Health Belief Model by illustrating how increased knowledge and awareness can positively influence health behavior and reduce inappropriate antimicrobial use.

2.9.4 Application of the Theoretical Framework to the Present Study

The integration of the One Health Approach and the Health Belief Model provides a comprehensive framework for understanding antimicrobial resistance among bacterial pathogens isolated from pregnant and non-pregnant women.

From the microbiological perspective, bacteria develop resistance through genetic mutations and horizontal gene transfer under antimicrobial selection pressure. From the behavioral perspective, inappropriate antibiotic use including self-medication, incomplete treatment courses, empirical prescribing without culture and susceptibility testing, and indiscriminate antibiotic access accelerates the selection and dissemination of resistant organisms.

Within obstetric care, these biological and behavioral factors interact to influence treatment outcomes. Inappropriate antibiotic use increases the likelihood of multidrug-resistant urinary and reproductive tract infections, which may subsequently contribute to maternal sepsis, pyelonephritis, preterm labour, miscarriage, postpartum infections, and neonatal complications. Conversely, evidence-based prescribing, antimicrobial stewardship, routine culture and susceptibility testing, and patient education reduce unnecessary antimicrobial exposure and improve maternal and neonatal outcomes.

Therefore, this study applies the integrated theoretical framework to examine the relationship between bacterial pathogens, antimicrobial susceptibility patterns, pregnancy status, and pregnancy outcomes while emphasizing the importance of responsible antibiotic use and antimicrobial stewardship.

2.9.5 Conceptual Framework

The conceptual framework for this study illustrates the relationships among the independent variables, mediating factors, and outcome variables.

Independent Variables

- Pregnancy status (pregnant and non-pregnant women)
- Age
- Clinical specimen type (urine, blood, high vaginal swab)
- Bacterial pathogens isolated
- Antibiotic prescribing practices
- Antibiotic misuse (self-medication, incomplete dosage, empirical treatment)

Mediating Variables

- Antimicrobial stewardship
- Culture and antimicrobial susceptibility testing
- Infection prevention and control measures
- Community health education
- Patient adherence to antibiotic therapy

Dependent Variables

- Antimicrobial resistance patterns
- Multidrug-resistant bacterial infections
- Treatment outcomes
- Maternal outcomes (pyelonephritis, sepsis, miscarriage, preterm labour)
- Neonatal outcomes (low birth weight, neonatal infection, adverse birth outcomes)

The framework proposes that inappropriate antimicrobial use and inadequate stewardship increase antimicrobial resistance, whereas effective stewardship, microbiological diagnosis, and patient education improve antibiotic effectiveness and reduce adverse pregnancy outcomes.

2.9.6 Summary of the Theoretical Framework

The integrated application of the One Health Approach and the Health Belief Model provides a strong theoretical basis for the present study. The One Health Approach explains the interconnected biological and environmental determinants of antimicrobial resistance, while the Health Belief Model explains how patient knowledge, perceptions, and behaviors influence antibiotic use. Together, these frameworks support the study's investigation into antimicrobial resistance among urinary and reproductive tract pathogens and reinforce the importance of laboratory-guided therapy, antimicrobial stewardship, infection prevention, and public health education in improving pregnancy and childbirth outcomes.

This theoretical foundation also aligns with the objectives of the study by providing a basis for interpreting antimicrobial susceptibility patterns, understanding the behavioral drivers of antibiotic resistance, and formulating recommendations for clinical practice and public health policy in Ghana and other sub-Saharan African settings.

2.10 Conceptual Framework of the Study

2.10.1 Introduction

A conceptual framework provides a visual and narrative representation of the relationships among the variables investigated in a research study. It translates the theoretical foundations into measurable constructs and illustrates how the independent variables influence the dependent variables through mediating factors. In antimicrobial resistance research, a conceptual framework is particularly important because resistance develops through complex interactions involving bacterial characteristics, patient-related factors, antimicrobial use, healthcare practices, and public health interventions.

The present study investigates antimicrobial resistance among bacterial pathogens isolated from urine, blood, and high vaginal swab (HVS) specimens collected from pregnant and non-pregnant women. It further examines how antimicrobial resistance influences the management of urinary and reproductive tract infections and its implications for pregnancy and childbirth outcomes.

Guided by the One Health Approach and the Health Belief Model, the conceptual framework integrates microbiological, clinical, behavioral, and healthcare system factors that contribute to antimicrobial resistance and treatment outcomes.

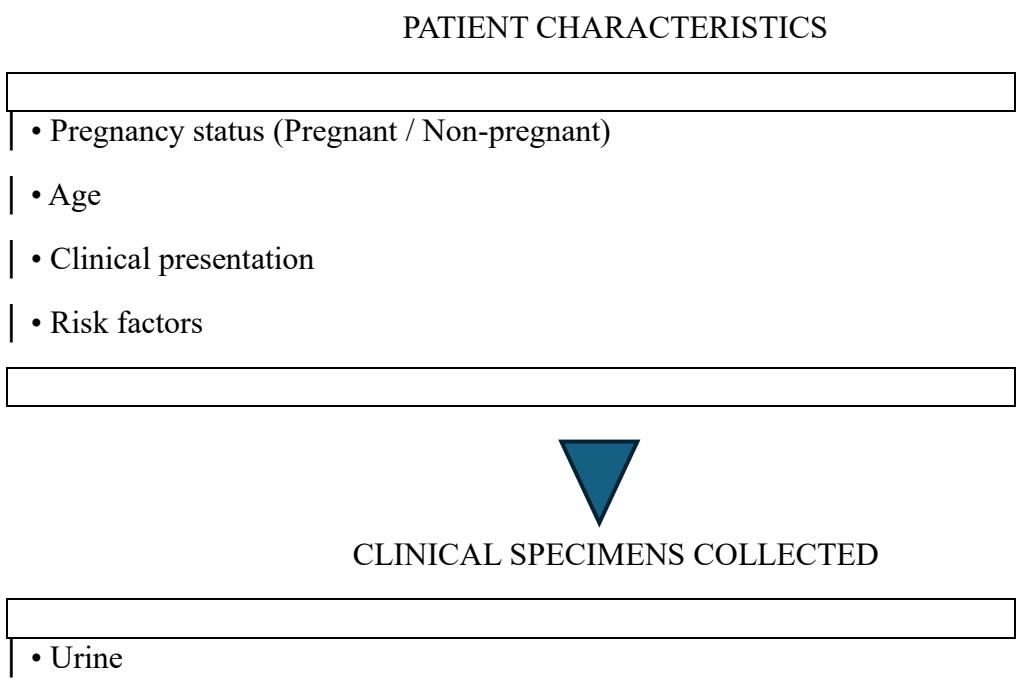
2.10.2 Conceptual Model

The conceptual framework proposes that patient characteristics and clinical factors influence the occurrence of bacterial infections. These infections are diagnosed through microbiological investigations, including culture and antimicrobial susceptibility testing (AST). The resulting susceptibility patterns determine the selection of appropriate antimicrobial therapy. However, the effectiveness of treatment is modified by antimicrobial stewardship practices, patient adherence to prescribed medications, and responsible antibiotic use. These factors collectively influence maternal health outcomes, pregnancy outcomes, and the emergence of multidrug-resistant (MDR) bacterial pathogens.

The framework also recognizes that inappropriate antibiotic use including self-medication, empirical prescribing without culture, indiscriminate antibiotic access, incomplete treatment courses, and poor adherence creates selective pressure that promotes antimicrobial resistance. Conversely, evidence-based prescribing, microbiological diagnosis, antimicrobial stewardship, and community health education reduce inappropriate antibiotic exposure and improve treatment outcomes.

2.10.3 Conceptual Framework Diagram

Figure 2.1: Conceptual Framework of the Study



- Blood
- High Vaginal Swab (HVS)



MICROBIOLOGICAL INVESTIGATION

- Culture and Identification
- Bacterial/Fungal Isolation
- Antimicrobial Susceptibility Testing (CLSI)



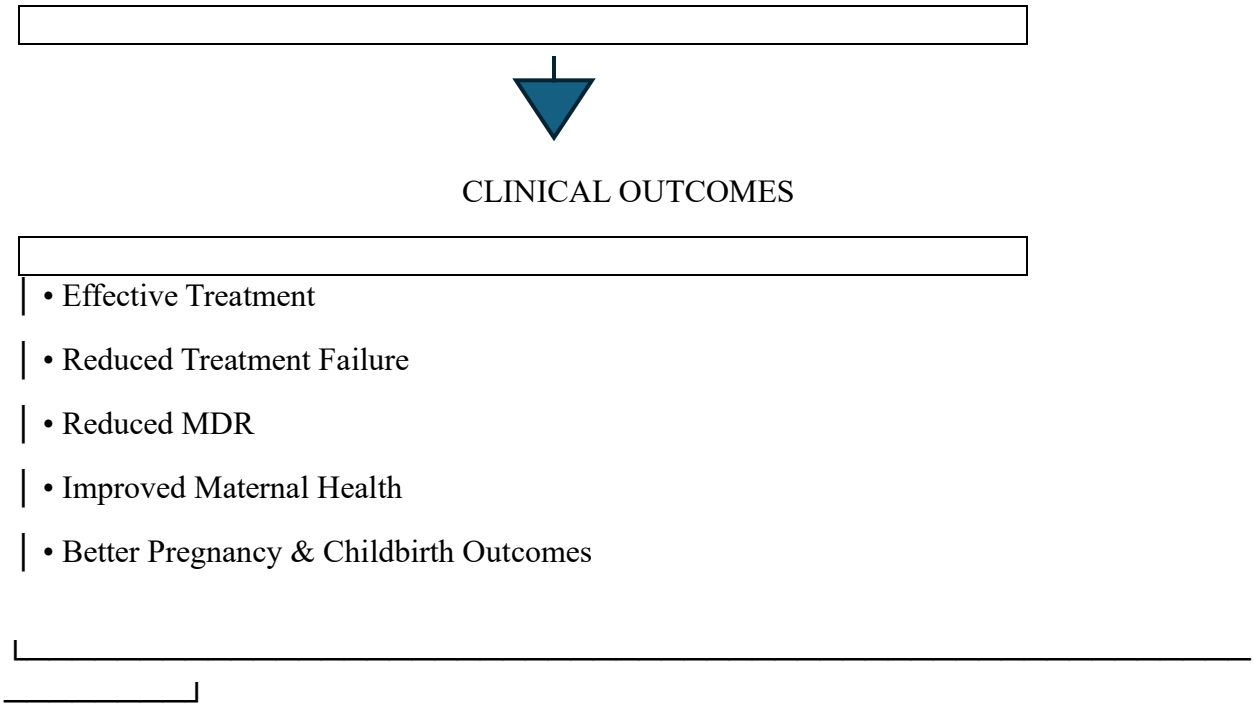
ANTIMICROBIAL RESISTANCE PATTERNS

- Susceptible (S)
- Intermediate (I)
- Resistant ®
- Multidrug Resistance (MDR)



MEDIATING FACTORS

- Antimicrobial Stewardship
- Culture-guided Antibiotic Therapy
- Infection Prevention & Control
- Community Health Education
- Patient Adherence



2.10.4 Explanation of the Conceptual Framework

The conceptual framework illustrates that pregnancy status, age, and clinical presentation influence the occurrence of urinary tract infections, reproductive tract infections, and bloodstream infections. Appropriate specimen collection (urine, blood, and HVS) allows laboratory identification of bacterial pathogens and determination of antimicrobial susceptibility using standardized CLSSI guidelines.

The laboratory findings generated through culture and susceptibility testing provide objective evidence for selecting effective antibiotics. Appropriate antimicrobial therapy improves treatment outcomes, whereas inappropriate antibiotic selection may result in persistent infection, treatment failure, and the development of multidrug-resistant organisms.

The framework further demonstrates that antimicrobial stewardship serves as a critical mediating factor between laboratory diagnosis and clinical outcomes. Stewardship interventions including culture-guided prescribing, patient education, infection prevention and control, and adherence to clinical guidelines reduce unnecessary antibiotic exposure and preserve the effectiveness of existing antimicrobial agents.

Conversely, inappropriate antibiotic use, including self-medication, empirical treatment without laboratory confirmation, indiscriminate antibiotic access, and incomplete treatment courses, accelerates the emergence of resistant bacterial strains. This relationship is supported by the findings of Appiah and Amakeh (2026), who demonstrated that community-based health education significantly improved responsible antibiotic use and reduced behaviors associated

with antibiotic misuse in urban Ghana. These findings emphasize that behavioral interventions complement microbiological surveillance in addressing antimicrobial resistance.

Ultimately, improved antimicrobial stewardship and evidence-based prescribing are expected to reduce antimicrobial resistance, improve treatment success, decrease maternal and neonatal complications, and promote safer pregnancy and childbirth outcomes.

Ultimately, improved antimicrobial stewardship and evidence-based prescribing are expected to reduce antimicrobial resistance, improve treatment success, decrease maternal and neonatal complications, and promote safer pregnancy and childbirth outcomes.

2.10.5 Relevance of the Conceptual Framework to the Present Study

The conceptual framework directly aligns with the objectives of this research by illustrating how laboratory diagnosis, antimicrobial susceptibility testing, and stewardship practices influence the management of bacterial infections among pregnant and non-pregnant women.

Specifically, the framework guided the study by:

- Identifying the independent variables (pregnancy status, age, specimen type, bacterial isolates, and antibiotic exposure).
- Defining the mediating variables (antimicrobial stewardship, culture-guided therapy, infection prevention and community health education).
- Identifying the dependent variables (antimicrobial resistance patterns, multidrug resistance, treatment outcomes, maternal outcomes, and pregnancy outcomes).
- Providing the analytical basis for examining relationships between bacterial pathogens, antimicrobial susceptibility patterns, and pregnancy outcomes.
- Supporting interpretation of the study findings within the broader context of antimicrobial stewardship and public health policy.

The framework also reinforces the study's central hypothesis that evidence-based antimicrobial prescribing, supported by microbiological diagnosis and strengthened antimicrobial stewardship, reduces antimicrobial resistance and improves maternal and neonatal health outcomes.

2.10.6 Chapter Summary

This chapter reviewed the current body of knowledge on antimicrobial resistance, urinary tract infections, reproductive tract infections, antimicrobial stewardship, mechanisms of bacterial resistance, and regional antimicrobial resistance trends in Ghana and sub-Saharan Africa. The chapter also established the theoretical and conceptual foundations of the study through the integration of the One Health Approach and the Health Belief Model. Together, these frameworks provide a comprehensive understanding of the biological, behavioral, and healthcare system factors influencing antimicrobial resistance.

The literature consistently demonstrates that inappropriate antibiotic use, inadequate antimicrobial stewardship, and limited access to microbiological diagnostics contribute substantially to the emergence and spread of multidrug-resistant bacterial pathogens. The review further highlights the critical importance of culture-guided antimicrobial therapy in improving maternal and neonatal outcomes and reducing the burden of antimicrobial resistance.

CHAPTER THREE

METHODOLOGY

3.1 Introduction

This chapter describes the methodological procedures employed to investigate the antimicrobial resistance patterns of bacterial pathogens associated with urinary and reproductive tract infections among pregnant and non-pregnant women and to assess their implications for pregnancy and childbirth outcomes. The chapter presents the research design, study setting, study population, eligibility criteria, sample size, sampling technique, specimen collection procedures, laboratory methods, antimicrobial susceptibility testing, quality assurance and quality control measures, data management, statistical analysis, ethical considerations, and study limitations.

The methodology was designed to ensure scientific rigor, reproducibility, and adherence to internationally recognized microbiological standards. Laboratory procedures for bacterial isolation, identification, and antimicrobial susceptibility testing were conducted according to the Clinical and Laboratory Standards Institute (CLSI) Performance Standards for Antimicrobial Susceptibility Testing (CLSI, 2024). Standard microbiological techniques were employed to isolate bacterial and fungal pathogens from urine, blood, and high vaginal swab (HVS) specimens, while the Kirby–Bauer disk diffusion method was used to determine antimicrobial susceptibility profiles.

This study adopted a quantitative laboratory-based approach to generate reliable evidence on the distribution of bacterial pathogens, antimicrobial resistance patterns, and multidrug resistance among pregnant and non-pregnant women attending healthcare services. The findings are expected to contribute to evidence-based antimicrobial prescribing, strengthen antimicrobial stewardship programs, and support interventions aimed at reducing pregnancy-related infectious complications and improving maternal and neonatal health outcomes.

Furthermore, the methodological approach was developed to ensure that the study findings are comparable with national and international antimicrobial resistance surveillance studies and are suitable for dissemination through peer-reviewed scientific publications. By integrating standardized laboratory procedures with robust statistical analysis, the study provides a comprehensive assessment of antimicrobial resistance among clinically significant pathogens responsible for urinary tract infections, reproductive tract infections, and bloodstream infections in women of reproductive age.

3.2 Research Design

This study employed a hospital-based analytical cross-sectional study design to investigate the antimicrobial resistance patterns of bacterial pathogens associated with urinary and reproductive tract infections among pregnant and non-pregnant women and to evaluate their implications for pregnancy and childbirth outcomes. An analytical cross-sectional design was considered

appropriate because it enabled the simultaneous collection of clinical specimens, microbiological data, and participant characteristics at a single point in time, thereby facilitating the comparison of antimicrobial resistance patterns between the two study populations without the need for long-term follow-up (Setia, 2016).

The study adopted a quantitative laboratory-based approach, integrating clinical microbiology with epidemiological analysis. Biological specimens, including urine, blood, and high vaginal swab (HVS) samples, were collected from eligible participants and processed using standardized microbiological techniques. Bacterial and fungal pathogens were isolated, identified, and subjected to antimicrobial susceptibility testing using the Kirby–Bauer disk diffusion method in accordance with the Clinical and Laboratory Standards Institute (CLSI) Performance Standards for Antimicrobial Susceptibility Testing (2024). This standardized approach ensured consistency, reliability, and comparability of laboratory findings with national and international antimicrobial resistance surveillance studies (CLSI, 2024).

The analytical component of the study involved comparing the prevalence of bacterial pathogens, antimicrobial susceptibility profiles, multidrug resistance (MDR) patterns, and selected pregnancy outcomes between pregnant and non-pregnant women. Sociodemographic characteristics, specimen types, bacterial isolates, and antimicrobial susceptibility results were analyzed using appropriate descriptive and inferential statistical methods to determine whether statistically significant differences existed between the two groups. The study further explored the relationship between antimicrobial resistance and adverse pregnancy outcomes, including preterm birth, miscarriage, low birth weight, and mode of delivery.

The selection of an analytical cross-sectional design was supported by several methodological advantages. First, it enabled the efficient assessment of antimicrobial resistance patterns within a relatively large study population of 400 participants, consisting of 200 pregnant women and 200 non-pregnant women, over a defined study period. Second, the design facilitated direct comparison of bacterial isolates and antimicrobial susceptibility patterns between the two groups, allowing identification of clinically relevant differences in resistance profiles. Third, the design was cost-effective and practical within the hospital laboratory setting, making optimal use of available microbiological resources while maintaining high scientific standards.

Although cross-sectional studies do not establish temporal or causal relationships, they are widely recommended for antimicrobial resistance surveillance because they provide robust estimates of pathogen distribution, antimicrobial susceptibility patterns, and resistance prevalence within defined populations. Such studies also generate essential baseline data for antimicrobial stewardship programs, infection prevention and control initiatives, and evidence-based empirical treatment guidelines (WHO, 2024).

To enhance the validity and reliability of the findings, all laboratory procedures were performed using standardized operating procedures (SOPs), quality-controlled culture media, validated antimicrobial discs, and internationally accepted interpretative criteria. Internal quality control

measures were implemented throughout specimen processing, bacterial identification, and antimicrobial susceptibility testing to minimize analytical error and ensure reproducibility of results.

Overall, the chosen research design provided a scientifically rigorous framework for evaluating antimicrobial resistance among clinically significant bacterial pathogens isolated from urine, blood, and high vaginal swab specimens. It also enabled the study to achieve its objectives of identifying resistance patterns, comparing findings between pregnant and non-pregnant women, and assessing the implications of antimicrobial resistance for pregnancy and childbirth outcomes.

3.3 Study Setting

This study was conducted at Ga East Municipal Hospital (GEMH), located in the Ga East Municipality of the Greater Accra Region, Ghana. The hospital is a government-owned secondary-level healthcare facility operating under the Ghana Health Service (GHS). It serves as one of the major referral hospitals within the municipality and provides comprehensive preventive, diagnostic, curative, emergency, and specialist healthcare services to residents of the municipality and surrounding communities. The hospital receives patients from both urban and peri-urban areas, making it an ideal setting for investigating bacterial infections and antimicrobial resistance patterns among women of reproductive age.

Ga East Municipal Hospital provides a wide range of clinical services through departments including the Obstetrics and Gynaecology Unit, Antenatal Clinic, Postnatal Clinic, Outpatient Department (OPD), Emergency Unit, Medical and Surgical Wards, Paediatric Unit, and the Pathology Department. These departments routinely manage patients presenting with urinary tract infections (UTIs), reproductive tract infections (RTIs), sexually transmitted infections (STIs), bloodstream infections, and pregnancy-related infectious complications, thereby providing a diverse clinical population suitable for this study.

The hospital's Pathology Department houses a well-equipped Medical Laboratory that offers diagnostic services in Microbiology, Haematology, Blood Transfusion (Blood Bank), Chemical Pathology, Serology, Immunology, Histopathology, and Parasitology. The Microbiology Laboratory performs routine culture and antimicrobial susceptibility testing for clinical specimens, including urine, blood, high vaginal swabs (HVS), wound swabs, sputum, and other body fluids. These laboratory services support evidence-based diagnosis and antimicrobial therapy for patients attending the hospital.

The microbiology laboratory follows standardized laboratory protocols consistent with the recommendations of the Clinical and Laboratory Standards Institute (CLSI) for bacterial isolation, identification, and antimicrobial susceptibility testing. Routine quality assurance procedures, standardized operating procedures (SOPs), quality-controlled culture media, and reference bacterial strains are utilized to ensure the accuracy, reliability, and reproducibility of laboratory results. These established laboratory systems provided a strong scientific foundation

for the present study and ensured that microbiological analyses were performed according to internationally accepted standards (CLSI, 2024).

The study population was recruited primarily from the Antenatal Clinic, Gynaecology Unit, Outpatient Department, and Medical Wards, where women presenting with symptoms suggestive of urinary tract infections, reproductive tract infections, bloodstream infections, or related clinical conditions were evaluated by attending clinicians. Eligible participants included both pregnant and non-pregnant women who met the study inclusion criteria. Clinical specimens comprising urine, blood, and high vaginal swabs were collected as part of routine diagnostic investigations and processed in the hospital microbiology laboratory.

The selection of Ga East Municipal Hospital as the study site was based on several considerations. First, the hospital manages a high volume of obstetric and gynaecological patients, providing access to a representative population of pregnant and non-pregnant women. Second, the availability of a functional microbiology laboratory capable of performing bacterial culture, organism identification, and antimicrobial susceptibility testing made it possible to generate high-quality microbiological data. Third, the hospital's role as a referral center within the municipality ensured that the study captured a broad spectrum of bacterial pathogens and antimicrobial resistance patterns encountered in routine clinical practice.

Additionally, the investigator's professional experience as a Medical Laboratory Scientist in the Pathology Department facilitated adherence to standardized specimen collection procedures, laboratory protocols, quality assurance practices, and accurate data management throughout the study. This familiarity with the laboratory environment enhanced the consistency and reliability of microbiological analyses while maintaining strict compliance with ethical principles, institutional policies, and professional laboratory standards.

Given the increasing burden of antimicrobial resistance in Ghana, Ga East Municipal Hospital provides an appropriate setting for evaluating the prevalence of bacterial pathogens and their antimicrobial susceptibility patterns among women of reproductive age. The findings generated from this setting are expected to contribute to local antimicrobial resistance surveillance, strengthen antimicrobial stewardship initiatives, inform empirical treatment guidelines, and improve the management of urinary and reproductive tract infections, particularly among pregnant women. Furthermore, the study provides valuable evidence to support national efforts aimed at reducing antimicrobial resistance and improving maternal and neonatal health outcomes in Ghana.

3.4 Study Population

The study population comprised women of reproductive age attending Ga East Municipal Hospital, Greater Accra Region, Ghana, who presented with clinical features suggestive of urinary tract infections (UTIs), reproductive tract infections (RTIs), bloodstream infections, or related infectious conditions requiring microbiological investigation. The population included

both pregnant and non-pregnant women, enabling comparative assessment of bacterial pathogens, antimicrobial susceptibility patterns, and multidrug resistance (MDR) between the two groups.

Women of reproductive age were selected because they constitute the population most affected by urinary and reproductive tract infections owing to anatomical, physiological, hormonal, and behavioral factors. Pregnancy further increases susceptibility to bacterial infections through physiological changes such as urinary stasis, hormonal alterations, reduced ureteral tone, and immunological adaptations that facilitate bacterial colonization and ascending infection (Monari et al., 2024). Consequently, comparing pregnant and non-pregnant women provides valuable insight into the influence of pregnancy on the epidemiology of bacterial infections and antimicrobial resistance.

The target population consisted of 400 participants, comprising 200 pregnant women receiving antenatal or obstetric care and 200 non-pregnant women attending outpatient, gynecological, or medical clinics during the study period. This equal representation was intentionally adopted to facilitate direct comparison of bacterial isolates, antimicrobial susceptibility profiles, multidrug resistance patterns, and clinical outcomes between the two study groups.

Participants were recruited from departments where urinary and reproductive tract infections are commonly diagnosed and managed, including the Antenatal Clinic (ANC), Obstetrics and Gynaecology Unit, Outpatient Department (OPD), Medical Wards, and Emergency Unit. These departments routinely evaluate women presenting with symptoms such as dysuria, urinary frequency, urgency, suprapubic pain, abnormal vaginal discharge, pelvic pain, fever, suspected bacteremia, and other signs suggestive of bacterial infection. Clinical assessment by attending physicians determined the need for microbiological investigations, after which eligible patients were invited to participate in the study.

The study population reflected a broad reproductive age range to capture the diversity of women commonly affected by these infections. Pregnant participants ranged in age from 18 to 45 years, representing the typical childbearing population receiving antenatal care. Non-pregnant participants ranged from 15 to 60 years, encompassing adolescent, reproductive-age, and peri-menopausal women who presented with urinary or reproductive tract infections. This wide age distribution allowed the study to examine antimicrobial resistance patterns across different reproductive age groups and enhanced the representativeness of the findings.

The study population was considered appropriate because urinary and reproductive tract infections remain among the leading causes of antibiotic prescription in women, and antimicrobial resistance has increasingly complicated their management. By including women from diverse clinical units within a major municipal referral hospital, the study captured a wide spectrum of bacterial pathogens, including Escherichia coli, Staphylococcus aureus, Klebsiella oxytoca, Enterococcus spp., Citrobacter spp., Proteus spp., Pseudomonas spp., and Candida spp.,

thereby providing comprehensive data on clinically important microorganisms associated with urinary, reproductive tract, and bloodstream infections.

Furthermore, the selected study population aligns with the objectives of the research, which sought to evaluate antimicrobial resistance among bacterial pathogens isolated from urine, blood, and high vaginal swab specimens and to determine their implications for pregnancy and childbirth outcomes. The inclusion of both pregnant and non-pregnant women strengthens the comparative nature of the study and enables assessment of whether pregnancy influences bacterial distribution, antimicrobial susceptibility, and multidrug resistance.

The study population also supports broader public health objectives by generating locally relevant antimicrobial resistance data that can inform evidence-based empirical treatment guidelines, antimicrobial stewardship programs, infection prevention and control strategies, and maternal healthcare policies in Ghana. Given the increasing burden of antimicrobial resistance in low- and middle-income countries, the findings derived from this population are expected to contribute meaningfully to national surveillance efforts and improve the clinical management of bacterial infections among women of reproductive age.

3.5 Inclusion and Exclusion Criteria

Establishing clear inclusion and exclusion criteria was essential to ensure that the study population accurately reflected the research objectives and that the findings were valid, reliable, and applicable to women at risk of urinary tract infections (UTIs), reproductive tract infections (RTIs), and bloodstream infections. These criteria were designed to recruit participants who were clinically relevant to the study while minimizing potential sources of bias and confounding.

3.5.1 Inclusion Criteria

Participants were eligible for inclusion in the study if they met all of the following criteria:

- Women aged 15–60 years attending Ga East Municipal Hospital during the study period.
- Pregnant women receiving antenatal, obstetric, or related maternal healthcare services.
- Non-pregnant women attending the Outpatient Department, Gynaecology Unit, Medical Wards, or Emergency Unit.
- Women presenting with clinical features suggestive of urinary tract infection, reproductive tract infection, bloodstream infection, or other bacterial infections requiring microbiological investigation.
- Women from whom at least one clinical specimen (urine, blood, or high vaginal swab) was collected for culture and antimicrobial susceptibility testing as part of routine clinical management.
- Participants who voluntarily agreed to participate in the study and provided written informed consent before enrollment.

- For participants younger than 18 years, written assent together with consent from a parent or legal guardian was obtained in accordance with institutional ethical requirements.

3.5.2 Exclusion Criteria

Participants were excluded from the study if they met one or more of the following criteria:

- Women who declined to participate or did not provide informed consent.
- Women whose clinical records or laboratory results were incomplete, missing, or inadequate for analysis.
- Clinical specimens that were improperly collected, inadequately labeled, contaminated, leaked during transportation, or otherwise unsuitable for microbiological processing.
- Duplicate specimens obtained from the same participant during the same episode of illness. Only the first eligible specimen was included to prevent duplication of microbiological data.
- Participants who had already been enrolled in the study during the data collection period.
- Specimens that failed laboratory quality control procedures or produced inconclusive microbiological results after repeat testing.
- Participants for whom essential demographic or clinical information required for statistical analysis was unavailable.

Applying these eligibility criteria ensured that only participants with reliable clinical and microbiological data were included in the final analysis. This approach enhanced the internal validity of the study, reduced selection bias, and improved the accuracy of comparisons between pregnant and non-pregnant women regarding bacterial isolates, antimicrobial susceptibility patterns, multidrug resistance, and pregnancy-related outcomes. Furthermore, the use of standardized eligibility criteria supports the reproducibility of the study and aligns with best practices for observational clinical and microbiological research.

3.6 Sample Size Determination

Sample size determination is a critical component of research methodology because it ensures that the study includes a sufficient number of participants to produce statistically reliable, valid, and generalizable findings. An adequate sample size increases the precision of statistical estimates, improves the power to detect significant differences between study groups, and minimizes sampling error (Charan & Biswas, 2013).

For this study, a total sample size of 400 women was used. The participants comprised 200 pregnant women and 200 non-pregnant women attending Ga East Municipal Hospital during the study period. The equal allocation of participants between the two groups was intentionally adopted to facilitate direct comparison of bacterial isolates, antimicrobial susceptibility patterns, multidrug resistance (MDR), and clinical outcomes.

The sample size was determined using Cochran’s sample size formula for cross-sectional studies:

$$n = \frac{Z^2 P(1 - P)}{d^2}$$

Where:

N = Minimum required sample size

Z = Standard normal deviate corresponding to a 95% confidence level (1.96)

P = Estimated prevalence of urinary and reproductive tract infections among women. In the absence of a single definitive prevalence estimate applicable to the study population, a prevalence of 50% (0.50) was assumed to maximize the required sample size.

D = Margin of error (0.05)

Substituting the values:

$$X = \frac{(1.96)^2 \text{ x } 0.05(1 - 0.05)}{(0.05)^2}$$

$$n = \frac{3.8416 \text{ x } 0.25}{0.0025}$$

n = 384.16

The minimum calculated sample size was therefore approximately 384 participants. To improve statistical precision, compensate for potential exclusions arising from contaminated specimens, incomplete laboratory records, or missing clinical information, and ensure balanced comparison between pregnant and non-pregnant women, the sample size was increased to 400 participants.

The final study population consisted of

Study Group	Number of Participants
Pregnant women	200
Non-pregnant women	200
Total	400

Clinical specimens were collected according to the participants' clinical indications. A total of:

- 400 urine specimens
- 300 high vaginal swab (HVS) specimens
- 200 blood specimens

Were processed for microbiological culture and antimicrobial susceptibility testing.

The selected sample size was considered adequate to achieve the study objectives by enabling reliable estimation of bacterial pathogen distribution, antimicrobial susceptibility profiles, and multidrug resistance patterns while providing sufficient statistical power for comparisons between pregnant and non-pregnant women. Furthermore, the sample size is consistent with similar hospital-based antimicrobial resistance surveillance studies conducted in Ghana and other sub-Saharan African countries, thereby enhancing the comparability and external validity of the findings (Charan & Biswas, 2013; WHO, 2024).

3.7 Sampling Technique

This study employed a consecutive sampling technique, a non-probability sampling method commonly used in hospital-based clinical and microbiological research. Under this approach, all eligible pregnant and non-pregnant women who met the inclusion criteria and presented to Ga East Municipal Hospital during the study period were consecutively recruited until the predetermined sample size of 400 participants was achieved. Consecutive sampling was considered appropriate because it minimizes selection bias associated with convenience sampling while ensuring that every eligible patient presenting during the study period had an equal opportunity to participate (Setia, 2016).

Participant recruitment was conducted across the Antenatal Clinic (ANC), Obstetrics and Gynaecology Unit, Outpatient Department (OPD), Medical Wards, and Emergency Unit. Women presenting with clinical signs and symptoms suggestive of urinary tract infections (UTIs), reproductive tract infections (RTIs), bloodstream infections, or related bacterial infections were evaluated by attending clinicians. Patients who satisfied the eligibility criteria and provided written informed consent were enrolled into the study.

To facilitate comparative analysis, recruitment continued until 200 pregnant women and 200 non-pregnant women had been enrolled. Equal representation of both study groups ensured adequate statistical power for comparing bacterial pathogen distribution, antimicrobial susceptibility patterns, multidrug resistance (MDR), and selected clinical outcomes between pregnant and non-pregnant participants.

Following enrollment, appropriate clinical specimens were collected according to the participants' presenting conditions and the attending clinician's diagnostic request. These included midstream urine specimens for suspected urinary tract infections, high vaginal swab (HVS) specimens for suspected reproductive tract infections, and blood specimens from patients

with suspected bloodstream infections or systemic bacterial disease. All specimens were collected using standardized aseptic techniques and transported promptly to the Microbiology Laboratory for culture, organism identification, and antimicrobial susceptibility testing.

The use of consecutive sampling offered several methodological advantages. It enabled efficient participant recruitment within the routine clinical workflow, reduced the likelihood of investigator selection bias, and ensured that the study population reflected the spectrum of patients encountered in everyday clinical practice. Furthermore, because participants were recruited prospectively as they presented to the hospital, the sampling method enhanced the representativeness of the study population and strengthened the external validity of the findings.

Although consecutive sampling is a non-probability sampling technique and may limit generalizability beyond the study setting, it is widely accepted in hospital-based observational studies where the objective is to describe disease patterns, microbiological characteristics, and antimicrobial resistance profiles among patients seeking healthcare. When combined with standardized eligibility criteria, rigorous laboratory procedures, and appropriate statistical analysis, consecutive sampling provides robust and reliable data for antimicrobial resistance surveillance and clinical epidemiological research.

The sampling technique therefore ensured systematic recruitment of eligible participants while maintaining consistency with the study objectives and supporting valid comparisons between pregnant and non-pregnant women regarding bacterial isolates, antimicrobial susceptibility patterns, and multidrug resistance.

3.8 Study Variables

Study variables are measurable characteristics that are observed, recorded, and analyzed to answer the research questions and achieve the study objectives. In this study, the variables were categorized into independent variables, dependent variables, and potential confounding variables. This classification provided a structured framework for data collection, statistical analysis, and interpretation of the relationships between antimicrobial resistance, bacterial pathogens, pregnancy status, and pregnancy outcomes.

3.8.1 Independent Variables

Independent variables are factors that may influence the occurrence of antimicrobial resistance or affect treatment outcomes. The independent variables investigated in this study included:

- Socio-demographic Variables
- Age of participant (years)
- Pregnancy status (Pregnant or Non-pregnant)
- Clinical Variables

Type of clinical specimen:

- Urine
- Blood
- High Vaginal Swab (HVS)

Clinical diagnosis

- Presence of urinary tract infection (UTI)
- Presence of reproductive tract infection (RTI)
- Presence of bloodstream infection

Microbiological Variables

- Bacterial species isolated:
- Escherichia coli
- Staphylococcus aureus
- Klebsiella oxytoca
- Citrobacter spp.
- Enterococcus spp.
- Proteus spp.
- Pseudomonas spp.

Fungal isolate:

- Candida spp.

Antibiotic Exposure Variables

Antimicrobial agents tested included:

Pregnancy-compatible antibiotics

- Penicillin G
- Penicillin V
- Ampicillin
- Amoxicillin
- Amoxicillin-Clavulanate
- Cephalexin
- Cefuroxime
- Ceftriaxone
- Cefotaxime
- Cefixime
- Azithromycin
- Erythromycin
- Clindamycin

- Nitrofurantoin
- Fosfomycin

Other antibiotics evaluated

- Ciprofloxacin
- Levofloxacin
- Ofloxacin
- Moxifloxacin
- Nalidixic Acid
- Doxycycline
- Tetracycline
- Minocycline
- Gentamicin
- Amikacin
- Tobramycin
- Trimethoprim-Sulfamethoxazole
- Trimethoprim
- Chloramphenicol
- Tigecycline
- Piperacillin-Tazobactam
- Meropenem
- Imipenem

3.8.2 Dependent Variables

The dependent variables were the primary outcomes measured in the study.

These included:

Microbiological Outcomes

- Presence or absence of bacterial growth
- Type of bacterial pathogen isolated
- Type of fungal isolate identified

Antimicrobial Resistance Outcomes

Antimicrobial susceptibility profile:

- Susceptible (S)
- Intermediate (I)
- Resistant ®

Multidrug-resistant (MDR) status

Overall resistance pattern of bacterial isolates

Clinical Outcomes

Among pregnant participants, pregnancy-related outcomes included:

- Preterm birth
- Low birth weight
- Miscarriage
- Caesarean section (CS)
- Normal vaginal delivery
- Maternal infection-related complications

These outcomes were analyzed in relation to the antimicrobial resistance profiles of the isolated pathogens.

3.8.3 Potential Confounding Variables

Confounding variables are factors that may influence both the independent and dependent variables, thereby affecting the observed associations.

Potential confounding variables considered in this study included:

- Age
- Pregnancy status
- Type of clinical specimen
- Type of infecting organism
- Previous antibiotic exposure
- Severity of infection
- Underlying medical conditions (where documented)
- Hospital department of recruitment

These variables were considered during statistical analysis to minimize bias and improve the validity of comparisons between pregnant and non-pregnant women.

3.8.4 Operational Definitions of Key Variables

To ensure consistency throughout the study, the following operational definitions were adopted:

Antimicrobial Resistance (AMR): The ability of a microorganism to survive or multiply despite exposure to an antimicrobial agent that would normally inhibit or kill it (WHO, 2024).

Multidrug Resistance (MDR): Resistance of a bacterial isolate to at least one antimicrobial agent in three or more antimicrobial classes, according to internationally accepted definitions (Magiorakos et al., 2012).

Urinary Tract Infection (UTI): A bacterial infection involving any part of the urinary system, confirmed by urine culture demonstrating significant microbial growth.

Reproductive Tract Infection (RTI): Infection affecting the female reproductive tract, confirmed by microbiological examination of high vaginal swab specimens.

Bloodstream Infection (BSI): Isolation of a pathogenic microorganism from a blood culture obtained from a patient with clinical signs suggestive of systemic infection.

Susceptibility Categories: Antimicrobial susceptibility results were interpreted as Susceptible (S), Intermediate (I), or Resistant ® according to the Clinical and Laboratory Standards Institute (CLSI) Performance Standards for Antimicrobial Susceptibility Testing (2024).

Table 3.1: Summary of Study Variables

Variable Category	Variables
Independent Variables	Age, pregnancy status, specimen type, bacterial isolate, fungal isolate, antibiotics tested
Dependent Variables	Culture positivity, susceptibility profile (S/I/R), multidrug resistance, pregnancy outcomes
Confounding Variables	Previous antibiotic use, severity of infection, specimen type, age, underlying medical conditions

The identification and classification of these variables provided a systematic basis for data collection, laboratory analysis, and statistical evaluation. This framework enabled the study to investigate associations between bacterial pathogens, antimicrobial resistance patterns, and pregnancy outcomes while accounting for factors that could potentially influence the observed relationships.

3.9 Sample Collection Procedures

The accurate collection and handling of clinical specimens are essential components of microbiological investigations because specimen quality directly influences the reliability of culture results, bacterial identification, and antimicrobial susceptibility testing. In this study, clinical specimens were collected from eligible pregnant and non-pregnant women according to standard microbiological procedures and institutional protocols at Ga East Municipal Hospital. Specimen collection was performed using aseptic techniques to minimize contamination and ensure the recovery of clinically significant microorganisms.

A total of 900 clinical specimens were investigated, comprising:

- 400 urine specimens
- 300 high vaginal swab (HVS) specimens
- 200 blood culture specimens

Specimens were collected based on clinical indications and processed in the Microbiology Laboratory using standard operating procedures. All samples were appropriately labeled with unique study identification numbers, transported promptly to the laboratory, and processed according to established microbiological guidelines.

3.9.1 Urine Sample Collection Procedure

Urine specimens were collected from participants with suspected urinary tract infections (UTIs). Participants were instructed on appropriate urine collection procedures to reduce contamination from external genital flora.

A midstream clean-catch urine collection method was used. Participants were provided with sterile, wide-mouthed, leak-proof universal containers and instructed to:

1. Wash their hands thoroughly before specimen collection.
2. Clean the external genital area with sterile water or according to hospital-approved procedures.
3. Begin urinating into the toilet to clear potential contaminants from the urethral opening.
4. Collect the midstream portion of urine into the sterile container without touching the inside of the container or lid.
5. Securely close the container immediately after collection.

The collected urine specimens were transported to the Microbiology Laboratory within the recommended timeframe for processing. Where immediate processing was not possible, specimens were stored under appropriate conditions to maintain bacterial viability and prevent overgrowth of contaminating organisms.

Urine specimens were subsequently subjected to microbiological examination, including culture, bacterial identification, and antimicrobial susceptibility testing.

3.9.2 High Vaginal Swab (HVS) Collection Procedure

High vaginal swab specimens were collected from participants presenting with symptoms suggestive of reproductive tract infections (RTIs), including abnormal vaginal discharge, itching, irritation, pelvic discomfort, or suspected sexually transmitted infections.

The procedure was performed by trained healthcare professionals using standard aseptic techniques.

The collection procedure involved:

1. Positioning the participant appropriately for gynecological examination.
2. Using a sterile speculum where clinically indicated.
3. Carefully inserting a sterile swab into the vaginal canal without contaminating the specimen with external skin flora.
4. Rotating the swab gently against the vaginal wall to collect epithelial cells and vaginal secretions.
5. Placing the swab immediately into an appropriate transport medium.
6. Labeling the specimen with the participant's unique study identification number.

The specimens were transported promptly to the Microbiology Laboratory for processing. Laboratory investigations included bacterial culture, identification of pathogenic organisms, and detection of yeast/fungal organisms such as Candida species.

3.9.3 Blood Sample Collection Procedure

Blood specimens were collected from participants with clinical suspicion of bloodstream infection (BSI), systemic bacterial infection, fever of unknown origin, or other indications requiring blood culture investigation.

Blood collection was performed using strict aseptic techniques to minimize contamination.

The procedure involved:

1. Cleaning the venipuncture site using an appropriate antiseptic preparation.
2. Allowing the antiseptic to dry completely before venipuncture.
3. Collecting blood using sterile equipment by trained laboratory personnel.
4. Inoculating the collected blood into appropriate blood culture bottles according to laboratory protocols.
5. Properly labeling culture bottles with participant identification details and collection information.
6. Transporting blood cultures immediately to the Microbiology Laboratory for incubation and further analysis.

Blood cultures were monitored for microbial growth, and positive cultures were subjected to organism identification and antimicrobial susceptibility testing.

3.9.4 Specimen Transportation and Handling

All specimens were handled according to established microbiological safety procedures. Each specimen was assigned a unique identification code to maintain confidentiality and ensure traceability throughout laboratory processing.

The following measures were implemented:

- Verification of patient identification before collection.
- Use of sterile, appropriately labeled collection materials.
- Maintenance of specimen integrity during transportation.
- Prompt delivery of specimens to the laboratory.
- Documentation of specimen receipt and processing.
- Appropriate storage conditions when immediate processing was not possible.

Specimens that were improperly labeled, contaminated, leaked, or unsuitable for analysis were excluded according to the predefined exclusion criteria.

3.9.5 Laboratory Reception and Processing of Specimens

Upon arrival at the Microbiology Laboratory, specimens were evaluated for adequacy before processing. Laboratory personnel recorded specimen type, date and time of collection, participant identification number, and relevant clinical information.

Specimens were then processed using standardized microbiological techniques, including:

- Direct microscopy where applicable.
- Culture on appropriate microbiological media.
- Identification of bacterial and fungal isolates.
- Antimicrobial susceptibility testing.

All procedures were performed following laboratory standard operating procedures and quality assurance guidelines to ensure the accuracy and reproducibility of results.

3.9.6 Biosafety Considerations During Specimen Collection

All specimen collection and handling procedures were performed according to established biosafety principles. Laboratory personnel used appropriate personal protective equipment (PPE), including laboratory coats, gloves, and other protective materials where necessary.

Universal precautions were maintained throughout specimen collection, transportation, and processing to minimize occupational exposure and prevent laboratory-acquired infections.

The standardized collection of urine, high vaginal swab, and blood specimens ensured the generation of reliable microbiological data for evaluating antimicrobial resistance patterns among bacterial pathogens isolated from pregnant and non-pregnant women. Proper specimen collection, transportation, and laboratory processing procedures reduced contamination risk and strengthened the validity of antimicrobial susceptibility findings.

3.10 Laboratory Procedures

Laboratory investigations were conducted in the Microbiology Laboratory of the Pathology Department at Ga East Municipal Hospital using standardized microbiological techniques for the isolation, identification, and antimicrobial susceptibility testing of bacterial and fungal pathogens. All laboratory procedures were performed in accordance with the Clinical and Laboratory Standards Institute (CLSI) Performance Standards for Antimicrobial Susceptibility Testing (CLSI, 2024) and established Standard Operating Procedures (SOPs) of the hospital laboratory. Strict aseptic techniques and quality control measures were maintained throughout specimen processing to ensure the accuracy, reliability, and reproducibility of laboratory findings.

Clinical specimens comprising urine, blood, and high vaginal swab (HVS) samples were processed immediately upon receipt in the laboratory. Each specimen was assigned a unique laboratory identification number and examined for completeness, integrity, and suitability before microbiological analysis. Appropriate culture media, incubation conditions, biochemical identification tests, and antimicrobial susceptibility testing methods were employed to identify bacterial and fungal isolates.

3.10.1 Specimen Reception and Initial Examination

Upon arrival in the laboratory, all specimens were inspected to verify:

- Correct patient identification
- Specimen type
- Adequate specimen volume
- Proper labeling
- Appropriate transportation conditions
- Absence of leakage or contamination

Specimens failing to meet laboratory acceptance criteria were rejected and documented according to laboratory quality management procedures.

3.10.2 Culture Media

The following microbiological media were used depending on the specimen type and suspected pathogen:

Culture Medium	Purpose
Cysteine Lactose Electrolyte Deficient (CLED) Agar	Isolation of urinary pathogens
MacConkey Agar	Isolation of Gram-negative enteric bacteria
Blood Agar	Growth of fastidious organisms and haemolysis observation

Chocolate Agar	Isolation of fastidious organisms such as Neisseria spp.
Mannitol Salt Agar	Isolation of Staphylococcus species
Sabouraud Dextrose Agar (SDA)	Isolation of yeasts and fungi including Candida spp.

All culture media were prepared and quality-checked according to the manufacturer's recommendations and laboratory standard operating procedures.

3.10.3 Processing of Urine Specimens

Urine specimens were mixed gently before inoculation.

Using a calibrated sterile inoculating loop (0.001 mL), urine samples were streaked onto:

- CLED Agar
- MacConkey Agar
- Blood Agar

The inoculated plates were incubated aerobically at 35–37°C for 18–24 hours.

Following incubation, colony counts were determined, and significant bacteriuria was interpreted according to accepted microbiological criteria. Colony morphology, pigmentation, lactose fermentation, haemolysis, and colony characteristics were recorded before further identification procedures.

3.10.4 Processing of High Vaginal Swab (HVS) Specimens

High vaginal swab specimens were inoculated onto:

- Blood Agar
- Cled agar
- Chocolate Agar
- MacConkey Agar
- Sabouraud Dextrose Agar (where fungal infection was suspected)

Culture plates were incubated under appropriate atmospheric conditions at 35–37°C for 24–48 hours depending on the suspected pathogen.

Microscopic examination using Gram staining was also performed to evaluate bacterial morphology, inflammatory cells, epithelial cells, yeast cells, and other microscopic findings.

3.10.5 Processing of Blood Culture Specimens

Blood culture bottles were incubated according to standard blood culture protocols.

Positive blood cultures were subcultured onto:

- Blood Agar
- MacConkey Agar
- Chocolate Agar

Following incubation, bacterial colonies were examined and identified using standard microbiological methods.

Negative blood cultures were maintained for the recommended incubation period before being reported as having no bacterial growth.

3.10.6 Identification of Bacterial Isolates

Presumptive bacterial identification was based on:

- Colony morphology
- Colony pigmentation
- Haemolytic reactions
- Gram stain characteristics

Further identification was performed using standard biochemical tests, including:

Gram-Positive Organisms

- Catalase Test
- Coagulase Test
- Growth in 6.5% Sodium Chloride

Gram-Negative Organisms

- Oxidase Test
- Indole Test
- Citrate Utilization Test
- Urease Test
- Triple Sugar Iron (TSI) Test
- Motility Test

These biochemical reactions were interpreted according to standard microbiological identification guidelines.

3.10.7 Identification of Fungal Isolates

Yeast isolates recovered from HVS and urine specimens were cultured on Sabouraud Dextrose Agar.

Identification of Candida species was based on:

- Colony morphology

- Gram stain appearance
- Microscopic examination

Fluconazole susceptibility testing was performed for clinically significant Candida isolates where indicated.

3.10.8 Bacterial Isolates Investigated

The principal organisms identified during the study included:

Gram-Positive Bacteria

- Staphylococcus aureus
- Staphylococcus saprophyticus
- Enterococcus spp.
- Streptococcus agalactiae

Gram-Negative Bacteria

- Escherichia coli
- Klebsiella oxytoca
- Proteus spp.
- Pseudomonas spp.
- Citrobacter spp.

Yeast

- Candida spp.

3.10.9 Recording of Laboratory Findings

For each specimen, the following laboratory findings were documented:

- Specimen type
- Presence or absence of bacterial growth
- Organism isolated
- Gram reaction
- Biochemical identification results
- Antimicrobial susceptibility profile
- Final laboratory diagnosis

Laboratory data were entered into structured data collection forms before statistical analysis.

3.10.10 Laboratory Biosafety

All microbiological procedures were performed in accordance with WHO Laboratory Biosafety Manual (4th Edition) recommendations.

Laboratory personnel adhered to biosafety practices including:

- Wearing laboratory coats and gloves.
- Proper hand hygiene before and after specimen handling.
- Routine disinfection of work surfaces.
- Safe disposal of infectious waste through autoclaving or approved biohazard disposal methods.
- Immediate reporting and management of accidental spills or exposures.

Compliance with biosafety protocols minimized occupational risks and ensured the safe handling of potentially infectious clinical specimens.

The laboratory procedures adopted in this study followed internationally accepted microbiological standards for specimen processing, bacterial isolation, organism identification, and fungal detection. Standardized laboratory methods, combined with rigorous quality assurance and biosafety practices, ensured the generation of accurate and reproducible microbiological data. These procedures formed the basis for the subsequent antimicrobial susceptibility testing and resistance analysis presented in the following section.

3.11 Antimicrobial Susceptibility Testing

Antimicrobial susceptibility testing (AST) was performed on all clinically significant bacterial isolates recovered from urine, blood, and high vaginal swab (HVS) specimens to determine their susceptibility to commonly prescribed antimicrobial agents. The primary objective of AST was to identify effective antibiotics for the treatment of bacterial infections, detect antimicrobial resistance patterns, and identify multidrug-resistant (MDR) organisms. The results generated from AST provided evidence to support appropriate antimicrobial therapy and informed the evaluation of resistance patterns among pregnant and non-pregnant women.

The Kirby–Bauer disk diffusion method was employed for antimicrobial susceptibility testing in accordance with the Clinical and Laboratory Standards Institute (CLSI) Performance Standards for Antimicrobial Susceptibility Testing (35th Edition) (CLSI, 2024). This standardized method is widely recommended because of its accuracy, reproducibility, cost-effectiveness, and suitability for routine clinical microbiology laboratories.

3.11.1 Preparation of Bacterial Inoculum

Pure bacterial colonies obtained from overnight cultures were used for susceptibility testing. Approximately three to five well-isolated colonies of each bacterial isolate were aseptically transferred into sterile normal saline and thoroughly mixed to produce a homogeneous bacterial suspension.

The turbidity of each suspension was adjusted to match the 0.5 McFarland standard, corresponding to approximately 1.5×10^8 colony-forming units (CFU)/mL. Standardization of

the inoculum ensured consistency in bacterial density and improved the reproducibility of susceptibility test results.

3.11.2 Inoculation of Test Plates

A sterile cotton swab was immersed in the standardized bacterial suspension, excess fluid was removed by pressing the swab against the inner wall of the tube, and the entire surface of a Mueller–Hinton agar plate was inoculated by streaking in three directions to produce a uniform bacterial lawn. The inoculated plates were allowed to stand at room temperature for approximately 3–5 minutes to permit absorption of excess surface moisture before antimicrobial discs were applied.

For fastidious organisms, susceptibility testing was performed using media and incubation conditions recommended by CLSI.

3.11.3 Application of Antibiotic Discs

Commercially prepared antimicrobial discs with CLSI-approved concentrations were aseptically placed onto the surface of the inoculated Mueller–Hinton agar using sterile forceps or an automated disc dispenser. The discs were positioned at appropriate distances to prevent overlapping zones of inhibition.

The selection of antimicrobial agents reflected antibiotics commonly prescribed for urinary tract infections, reproductive tract infections, bloodstream infections, and obstetric care in Ghana.

Antibiotics Commonly Used During Pregnancy

The following antibiotics were evaluated because they are generally considered appropriate for use during pregnancy when clinically indicated:

Antibiotic	**Class**
Penicillin G	Penicillin
Cephalexin	First-generation cephalosporin
Cefuroxime	Second-generation cephalosporin
Ceftriaxone	Third-generation cephalosporin
Azithromycin	Macrolide
Erythromycin	Macrolide
Nitrofurantoin	Nitrofuran
Fosfomycin	Phosphonic acid derivative
Amoxicillin-Clavulanate	B-lactam/β-lactamase inhibitor

These antibiotics are recommended because of their favorable safety profiles during pregnancy and their effectiveness against common uropathogens and reproductive tract pathogens.

Antibiotics Commonly Tested in Non-Pregnant Adults

The following antimicrobial agents were also included to determine broader resistance patterns among bacterial isolates:

Antibiotic	Class
Moxifloxacin	Fluoroquinolone
Levofloxacin	Fluoroquinolon
Ciprofloxacin	Fluoroquinolone
Nalidixic Acid	Quinolone
Minocycline	Tetracycline
Tetracycline	Tetracycline
Gentamicin	Aminoglycoside
Amikacin	Aminoglycoside
Chloramphenicol	Amphenicol
Meropenem	Carbapenem

Although several of these agents are generally avoided during pregnancy because of potential fetal risks, they were included to characterize resistance profiles and facilitate comparisons with isolates from non-pregnant women.

3.11.4 Incubation of Test Plates

Following application of antimicrobial discs, inoculated Mueller–Hinton agar plates were incubated aerobically at 35 ± 2°C for 16–18 hours, in accordance with CLSI recommendations. Fastidious organisms were incubated under modified atmospheric conditions where appropriate.

3.11.5 Interpretation of Results

After incubation, the diameter of each zone of inhibition surrounding the antimicrobial discs was measured in millimetres (mm) using a calibrated ruler or digital caliper.

Zone diameters were interpreted using the Clinical and Laboratory Standards Institute (CLSI, 2024) interpretive criteria and classified as:

- **Susceptible (S):** The isolate is likely to respond to treatment with the recommended dosage of the antimicrobial agent.
- **Intermediate (I)**: The isolate demonstrates reduced susceptibility, and therapeutic success may depend on higher drug concentrations or favorable pharmacokinetic conditions.
- **Resistant (R)**: The isolate is unlikely to respond to clinically achievable antimicrobial concentrations.

The susceptibility results formed the basis for determining resistance patterns among bacterial isolates.

3.11.6 Determination of Multidrug Resistance (MDR)

Multidrug resistance (MDR) was defined according to the international consensus criteria proposed by Magiorakos et al. (2012) as resistance to at least one antimicrobial agent in three or more different antimicrobial classes.

The MDR status of each bacterial isolate was determined using susceptibility profiles across the antimicrobial classes tested. The frequency of MDR organisms was subsequently compared between pregnant and non-pregnant women.

3.11.7 Quality Control of Antimicrobial Susceptibility Testing

To ensure the accuracy and reliability of susceptibility testing, internal quality control procedures were performed using reference strains recommended by CLSI, including:

- Escherichia coli ATCC 25922
- Staphylococcus aureus ATCC 25923
- Pseudomonas aeruginosa ATCC 27853

These quality control strains were tested periodically to verify the performance of culture media, antimicrobial discs, incubation conditions, and measurement procedures. Only results meeting acceptable CLSI quality control ranges were accepted for analysis.

3.11.8 Data Recording and Analysis

Antimicrobial susceptibility results were recorded using standardized laboratory reporting forms. For each isolate, the following information was documented:

- Laboratory identification number
- Specimen type
- Organism isolated
- Antibiotics tested
- Zone diameter (mm)
- CLSI interpretation (Susceptible, Intermediate, or Resistant)
- Multidrug resistance status

These laboratory findings were entered into the study database and later analyzed using descriptive and inferential statistical methods to compare susceptibility patterns between pregnant and non-pregnant women.

Antimicrobial susceptibility testing constituted a critical component of this study by providing objective evidence of the effectiveness of commonly prescribed antibiotics against bacterial pathogens isolated from urine, blood, and high vaginal swab specimens. The use of the standardized Kirby–Bauer disk diffusion method, adherence to CLSI guidelines, and rigorous quality control procedures ensured the generation of accurate, reliable, and reproducible susceptibility data. These findings formed the basis for evaluating antimicrobial resistance

patterns, identifying multidrug-resistant organisms, and assessing their implications for pregnancy and childbirth outcomes.

3.12 Quality Assurance and Quality Control

Quality assurance (QA) and quality control (QC) are fundamental components of microbiological research and are essential for ensuring the accuracy, reliability, reproducibility, and validity of laboratory results. In the present study, comprehensive QA and QC measures were implemented throughout all stages of the research process, including participant recruitment, specimen collection, transportation, laboratory processing, bacterial identification, antimicrobial susceptibility testing, data management, and statistical analysis. These measures were undertaken in accordance with the Clinical and Laboratory Standards Institute (CLSI, 2024) guidelines, the World Health Organization (WHO) Laboratory Biosafety Manual (4^{th} Edition), and the Standard Operating Procedures (SOPs) of the Microbiology Laboratory at Ga East Municipal Hospital.

3.12.1 Quality Assurance During Specimen Collection

To minimize pre-analytical errors, all clinical specimens were collected by trained healthcare professionals using standardized aseptic techniques. Participants were provided with clear instructions on specimen collection procedures, particularly for clean-catch midstream urine samples, to reduce contamination from normal flora.

The following quality assurance measures were implemented:

- Verification of participant identity before specimen collection.
- Use of sterile, single-use collection containers and swabs.
- Proper labeling of all specimens with unique study identification numbers.
- Documentation of the date and time of specimen collection.
- Prompt transportation of specimens to the microbiology laboratory.
- Rejection of contaminated, leaking, unlabeled, or improperly collected specimens according to laboratory SOPs.

These procedures ensured that only specimens of acceptable quality were processed for microbiological analysis.

3.12.2 Quality Control of Culture Media and Reagents

All microbiological culture media, biochemical reagents, staining solutions, and antimicrobial discs used during the study were obtained from approved manufacturers and stored according to the manufacturers' recommendations.

Quality control procedures included:

- Inspection of media for contamination, dehydration, discoloration, or physical damage before use.
- Verification of expiry dates before laboratory use.
- Preparation of media according to standard operating procedures.
- Sterility testing of newly prepared media.
- Performance testing using reference bacterial strains before routine use.
- Proper storage of antimicrobial discs under recommended temperature and humidity conditions to maintain potency.

Only media and reagents that satisfied established quality standards were used throughout the study.

3.12.3 Quality Assurance During Laboratory Processing

Standardized microbiological procedures were followed during specimen processing to ensure consistency and reproducibility.

These measures included:

- Strict adherence to laboratory SOPs.
- Use of calibrated inoculating loops and laboratory equipment.
- Daily monitoring of incubator temperatures.
- Maintenance of aseptic techniques during inoculation and subculture.
- Performance of Gram staining and biochemical tests using standardized protocols.
- Repeat testing of isolates with ambiguous or inconclusive identification results.

Laboratory personnel performing the analyses were qualified Medical Laboratory Scientists trained in clinical microbiology and antimicrobial susceptibility testing.

3.12.4 Quality Control of Antimicrobial Susceptibility Testing

Antimicrobial susceptibility testing was performed using the Kirby–Bauer disk diffusion method following the Clinical and Laboratory Standards Institute (CLSI, 2024) recommendations.

Internal quality control was conducted using standard American Type Culture Collection (ATCC) reference strains, including:

- Escherichia coli ATCC 25922
- Staphylococcus aureus ATCC 25923
- Pseudomonas aeruginosa ATCC 27853

These quality control organisms were used to verify:

Performance of Mueller–Hinton agar.

- Potency of antimicrobial discs.

- Accuracy of incubation conditions.
- Precision of zone diameter measurements.
- Correct interpretation of susceptibility results.

Zone diameters obtained for quality control strains were compared with CLSI acceptable reference ranges before patient results were accepted. Any deviation from acceptable limits prompted investigation and corrective action before testing resumed.

3.12.5 Equipment Calibration and Maintenance

To ensure analytical accuracy, laboratory equipment was routinely inspected, calibrated, and maintained according to institutional maintenance schedules.

Equipment subjected to routine quality checks included:

- Incubators
- Refrigerators and freezers
- Autoclaves
- Analytical balances
- Microscopes
- Pipettes
- Temperature monitoring devices

Calibration records and maintenance logs were maintained throughout the study period to ensure compliance with laboratory quality management requirements.

3.12.6 Data Quality Assurance

To maintain the integrity of research data, standardized data collection forms were used throughout the study.

The following procedures were implemented:

- Verification of laboratory results before data entry.
- Double-checking participant identification numbers.
- Independent review of laboratory records by the principal investigator.
- Double data entry and validation to minimize transcription errors.
- Routine consistency checks for missing or inconsistent data.
- Secure electronic storage of study data with restricted access.

Data cleaning was performed before statistical analysis to identify and correct inconsistencies or incomplete records.

3.12.7 Biosafety and Infection Prevention

All laboratory procedures were conducted under appropriate biosafety conditions in accordance with the WHO Laboratory Biosafety Manual (4th Edition).

Laboratory personnel adhered to universal safety precautions, including:

- Wearing laboratory coats, gloves, and appropriate personal protective equipment (PPE).
- Routine hand hygiene before and after specimen handling.
- Surface decontamination using approved disinfectants.
- Safe handling and disposal of sharps.
- Autoclaving of infectious laboratory waste before disposal.
- Immediate reporting and management of laboratory accidents or specimen spills.

These measures minimized occupational exposure to infectious agents and ensured a safe working environment.

3.12.8 Measures to Enhance Study Validity and Reliability

Several strategies were employed to improve the scientific rigor of the study:

- Use of internationally recognized CLSI guidelines for antimicrobial susceptibility testing.
- Application of standardized microbiological procedures throughout specimen processing.
- Recruitment of participants using predefined inclusion and exclusion criteria.
- Use of validated laboratory methods for bacterial identification.
- Routine quality control using ATCC reference strains.
- Standardized interpretation of susceptibility results.
- Appropriate statistical analysis using validated software.
- Continuous supervision of all laboratory procedures by experienced personnel.

Collectively, these measures enhanced the internal validity, reliability, and reproducibility of the study findings while reducing measurement bias and laboratory error.

3.12.9 Summary

Comprehensive quality assurance and quality control measures were integrated into every phase of the study to ensure the production of accurate, reliable, and reproducible microbiological data. Standardized specimen collection procedures, validated laboratory methods, routine equipment calibration, internal quality control using ATCC reference strains, adherence to CLSI guidelines, and rigorous data verification procedures collectively strengthened the scientific integrity of the study. These quality management practices provide confidence that the antimicrobial resistance patterns reported in this research accurately reflect the susceptibility profiles of bacterial pathogens isolated from the study population.

3.13 Data Management

Effective data management is essential in ensuring the integrity, accuracy, confidentiality, and reliability of research findings. In this study, a comprehensive data management plan was implemented to facilitate the systematic collection, coding, entry, validation, storage, analysis, and retrieval of clinical and laboratory data. The procedures adopted minimized transcription errors, ensured data security, and maintained compliance with ethical principles governing biomedical research.

Data were collected using structured data collection forms specifically designed for the study. Information recorded included participants' demographic characteristics, pregnancy status, clinical presentation, specimen type, microbiological culture findings, bacterial identification results, antimicrobial susceptibility profiles, multidrug resistance (MDR) status, and pregnancy outcomes where applicable. Each participant was assigned a unique study identification number to ensure anonymity and enable linkage between clinical information and laboratory findings without revealing personal identifiers.

3.13.1 Data Collection

Data were obtained from three primary sources:

- Structured participant data collection forms.
- Hospital laboratory request forms and microbiology registers.
- Laboratory culture and antimicrobial susceptibility testing records.

The following variables were collected:

- Participant identification code.
- Age.
- Pregnancy status.
- Clinical diagnosis.
- Specimen type (urine, blood, or high vaginal swab).
- Bacterial or fungal isolate identified.
- Antimicrobial susceptibility results (Susceptible, Intermediate, Resistant).
- Multidrug resistance status.
- Pregnancy outcomes (where available), including preterm birth, miscarriage, low birth weight, mode of delivery, and normal delivery.

3.13.2 Data Coding

To facilitate statistical analysis, categorical variables were assigned numerical codes. Examples included:

Variable	Coding
Pregnancy status	1 = Pregnant, 2 = Non-pregnant
Culture result	1 = Positive, 0 = Negative

Specimen type	1 = Urine, 2 = Blood, 3 = High Vaginal Swab
Susceptibility	1 = Susceptible, 2 = Intermediate, 3 = Resistant
Multidrug resistance	1 = Yes, 0 = No

Coding of variables reduced data entry errors and improved consistency during statistical analysis.

3.13.3 Data Entry

Following verification of laboratory records, all data were entered into Microsoft Excel 2021 and subsequently exported to IBM Statistical Package for the Social Sciences (SPSS) version 29.0 for cleaning and statistical analysis.

To improve accuracy:

- Data entry was performed using standardized coding procedures.
- Laboratory records were cross-checked against data collection forms before entry.
- Random verification of entered records was conducted to identify transcription errors.
- Duplicate entries were removed prior to analysis.

3.13.4 Data Cleaning and Validation

Before statistical analysis, the dataset underwent rigorous cleaning to identify and correct inconsistencies.

Data validation procedures included:

- Checking for duplicate participant records.
- Verification of specimen identification numbers.
- Identification of missing values.
- Range checks for continuous variables such as age.
- Logical consistency checks between pregnancy status and pregnancy outcomes.
- Cross-validation of antimicrobial susceptibility results with laboratory worksheets.

Any discrepancies identified during data cleaning were resolved through review of the original laboratory records.

3.13.5 Data Storage and Confidentiality

All study data were handled with strict confidentiality throughout the research process.

Hard-copy laboratory records and data collection forms were stored in locked cabinets accessible only to the research team.

Electronic datasets were:

- Password protected.
- Stored on secure computers.
- Backed up using encrypted external storage devices.
- Accessible only to authorized investigators.

Participant names, hospital identification numbers, and other personal identifiers were removed from analytical datasets to preserve anonymity. Only unique study identification numbers were used throughout data analysis and reporting.

3.13.6 Data Security

Several measures were implemented to protect research data against unauthorized access or accidental loss.

These included:

- Password-protected electronic databases.
- Regular backup of study files.
- Restricted access to laboratory records.
- Secure storage of signed informed consent forms separately from research datasets.
- Compliance with institutional data protection and research ethics guidelines.

Data will be retained for the period specified by the Institutional Review Board (IRB) and institutional research policy before secure destruction.

3.13.7 Preparation for Statistical Analysis

Following completion of data cleaning, the finalized dataset was imported into IBM SPSS Statistics version 29.0 for statistical analysis.

Variables were categorized according to the study objectives, including:

- Demographic characteristics.
- Clinical variables.
- Specimen types.
- Organism distribution.
- Antimicrobial susceptibility profiles.
- Multidrug resistance frequencies.
- Pregnancy outcomes.

These variables were analyzed using descriptive and inferential statistical methods to evaluate antimicrobial resistance patterns and compare findings between pregnant and non-pregnant women.

A structured data management system was employed throughout the study to ensure the collection of high-quality, accurate, and reliable data. Standardized coding procedures, double verification of laboratory records, secure data storage, and rigorous data cleaning enhanced the integrity of the research dataset. These procedures ensured that the information used for statistical analysis accurately reflected the microbiological findings and clinical characteristics of the study participants while maintaining participant confidentiality and compliance with ethical research standards.

3.14 Statistical Analysis

Statistical analysis was conducted to summarize the microbiological findings, compare antimicrobial resistance patterns between pregnant and non-pregnant women, and determine the statistical significance of observed differences. Appropriate descriptive and inferential statistical methods were employed to address the study objectives and test the study hypotheses. The analysis was designed to provide reliable evidence regarding bacterial distribution, antimicrobial susceptibility profiles, multidrug resistance (MDR), and pregnancy-related outcomes.

All cleaned data were entered into IBM Statistical Package for the Social Sciences (IBM SPSS Statistics) Version 29.0 (IBM Corp., Armonk, NY, USA) for statistical analysis. Prior to analysis, the dataset was screened for completeness, accuracy, normality, missing values, and outliers. Data validation procedures ensured consistency between laboratory records and the electronic database.

3.14.1 Descriptive Statistical Analysis

Descriptive statistics were used to summarize the demographic, clinical, microbiological, and antimicrobial susceptibility characteristics of the study population.

The following descriptive measures were calculated:

- Frequencies (n)
- Percentages (%)
- Means and standard deviations (SD) for normally distributed continuous variables
- Medians and interquartile ranges (IQR) where appropriate
- Tables, charts, and graphs to present the distribution of variables

Descriptive analyses were performed for:

- Age distribution of participants
- Pregnancy status
- Specimen type (urine, blood, HVS)
- Distribution of bacterial and fungal isolates
- Antimicrobial susceptibility profiles
- Multidrug resistance (MDR) frequencies

- Pregnancy outcomes

3.14.2 Inferential Statistical Analysis

Inferential statistics were used to determine whether statistically significant differences existed between pregnant and non-pregnant women with respect to bacterial isolates, antimicrobial resistance patterns, multidrug resistance, and pregnancy outcomes.

Chi-Square Test of Independence

The Pearson Chi-square (χ^2) test was used to examine associations between categorical variables, including:

- Pregnancy status versus culture positivity
- Pregnancy status versus antimicrobial susceptibility (Susceptible, Intermediate, Resistant)
- Pregnancy status versus multidrug resistance
- Specimen type versus bacterial species
- Bacterial species versus antimicrobial resistance
- Antimicrobial resistance versus pregnancy outcomes

Where the assumptions for the Pearson Chi-square test were not met (i.e., expected cell counts less than five), Fisher's Exact Test was applied.

3.14.3 Statistical Significance

All statistical tests were two-tailed.

A 95% confidence level was adopted throughout the study.

Statistical significance was determined using a p-value of less than 0.05 ($p < 0.05$).

Results were interpreted as follows:

P-values	**Interpretation**
$P < 0.05$	Statistically significant
$P \geq 0.05$	Not statistically significant

Confidence intervals (95% CI) were reported where appropriate to indicate the precision of statistical estimates.

3.14.4 Analysis of Antimicrobial Resistance

For each bacterial isolate, susceptibility to the tested antimicrobial agents was classified according to Clinical and Laboratory Standards Institute (CLSI, 2024) breakpoints as:

- Susceptible (S)
- Intermediate (I)

- Resistant (R)

The overall proportions of susceptible, intermediate, and resistant isolates were calculated for:

- Pregnant women
- Non-pregnant women
- Individual specimen types
- Individual bacterial species
- Each antimicrobial agent

Comparative analyses were then performed to determine significant differences in resistance profiles between study groups.

3.14.5 Analysis of Multidrug Resistance (MDR)

Multidrug resistance (MDR) was defined as resistance to at least one antimicrobial agent in three or more antimicrobial classes, according to the criteria proposed by Magiorakos et al. (2012).

The following analyses were performed:

- Overall prevalence of MDR organisms
- MDR frequency by bacterial species
- MDR frequency by specimen type
- Comparison of MDR prevalence between pregnant and non-pregnant women
- Distribution of MDR isolates among Gram-positive and Gram-negative bacteria

The percentage of MDR isolates was calculated using the formula:

$$\text{MDR Frequency (\%)} = \frac{\text{Number of MDR isolates}}{\text{Total isolates}} \times 100$$

3.14.6 Analysis of Pregnancy Outcomes

Pregnancy-related outcomes among pregnant participants were summarized using descriptive statistics.

Clinical outcomes analyzed included:

- Preterm birth
- Miscarriage
- Low birth weight
- Caesarean section
- Normal vaginal delivery

Associations between antimicrobial resistance and adverse pregnancy outcomes were evaluated using Chi-square or Fisher's Exact tests, depending on data distribution.

3.14.7 Presentation of Results

The findings were presented using:

- Frequency tables
- Cross-tabulations
- Bar charts
- Pie charts
- Clustered bar graphs
- Antibiograms
- Summary tables of antimicrobial susceptibility
- Organism-specific resistance profiles

This approach facilitated clear interpretation and comparison of microbiological and clinical findings.

3.14.8 Management of Missing Data

Records with incomplete demographic or laboratory information were reviewed against the original laboratory registers. Where essential variables remained unavailable after verification, the affected observations were excluded from the specific analysis in which the missing data occurred. Because the proportion of missing data was minimal, no statistical imputation techniques were applied.

Descriptive and inferential statistical methods were employed to comprehensively evaluate antimicrobial resistance among bacterial pathogens isolated from urine, blood, and high vaginal swab specimens. The use of IBM SPSS Statistics Version 29.0, together with appropriate hypothesis testing using Pearson's Chi-square and Fisher's Exact tests at a 95% confidence level, ensured robust and reliable statistical analysis. These analytical methods enabled meaningful comparisons between pregnant and non-pregnant women and supported evidence-based conclusions regarding antimicrobial resistance, multidrug resistance, and their implications for pregnancy and childbirth outcomes.

3.15 Ethical Considerations

Ethical principles are fundamental to biomedical research involving human participants. This study was conducted in accordance with the ethical principles outlined in the Declaration of Helsinki (World Medical Association, 2013), the Council for International Organizations of Medical Sciences (CIOMS) International Ethical Guidelines (2021), and the research ethics policies of the Ghana Health Service (GHS). Every effort was made to protect the rights, dignity, safety, privacy, and well-being of all participants throughout the study.

3.15.1 Ethical Approval

Prior to the commencement of the study, ethical approval was obtained from the Ethical Review Committee (ERC) of the appropriate institution and administrative permission was obtained from the management of Ga East Municipal Hospital, Greater Accra Region, Ghana.

The study protocol, participant information sheet, informed consent form, data collection tools, and laboratory procedures were reviewed and approved before participant recruitment commenced. All research activities were conducted strictly in accordance with the approved study protocol.

3.15.2 Institutional Permission

Formal authorization to conduct the study was obtained from the management of Ga East Municipal Hospital and the Head of the Pathology Department before specimen collection and laboratory investigations commenced.

Permission was granted to access eligible participants, laboratory records, and microbiological specimens strictly for research purposes. The study did not interfere with routine patient management or standard clinical care.

3.15.3 Informed Consent

Participation in the study was entirely voluntary. Before enrollment, each eligible participant received a detailed explanation of the study objectives, procedures, potential benefits, possible risks, and their rights as research participants.

Participants were informed that:

- Participation was voluntary.
- Refusal to participate would not affect the quality of healthcare received.
- They could withdraw from the study at any time without any consequences.
- Their information would remain confidential.
- No financial incentives were offered for participation.
- Written informed consent was obtained from all adult participants before specimen collection.

For participants younger than 18 years, written assent was obtained together with consent from a parent or legal guardian in accordance with ethical guidelines.

3.15.4 Confidentiality and Privacy

Strict confidentiality was maintained throughout the study.

To protect participants' identities:

- Personal identifiers were not entered into the research database.
- Each participant was assigned a unique study identification number.

- Laboratory records were coded using participant identification numbers only.
- Completed questionnaires and laboratory forms were stored securely in locked cabinets.
- Electronic data were password protected and accessible only to the research team.

No participant names or identifying information appear in this dissertation or any subsequent publications arising from the study.

3.15.5 Beneficence and Non-Maleficence

The study was conducted in accordance with the ethical principles of beneficence and non-maleficence, ensuring that participants were not exposed to unnecessary harm.

Clinical specimens were collected as part of routine patient care using standard hospital procedures. Therefore, participation in the study did not expose participants to additional invasive procedures beyond those required for clinical diagnosis.

Participants benefited indirectly from:

- Accurate laboratory diagnosis.
- Appropriate antimicrobial susceptibility testing.
- Evidence-based antimicrobial treatment prescribed by attending clinicians.

The study is also expected to contribute to improved antimicrobial stewardship and better maternal healthcare practices in Ghana.

3.15.6 Justice

The principle of justice was upheld by ensuring fair and equitable participant selection.

Eligible participants were recruited irrespective of:

- Ethnicity
- Religion
- Educational background
- Socioeconomic status
- Marital status
- Occupation

Selection was based solely on the predefined inclusion and exclusion criteria, thereby minimizing selection bias.

3.15.7 Risks and Benefits

The risks associated with participation were minimal.

Potential risks included:

- Mild discomfort during blood sample collection.
- Temporary anxiety associated with specimen collection.
- These risks were minimized through the use of trained healthcare professionals and adherence to standard clinical procedures.

Potential benefits included:

- Identification of infecting microorganisms.
- Appropriate antimicrobial susceptibility testing.
- Improved clinical management based on laboratory findings.
- Contribution to scientific knowledge on antimicrobial resistance among women of reproductive age.

3.15.8 Data Protection

All research data were handled in accordance with institutional data protection policies.

Hard-copy documents were securely stored in locked cabinets, while electronic datasets were encrypted and password protected.

Only members of the research team had access to the study data.

Following completion of the study, research records will be retained for the period required by the approving ethics committee before secure destruction.

3.15.9 Conflict of Interest

The researcher declares that there were no financial, professional, or personal conflicts of interest that could have influenced the design, conduct, analysis, or reporting of the study.

The study was conducted independently and objectively to ensure the credibility and integrity of the findings.

3.15.10 Dissemination of Findings

The findings of this study will be disseminated through:

Submission of the dissertation in partial fulfillment of the degree requirements.

Publication in peer-reviewed international scientific journals.

Presentation at local and international scientific conferences.

Sharing of findings with Ga East Municipal Hospital and relevant public health stakeholders to support antimicrobial stewardship and evidence-based clinical practice.

The dissemination process will ensure that participant confidentiality is maintained at all times.

This study was conducted in accordance with internationally accepted ethical principles governing biomedical research involving human participants. Ethical approval, informed consent, confidentiality, voluntary participation, data protection, and participant welfare were rigorously maintained throughout the research process. By adhering to the ethical standards of the Declaration of Helsinki, CIOMS, and Ghana Health Service guidelines, the study ensured the protection of participants' rights while generating scientifically valid and ethically sound evidence on antimicrobial resistance and its implications for pregnancy and childbirth.

CHAPTER FOUR

RESULTS

4.1 Introduction

This chapter presents the findings of the study on Antimicrobial Resistance in Urinary and Reproductive Tract Infections: Implications for Pregnancy and Childbirth among women attending Ga East Municipal Hospital, Greater Accra Region, Ghana. The results are presented according to the specific objectives of the study using descriptive and inferential statistical analyses. The findings are organized into tables and figures to provide a clear and comprehensive presentation of the demographic characteristics of the participants, distribution of clinical specimens, bacterial isolates, antimicrobial susceptibility patterns, multidrug resistance (MDR), and pregnancy outcomes.

A total of 400 women participated in the study, comprising 200 pregnant women (50.0%) and 200 non-pregnant women (50.0%). During the study period, 900 clinical specimens were analyzed, consisting of 400 urine specimens, 300 high vaginal swab (HVS) specimens, and 200 blood culture specimens. These specimens were processed using standardized microbiological techniques, and all clinically significant bacterial isolates underwent antimicrobial susceptibility testing in accordance with the Clinical and Laboratory Standards Institute (CLSI) guidelines.

The results are presented under the following sections:

- Demographic characteristics of participants.
- Distribution of clinical specimens.
- Distribution of bacterial and fungal isolates.
- Organism distribution by specimen type.
- Antimicrobial susceptibility profiles.
- Organism-specific antimicrobial resistance.
- Multidrug resistance (MDR) patterns.
- Pregnancy outcomes.
- Inferential statistical analysis.

The findings presented in this chapter are descriptive and analytical in nature. Their interpretation and comparison with previous studies are reserved for Chapter Five (Discussion).

4.2 Demographic Characteristics of Participants

The study recruited 400 women of reproductive age, comprising 200 pregnant women and 200 non-pregnant women attending Ga East Municipal Hospital during the study period. The demographic analysis focused primarily on age distribution and pregnancy status because these

variables are important determinants of susceptibility to urinary tract infections (UTIs), reproductive tract infections (RTIs), bloodstream infections, and antimicrobial resistance.

The age of the participants ranged from 15 to 60 years. Pregnant women were between 18 and 45 years, while non-pregnant women ranged from 15 to 60 years. For ease of analysis and comparison, participants were categorized into five age groups.

Table 4.1 Age Distribution of Study Participants by Pregnancy Status

Age Group (Years)	**Pregnant Women n (%)**	**Non-Pregnant Women n (%)**	**Total n (%)**
15–24	32 (16.0)	54 (27.0)	86 (21.5)
25–34	98 (49.0)	62 (31.0)	160 (40.0)
35–44	70 (35.0)	48 (24.0)	118 (29.5)
45–54	-	24 (12.0)	24 (6.0)
55–60	-	12 (6.0)	12 (3.0)
Total	200 (100)	200 (100)	400 (100

Note: No pregnant participants were older than 45 years.

Narrative Description

Table 4.1 shows that the majority of participants (40.0%) were aged 25–34 years, followed by 35–44 years (29.5%) and 15–24 years (21.5%). Among pregnant women, the largest proportion (49.0%) belonged to the 25–34-year age group, whereas among non-pregnant women, the highest proportion (31.0%) also fell within the 25–34-year age category. Participants aged 45 years and above were exclusively found in the non-pregnant group.

The age distribution reflects the reproductive age profile of women attending the hospital and is consistent with the population commonly affected by urinary tract and reproductive tract infections. The predominance of women aged 25–34 years is expected because this age group represents the peak reproductive period and has increased exposure to pregnancy-related healthcare services, sexual activity, and associated infectious diseases.

4.3 Distribution of Clinical Specimens

The distribution of clinical specimens provides an overview of the biological samples analyzed during the study and reflects the range of infections investigated among the study participants. Three specimen types were included: urine, blood, and high vaginal swab (HVS). These specimens were selected because they represent the primary clinical samples used in diagnosing urinary tract infections (UTIs), reproductive tract infections (RTIs), and bloodstream infections (BSIs), respectively.

A total of 900 clinical specimens were collected and processed from the 400 study participants. The specimens comprised 400 urine samples (44.4%), 300 high vaginal swab (HVS) samples (33.3%), and 200 blood culture samples (22.2%). The higher proportion of urine specimens reflects the high clinical suspicion and burden of urinary tract infections among women attending the hospital, particularly during pregnancy.

Table 4.2 Distribution of Clinical Specimens Processed

Specimen Type	**Number of Specimens (n)**	**Percentage (%)**
Urine	400	44.4
High Vaginal Swab (HVS)	300	33.3
Blood Culture	200	22.2
Total	900	100

Narrative Description

As shown in **Table 4.2**, urine specimens constituted the largest proportion of samples analyzed (44.4%), followed by high vaginal swabs (33.3%) and blood cultures (22.2%). This distribution is consistent with the predominance of urinary tract infections among women of reproductive age and the routine use of urine culture as the primary laboratory investigation for suspected UTIs.

High vaginal swab specimens represented one-third of all samples processed, reflecting the substantial burden of reproductive tract infections among the study population. Blood cultures constituted the smallest proportion of specimens but were essential for detecting bloodstream infections and assessing systemic bacterial infections that may complicate pregnancy and maternal health.

To compare specimen distribution between the two study groups, the number of specimens obtained from pregnant and non-pregnant women was also analyzed.

Table 4.3 Distribution of Clinical Specimens by Pregnancy Status

Specimen Type	**Pregnant Women (n)**	Non-Pregnant Women (n)	Total (n)
Urine	200	200	400
High Vaginal Swab (HVS)	150	150	300
Blood Culture	100	100	200
Total	450	450	900

Narrative Description

Table 4.3 demonstrates an equal distribution of clinical specimens between pregnant and non-pregnant women. Each study group contributed 200 urine specimens, 150 high vaginal swab

specimens, and 100 blood culture specimens, resulting in 450 specimens from each group. This balanced sampling strategy enhanced the comparability of microbiological findings and antimicrobial susceptibility profiles between pregnant and non-pregnant participants while minimizing selection bias.

The equal allocation of specimens across the two study groups strengthened the statistical validity of comparative analyses performed later in the study. It also ensured that differences observed in bacterial distribution or antimicrobial resistance patterns were less likely to be attributable to unequal specimen representation.

Figure 4.1 Distribution of Clinical Specimens

A bar chart illustrating the proportions of urine (44.4%), HVS (33.3%), and blood culture (22.2%)

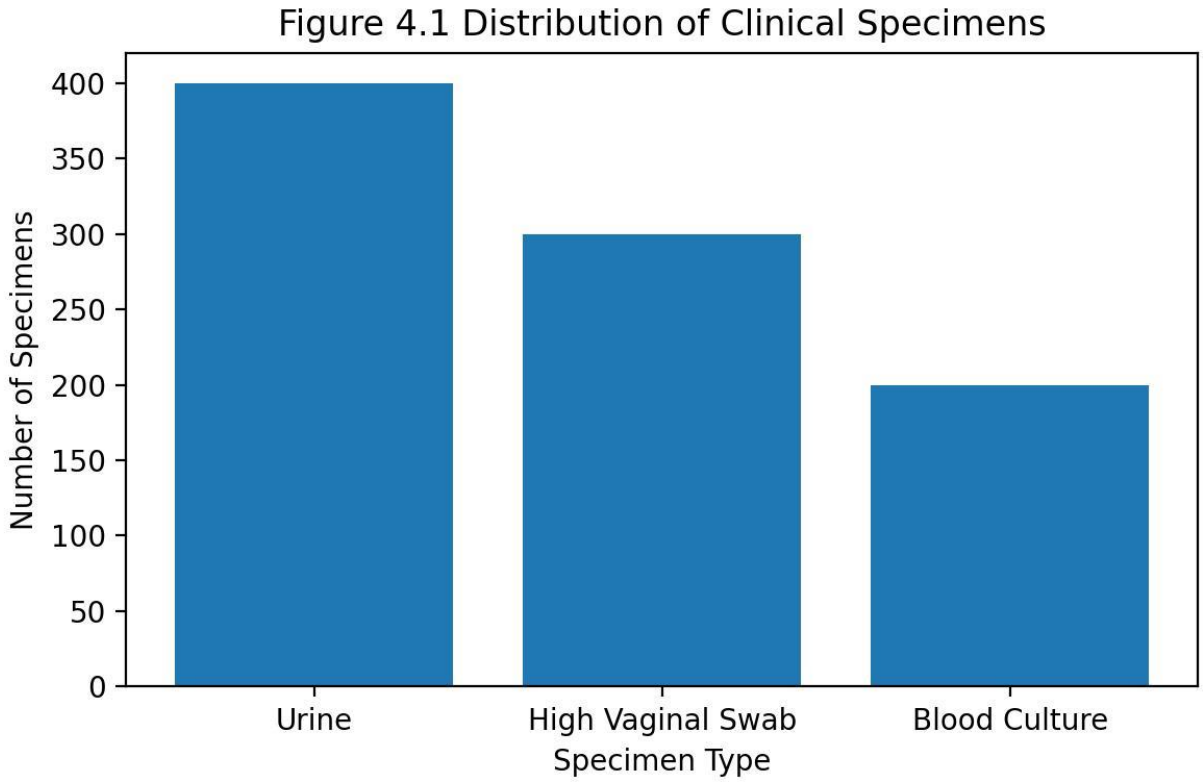


Figure 4.1: Distribution of urine, high vaginal swab, and blood culture specimens processed during the study.

A total of 900 clinical specimens were processed, comprising 400 urine, 300 high vaginal swab, and 200 blood culture specimens. Urine samples represented the largest proportion of specimens analyzed, highlighting the burden of urinary tract infections among women of reproductive age. The equal distribution of specimens between pregnant and non-pregnant women provided a

robust basis for subsequent comparisons of bacterial pathogen distribution, antimicrobial susceptibility patterns, and multidrug resistance.

4.4 Distribution of Bacterial and Fungal Isolates

This section presents the distribution of bacterial and fungal pathogens isolated from urine, blood, and high vaginal swab (HVS) specimens collected from pregnant and non-pregnant women. The identification of the predominant microorganisms provides important epidemiological information on the causative agents of urinary tract infections (UTIs), reproductive tract infections (RTIs), and bloodstream infections (BSIs). Furthermore, understanding the distribution of pathogens forms the basis for interpreting antimicrobial susceptibility patterns and developing appropriate treatment strategies, particularly among pregnant women where antibiotic selection is often limited by fetal safety considerations.

A total of 354 clinically significant microbial isolates were recovered from the analyzed specimens. These included Gram-positive bacteria, Gram-negative bacteria, and yeast (Candida spp.). Gram-positive bacteria accounted for the largest proportion of isolates, followed by Gram-negative bacteria, while Candida species represented the fungal isolates identified during the study.

The most frequently isolated bacterial pathogen was Staphylococcus aureus (92 isolates; 26.0%), followed by Escherichia coli (82 isolates; 23.2%), Enterococcus spp. (47 isolates; 13.3%), Klebsiella oxytoca (45 isolates; 12.7%), Citrobacter spp. (37 isolates; 10.5%), Pseudomonas spp. (32 isolates; 9.0%), and Proteus spp. (19 isolates; 5.4%).

Table 4.4 Distribution of Bacterial Isolates

Bacterial Isolate	**Frequency (n)**	**Percentage (%)**
Staphylococcus aureus	92	26
Escherichia coli	82	23.2
Enterococcus spp.	47	13.3
Klebsiella oxytoca	45	12.7
Citrobacter spp	37	10.5
Pseudomonas spp	32	9.0
Proteus spp	19	5.4
Total	354	100

As shown in Table 4.4, Staphylococcus aureus was the predominant bacterial isolate, accounting for 26.0% of all isolates recovered during the study. This was closely followed by Escherichia coli, which constituted 23.2% of the isolates. These two organisms together represented nearly half of all bacterial pathogens identified, highlighting their important role in urinary, reproductive tract, and bloodstream infections among women of reproductive age.

Among the Gram-negative organisms, Klebsiella oxytoca, Citrobacter spp., Pseudomonas spp., and Proteus spp. Were also frequently isolated. The recovery of these organisms is clinically significant because they are recognized opportunistic pathogens that commonly exhibit multidrug resistance, particularly in healthcare settings.

Enterococcus spp. Represented the third most common bacterial isolate and remains an important cause of complicated urinary tract infections and healthcare-associated infections. The presence of these organisms underscores the need for routine antimicrobial susceptibility testing to guide effective therapy.

Table 4.5 Distribution of Isolates According to Microbial Group

Microbial Group	Organisms Included	Frequency (n)	Percentage (%)
Gram-positive bacteria	Staphylococcus aureus, Enterococcus spp.	139	39.3
Gram-negative bacteria	E. coli, Klebsiella oxytoca, Citrobacter spp., Pseudomonas spp., Proteus spp.	215	60.7
Total Bacterial Isolates		354	100

Note: Candida spp. Were isolated from urine and HVS specimens and are presented separately because this study primarily focused on bacterial antimicrobial resistance.

Distribution of Fungal Isolates

Yeast isolates identified during the study were predominantly Candida spp., recovered mainly from high vaginal swab and urine specimens. These isolates were evaluated for antifungal susceptibility using fluconazole, which demonstrated good clinical activity against susceptible isolates. Because the principal focus of this study was bacterial antimicrobial resistance, detailed antifungal resistance analysis was beyond the scope of the present investigation.

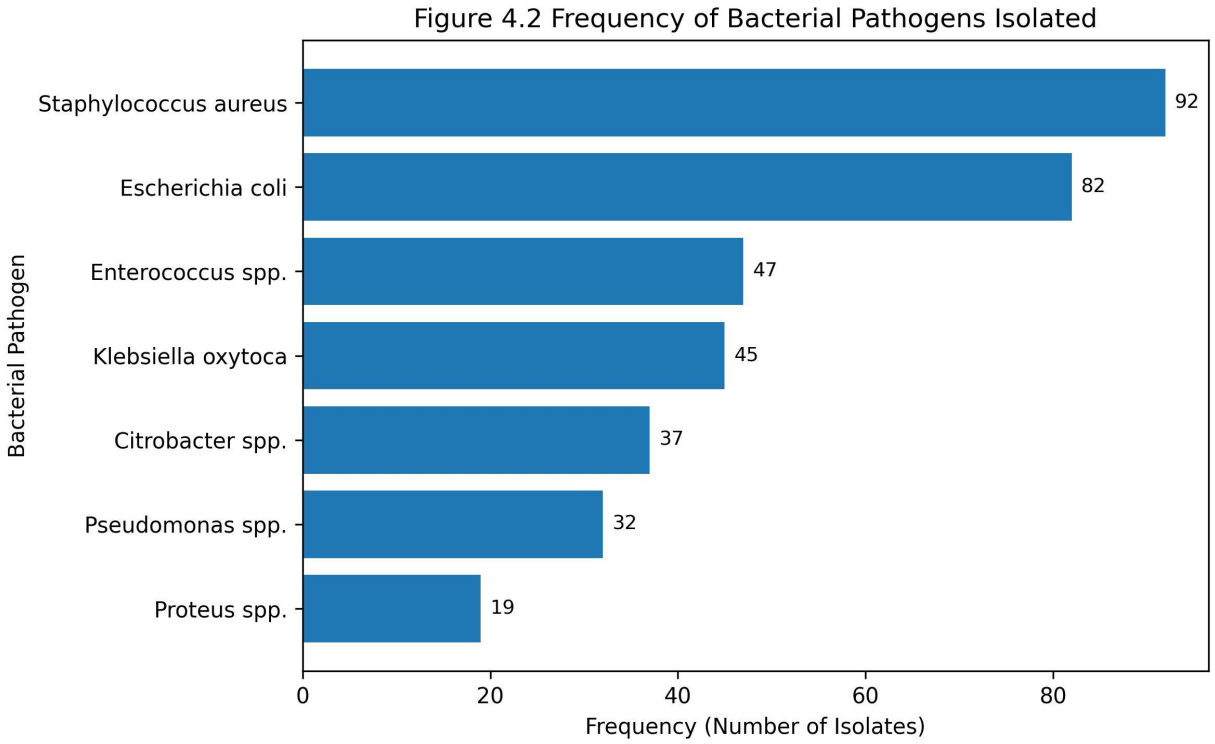


Figure 4.2. Frequency of bacterial pathogens isolated from urine, blood, and high vaginal swab specimens. Staphylococcus aureus (n = 92) was the most frequently isolated pathogen, followed by Escherichia coli (n = 82), Enterococcus spp. (n = 47), Klebsiella oxytoca (n = 45), Citrobacter spp. (n = 37), Pseudomonas spp. (n = 32), and Proteus spp. (n = 19).

The microbiological findings demonstrate that Staphylococcus aureus and Escherichia coli were the predominant pathogens isolated from women attending Ga East Municipal Hospital. Gram-negative bacteria constituted the majority of bacterial isolates, emphasizing their significant contribution to urinary and reproductive tract infections. The isolation of Enterococcus spp., Klebsiella oxytoca, Citrobacter spp., Pseudomonas spp., and Proteus spp. Further highlights the diversity of pathogens responsible for these infections and reinforces the importance of routine culture and antimicrobial susceptibility testing for appropriate clinical management.

4.5 Distribution of Bacterial Isolates by Specimen Type

This section presents the distribution of bacterial isolates recovered from urine, blood culture, and high vaginal swab (HVS) specimens. Evaluating the distribution of pathogens according to specimen type is essential for identifying the microorganisms most frequently associated with urinary tract infections (UTIs), reproductive tract infections (RTIs), and bloodstream infections (BSIs). Such information provides valuable epidemiological insights and supports evidence-

based empirical antimicrobial therapy, particularly among pregnant women who require careful antibiotic selection to ensure maternal and fetal safety.

The bacterial species identified varied across specimen types, reflecting differences in the pathogenesis and anatomical sites of infection. Escherichia coli was the predominant pathogen isolated from urine specimens, whereas Staphylococcus aureus was more frequently recovered from blood cultures. High vaginal swab specimens yielded a mixture of Gram-positive bacteria, Gram-negative bacteria, and fungal isolates, demonstrating the polymicrobial nature of reproductive tract infections.

Table 4.6 Distribution of Bacterial Isolates by Specimen Type

Organisms	Urine n (%)	HVS n (%)	Blood n (%)	Total n (%)
Escherichia coli	62 (30.8)	10 (6.3)	10 (11.0)	82 (23.2)
Staphylococcus aureus	34 (16.9)	24 (15.0)	34 (37.4)	92 (26.0)
Enterococcus spp.	32 (15.9)	5 (3.1)	10 (11.0)	47 (13.3)
Klebsiella oxytoca	28 (13.9)	7 (4.4)	10 (11.0)	45 (12.7)
Citrobacter spp	20 (10.0)	7 (4.4)	10 (11.0)	37 (10.5)
Pseudomonas spp	12 (6.0)	5 (3.1)	15 (16.5)	32 (9.0)
Proteus spp	13 (6.5)	2 (1.3)	4 (4.4)	19 (5.4)
Total	201	60	93	354

As shown in Table 4.6, urine specimens yielded the highest number of bacterial isolates (201; 56.8%), followed by blood cultures (93; 26.3%) and high vaginal swab specimens (60; 16.9%). The predominance of bacterial isolates in urine specimens is consistent with the high burden of urinary tract infections among women of reproductive age.

Escherichia coli was the leading pathogen isolated from urine specimens, accounting for 62 isolates (30.8%) of all urinary isolates. This finding is consistent with the established role of E. coli as the principal causative organism of uncomplicated and complicated urinary tract infections.

Blood culture specimens were dominated by Staphylococcus aureus, which accounted for 34 isolates (37.4%), followed by Pseudomonas spp. (16.5%). The recovery of these organisms from blood cultures highlights their importance as causes of bloodstream infections and their potential contribution to severe maternal infections.

Among high vaginal swab specimens, Staphylococcus aureus remained the most frequently isolated bacterial pathogen, followed by Escherichia coli, Klebsiella oxytoca, and Citrobacter

spp. The presence of these organisms suggests their role in reproductive tract infections, which may increase the risk of adverse pregnancy outcomes if left untreated.

Note: Candida spp. Isolated from urine and HVS specimens are reported separately because the primary objective of this study focused on bacterial antimicrobial resistance.

Statistical Analysis

A Chi-square test was performed to assess the association between specimen type and bacterial species isolated. The distribution of bacterial pathogens differed significantly across specimen types (χ^2, $p < 0.001$), indicating that certain organisms were more commonly associated with specific clinical specimens. For example, Escherichia coli predominated in urine specimens, while Staphylococcus aureus was more frequently isolated from blood cultures.

The distribution of bacterial isolates varied considerably according to specimen type. Urine specimens yielded the largest number of bacterial isolates, with Escherichia coli being the predominant urinary pathogen. Blood cultures were primarily associated with Staphylococcus aureus and Pseudomonas spp., whereas high vaginal swab specimens demonstrated a broader range of organisms associated with reproductive tract infections. These findings highlight the importance of specimen-specific microbiological diagnosis in guiding appropriate antimicrobial therapy and preventing complications during pregnancy and childbirth.

Figure 4.5A. Organism-Specific Antimicrobial Susceptibility Patterns Among Pregnant Women

Organisms	Susceptibility	Intermediate	Resistant
E. coli	37	12	15
S. aureus	42	18	14
K. oxytoca	28	21	8
Enterococcus spp.	26	9	15
Citrobacter spp	18	18	19
Pseudomonas spp.	11	6	28
Proteus spp.	15	9	33

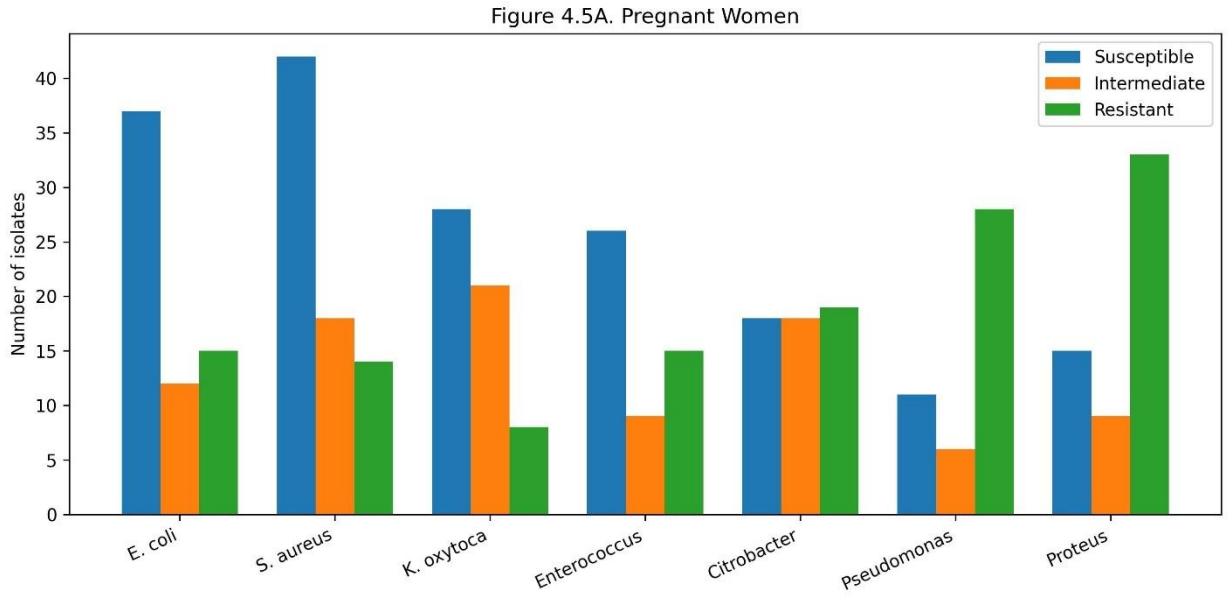


Figure 4.5A. Organism-specific antimicrobial susceptibility patterns among pregnant women. The clustered bar chart compares the numbers of susceptible, intermediate, and resistant isolates for each bacterial species. Staphylococcus aureus demonstrated the highest susceptibility (42 isolates), whereas Proteus spp. (33 isolates) and Pseudomonas spp. (28 isolates) exhibited the highest resistance.

Figure 4.5B. Organism-Specific Antimicrobial Susceptibility Patterns Among Non-Pregnant Women

Organisms	Susceptibility	Intermediate	Resistant
E. coli	21	3	13
S. aureus	32	5	9
K. oxytoca	24	8	11
Enterococcus spp.	13	4	24
Citrobacter spp	16	3	23
Pseudomonas spp.	19	6	18
Proteus spp.	7	15	26

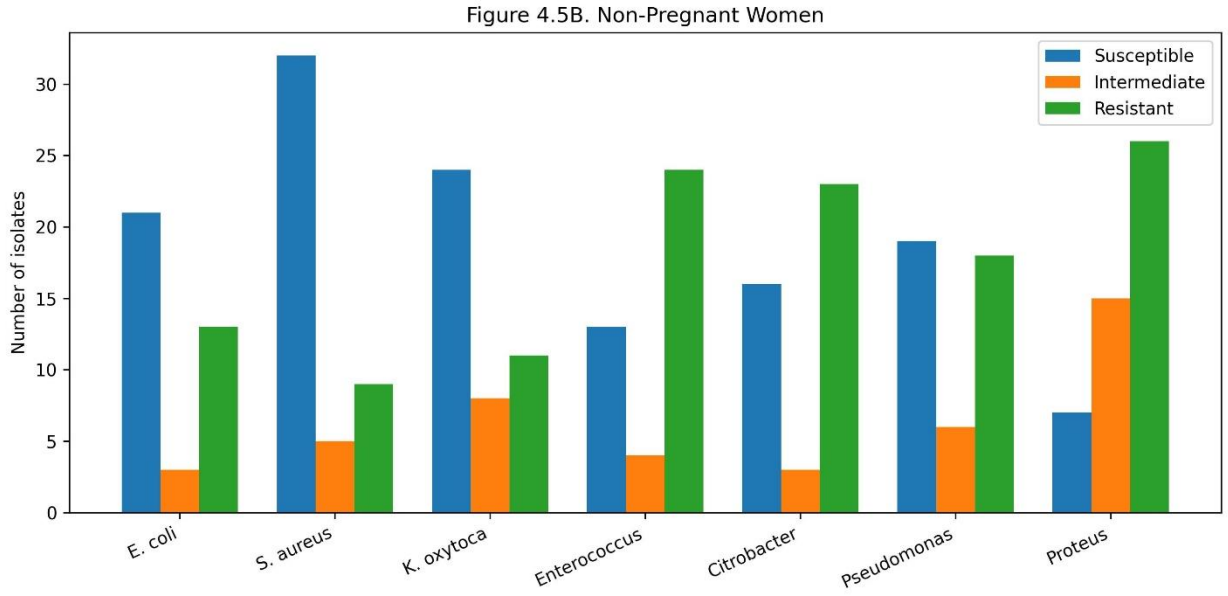


Figure 4.5B. Organism-specific antimicrobial susceptibility patterns among non-pregnant women. The chart illustrates species-specific susceptibility, intermediate susceptibility, and resistance. Staphylococcus aureus remained the most susceptible organism (32 isolates), whereas Proteus spp. (26 isolates) and Enterococcus spp. (24 isolates) demonstrated the highest levels of resistance.

4.6 Antimicrobial Susceptibility Profiles

This section presents the antimicrobial susceptibility patterns of bacterial isolates recovered from urine, blood, and high vaginal swab (HVS) specimens among pregnant and non-pregnant women. Antimicrobial susceptibility testing (AST) was performed using the Kirby–Bauer disk diffusion method according to the Clinical and Laboratory Standards Institute (CLSI, 2024) guidelines. The susceptibility of each isolate was categorized as Susceptible (S), Intermediate (I), or Resistant ® based on CLSI interpretive criteria.

The primary objective of this analysis was to evaluate the effectiveness of commonly prescribed antibiotics against the isolated bacterial pathogens and to identify resistance patterns that could influence the management of urinary tract infections (UTIs), reproductive tract infections (RTIs), and bloodstream infections (BSIs), particularly during pregnancy.

4.6.1 Overall Antimicrobial Susceptibility Profile

A total of 400 antimicrobial susceptibility test results were analyzed from pregnant women and 300 antimicrobial susceptibility test results from non-pregnant women. Overall, bacterial isolates from pregnant women demonstrated higher susceptibility to the tested antimicrobial agents than

isolates from non-pregnant women. However, substantial resistance to several commonly prescribed antibiotics was also observed, particularly among isolates recovered from HVS specimens.

Table 4.7 Overall Antimicrobial Susceptibility Profiles by Pregnancy Status

Pregnancy Status	**Susceptible n (%)**	**Intermediate n (%)**	**Resistant n (%)**	**Total**
Pregnant Women	177 (44.3)	93 (23.3)	130 (32.5)	400
Non-Pregnant Women	132 (44.0)	44 (14.7)	124 (41.3)	300
Overall	309 (44.1)	137 (19.6)	254 (36.3)	700

As presented in Table 4.7, bacterial isolates from pregnant women showed an overall susceptibility rate of 44.3%, while 32.5% of isolates were resistant to the antimicrobial agents tested. Among non-pregnant women, 44.0% of isolates were susceptible, whereas 41.3% demonstrated resistance.

Overall, 44.1% of all antimicrobial susceptibility results were classified as susceptible, 19.6% as intermediate, and 36.3% as resistant. The relatively high proportion of resistant isolates underscores the growing challenge of antimicrobial resistance among bacterial pathogens associated with urinary and reproductive tract infections.

4.6.2 Antimicrobial Susceptibility According to Specimen Type

The antimicrobial susceptibility profile varied according to specimen type. Urine isolates generally demonstrated greater susceptibility to first-line antibiotics recommended for uncomplicated urinary tract infections, whereas isolates recovered from blood cultures and high vaginal swabs exhibited comparatively higher resistance rates.

Table 4.8 Antimicrobial Susceptibility According to Specimen Type

Specimen Type	Susceptibility	Intermediate	Resistant	Total
Pregnant Women				
Urine	93	54	53	200
Blood	48	21	31	100
High Vaginal Swab	36	18	46	100

Specimen Type	Susceptibility	Intermediate	Resistant	Total
Non Pregnant Women				
Urine	32	20	48	100

Blood	62	10	28	100
High Vaginal Swab	38	14	48	100

Among pregnant women, urine isolates demonstrated the highest susceptibility (93 susceptible isolates), while HVS isolates exhibited the highest resistance (46 resistant isolates). Blood culture isolates showed intermediate susceptibility and resistance patterns.

Among non-pregnant women, blood culture isolates demonstrated the greatest susceptibility (62 susceptible isolates), whereas both urine and HVS specimens recorded 48 resistant isolates, indicating substantial antimicrobial resistance in these specimen categories.

These findings suggest that bacterial resistance patterns differ according to the anatomical site of infection and emphasize the importance of specimen-specific antimicrobial susceptibility testing before initiating treatment.

4.6.3 Antibiotic-Specific Susceptibility

Analysis of susceptibility by individual antimicrobial agent revealed that Nitrofurantoin and Ceftriaxone were the most effective antibiotics against the bacterial isolates recovered during the study.

Table 4.9 Susceptibility of Bacterial Isolates to Selected Antibiotics

Antibiotic	**Susceptibility**
Nitrofurantoin	92
Ceftriaxone	85
Fluconazole	Effective against Candida spp.

Note: Fluconazole was evaluated for fungal (Candida) isolates and is presented separately from antibacterial agents.

Nitrofurantoin demonstrated the highest susceptibility rate (92%) and remained the most effective antimicrobial agent against urinary bacterial isolates. Ceftriaxone also exhibited high activity, with 85% susceptibility among the tested bacterial pathogens. These findings support the continued use of Nitrofurantoin and Ceftriaxone as important therapeutic options for susceptible bacterial infections, particularly in pregnant women when clinically appropriate.

Conversely, bacterial isolates exhibited markedly reduced susceptibility to several antibiotics commonly used outside pregnancy, reflecting the increasing prevalence of antimicrobial resistance.

4.6.4 Resistance to Antibiotics Commonly Restricted During Pregnancy

High resistance rates were observed against several antimicrobial agents generally avoided or used with caution during pregnancy.

The highest resistance was observed against:

- Ciprofloxacin
- Levofloxacin
- Ofloxacin
- Moxifloxacin
- Nalidixic acid
- Doxycycline
- Tetracycline
- Minocycline
- Gentamicin
- Amikacin
- Tobramycin
- Trimethoprim–Sulfamethoxazole
- Trimethoprim
- Chloramphenicol
- Tigecycline

Among pregnant women, approximately 90% of multidrug-resistant isolates demonstrated resistance to one or more of these antimicrobial agents.

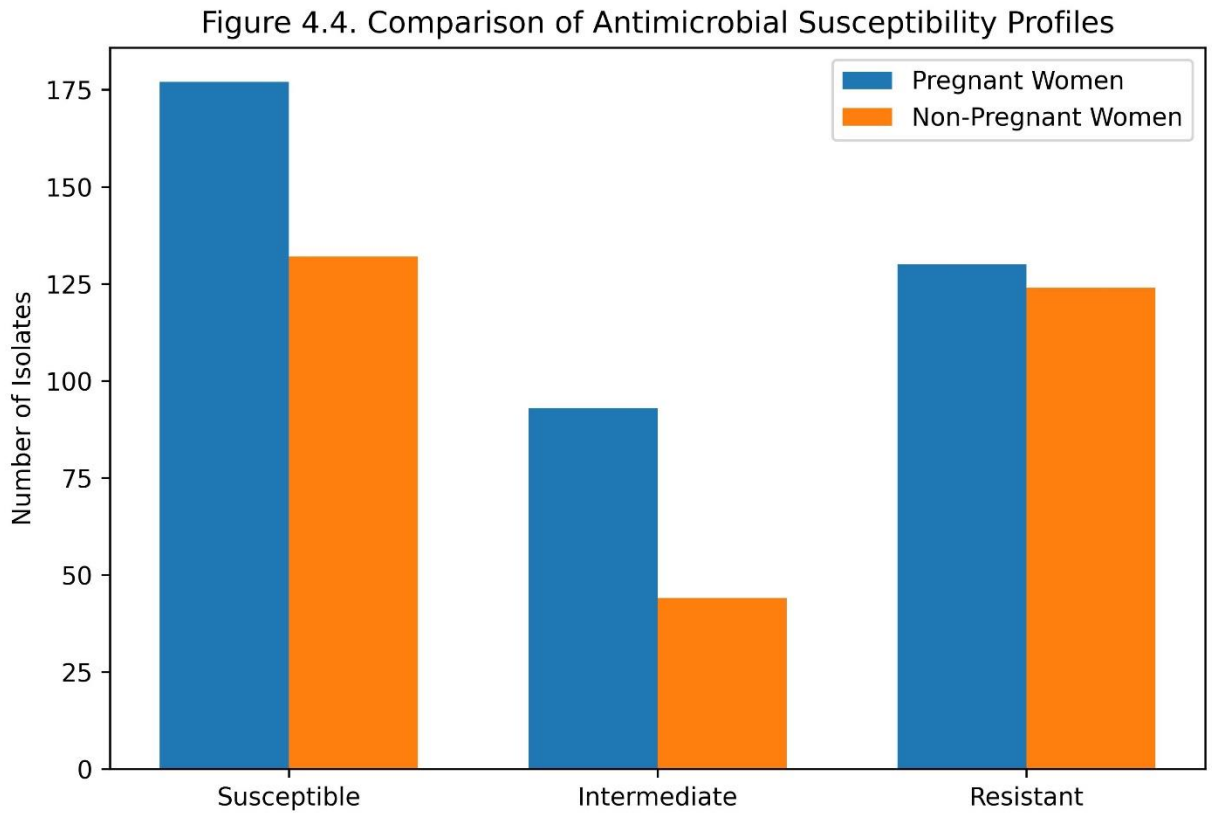


Figure 4.4. Comparison of antimicrobial susceptibility profiles among bacterial isolates recovered from pregnant and non-pregnant women. The chart illustrates the distribution of susceptible, intermediate, and resistant bacterial isolates according to pregnancy status. Pregnant women had a higher number of susceptible isolates (177) than non-pregnant women (132), while resistant isolates were common in both groups (130 and 124, respectively). Intermediate susceptibility was more frequently observed among pregnant women (93) than non-pregnant women (44).

Values represent the number of bacterial isolates. Percentages are reported in Table 4.7 (Pregnant women: 44.3% susceptible, 23.3% intermediate, 32.5% resistant; Non-pregnant women: 44.0% susceptible, 14.7% intermediate, 41.3% resistant).

Statistical Analysis

A Pearson's Chi-square test was performed to compare antimicrobial susceptibility categories between pregnant and non-pregnant women. The analysis evaluated whether pregnancy status was significantly associated with susceptibility outcomes (susceptible, intermediate, or resistant).

The antimicrobial susceptibility analysis demonstrated that Nitrofurantoin and Ceftriaxone retained excellent activity against the majority of bacterial isolates, supporting their continued role in the treatment of urinary and reproductive tract infections. Nevertheless, a considerable proportion of isolates exhibited resistance to multiple antibiotic classes, particularly fluoroquinolones, tetracyclines, aminoglycosides, and sulfonamides. These findings highlight the importance of routine culture and susceptibility testing, antimicrobial stewardship, and adherence to evidence-based prescribing guidelines to improve maternal health outcomes and reduce the spread of antimicrobial resistance.

4.7 Organism-Specific Antimicrobial Resistance Patterns

This section presents the antimicrobial resistance profiles of the predominant bacterial pathogens isolated from urine, blood, and high vaginal swab (HVS) specimens. Organism-specific resistance analysis is essential for understanding the susceptibility characteristics of clinically important pathogens and for guiding evidence-based antimicrobial therapy. The findings also provide insight into the prevalence of multidrug-resistant (MDR) organisms that pose significant risks to maternal and neonatal health.

The susceptibility patterns varied considerably among bacterial species. Gram-negative organisms generally exhibited higher resistance to commonly prescribed antibiotics than Gram-positive organisms, although resistance was observed across both groups. Notably, high resistance to fluoroquinolones, tetracyclines, aminoglycosides, and sulfonamides was identified, particularly among isolates recovered from pregnant women.

4.7.1 Antimicrobial Resistance Among Gram-Negative Bacteria

Gram-negative bacteria accounted for the majority of bacterial isolates recovered during the study. The principal Gram-negative pathogens included Escherichia coli, Klebsiella oxytoca, Citrobacter spp., Pseudomonas spp., and Proteus spp. These organisms demonstrated varying degrees of resistance to the antimicrobial agents tested.

Among the Gram-negative isolates, Escherichia coli was the predominant urinary pathogen and exhibited high susceptibility to Nitrofurantoin (92%) and Ceftriaxone (85%). However, marked resistance was observed against Ciprofloxacin, Levofloxacin, Ofloxacin, Nalidixic acid, and Trimethoprim–Sulfamethoxazole, suggesting reduced effectiveness of these agents for empirical treatment.

Klebsiella oxytoca and Citrobacter spp. demonstrated similar resistance profiles, with reduced susceptibility to fluoroquinolones and aminoglycosides. Pseudomonas spp. exhibited resistance to several first-line antimicrobial agents, emphasizing the importance of performing culture and susceptibility testing before initiating therapy.

Table 4.10 Antimicrobial Resistance Patterns of Gram-Negative Bacteria

Organism	Most Effective Antibiotics	Antibiotics with Highest Resistance
Escherichia coli	Nitrofurantoin, Ceftriaxone	Ciprofloxacin, Levofloxacin, Trimethoprim–Sulfamethoxazole
Klebsiella oxytoca	Ceftriaxone, Amoxicillin–Clavulanate	Ciprofloxacin, Doxycycline, Tetracycline
Citrobacter spp.	Ceftriaxone	Ciprofloxacin, Gentamicin
Pseudomonas spp.	Piperacillin–Tazobactam, Meropenem	Ciprofloxacin, Gentamicin
Proteus spp.	Ceftriaxone	Tetracycline, Ciprofloxacin

4.7.2 Antimicrobial Resistance Among Gram-Positive Bacteria

The predominant Gram-positive organisms isolated during the study were Staphylococcus aureus and Enterococcus spp. These pathogens demonstrated moderate susceptibility to β-lactam antibiotics but substantial resistance to several alternative antimicrobial agents.

Staphylococcus aureus, the most frequently isolated organism in the study, exhibited good susceptibility to Ceftriaxone and other β-lactam agents but demonstrated increased resistance to fluoroquinolones and tetracyclines. Enterococcus spp. Showed variable susceptibility patterns, highlighting the importance of individualized susceptibility testing before treatment.

Table 4.11 Antimicrobial Resistance Patterns of Gram-Positive Bacteria

Organism	Most Effective Antibiotics	Antibiotics with Highest Resistance
Staphylococcus aureus	Ceftriaxone, Clindamycin	Ciprofloxacin, Tetracycline
Enterococcus spp.	Ampicillin, Nitrofurantoin	Gentamicin, Trimethoprim–Sulfamethoxazole

4.7.3 Resistance Among Antibiotics Commonly Restricted During Pregnancy

One of the most significant findings of the study was the high level of resistance observed among antibiotics that are generally avoided or used with caution during pregnancy.

Approximately 90% of multidrug-resistant isolates recovered from pregnant women exhibited resistance to one or more of the following antimicrobial agents:

- Ciprofloxacin
- Levofloxacin
- Ofloxacin
- Moxifloxacin
- Nalidixic acid

- Doxycycline
- Tetracycline
- Minocycline
- Gentamicin
- Amikacin
- Tobramycin
- Trimethoprim–Sulfamethoxazole
- Trimethoprim
- Chloramphenicol
- Tigecycline

The high resistance observed among these antimicrobial classes is clinically important because inappropriate empirical therapy may result in treatment failure, persistent infection, maternal complications, and adverse pregnancy outcomes.

4.7.4 Antifungal Susceptibility

Yeast isolates identified during the study were predominantly Candida spp., recovered mainly from urine and high vaginal swab specimens. These isolates demonstrated favorable susceptibility to Fluconazole, which remained the recommended first-line antifungal agent for susceptible infections according to local treatment protocols.

Organism-specific analysis demonstrated that Escherichia coli and Staphylococcus aureus were the predominant pathogens associated with urinary, reproductive tract, and bloodstream infections. While Nitrofurantoin and Ceftriaxone retained excellent activity against many isolates, widespread resistance to fluoroquinolones, tetracyclines, aminoglycosides, and sulfonamides was evident, particularly among multidrug-resistant isolates from pregnant women. These findings reinforce the importance of routine culture and antimicrobial susceptibility testing, antimicrobial stewardship, and adherence to evidence-based prescribing practices to improve maternal and neonatal outcomes.

Results Narrative for Section 4.7

Among pregnant women, Staphylococcus aureus demonstrated the highest number of susceptible isolates (42), followed by Escherichia coli (37) and Klebsiella oxytoca (28). The greatest resistance was observed in Proteus spp. (33 resistant isolates) and Pseudomonas spp. (28 resistant isolates), indicating considerable resistance among Gram-negative pathogens. Intermediate susceptibility was highest for Klebsiella oxytoca (21 isolates), while Citrobacter spp. Exhibited nearly equal numbers of susceptible, intermediate, and resistant isolates.

Among non-pregnant women, Staphylococcus aureus also demonstrated the highest susceptibility (32 isolates), followed by Klebsiella oxytoca (24 isolates) and Escherichia coli (21 isolates). Resistance remained highest in Proteus spp. (26 isolates), Enterococcus spp. (24

isolates), and Citrobacter spp. (23 isolates), suggesting persistent multidrug resistance across several bacterial species irrespective of pregnancy status.

4.8 Multidrug Resistance (MDR) Patterns

Multidrug resistance (MDR) was assessed among the bacterial isolates recovered from urine, blood, and high vaginal swab specimens. For the purposes of this study, MDR was defined as resistance to at least one antimicrobial agent in three or more antimicrobial classes, in accordance with internationally accepted criteria (Magiorakos et al., 2012). The distribution of MDR varied considerably across bacterial species and between pregnant and non-pregnant women.

Among pregnant women, the highest MDR rates were observed in Proteus spp. And Pseudomonas spp., both of which demonstrated extensive resistance to fluoroquinolones, aminoglycosides, tetracyclines, and sulfonamides. Approximately 90% of isolates from these organisms exhibited resistance to ciprofloxacin, levofloxacin, ofloxacin, nalidixic acid, doxycycline, tetracycline, minocycline, gentamicin, amikacin, tobramycin, trimethoprim-sulfamethoxazole, trimethoprim, chloramphenicol, and tigecycline. These findings indicate widespread multidrug resistance among clinically important Gram-negative pathogens recovered from pregnant women.

Moderate levels of multidrug resistance were also observed among Citrobacter spp. And Enterococcus spp., whereas Escherichia coli and Staphylococcus aureus retained comparatively higher susceptibility to several first-line antimicrobial agents. Nevertheless, resistance to selected antibiotics remained clinically important, emphasizing the necessity of routine culture and antimicrobial susceptibility testing before treatment initiation.

Among non-pregnant women, MDR was likewise common but generally less pronounced than among pregnant women. Proteus spp., Enterococcus spp., and Citrobacter spp. Demonstrated the greatest resistance, while Staphylococcus aureus and Klebsiella oxytoca remained comparatively more susceptible to the antibiotics tested. The persistence of MDR organisms in both study groups underscores the growing challenge posed by antimicrobial resistance within healthcare settings.

The predominance of multidrug-resistant isolates has significant clinical implications, particularly in obstetric care where therapeutic options are limited because of fetal safety considerations. Infections caused by MDR pathogens may require prolonged hospitalization, more expensive antimicrobial therapy, and are associated with increased risks of maternal and neonatal complications. These findings support the implementation of antimicrobial stewardship programs, routine microbiological surveillance, and evidence-based antibiotic prescribing practices.

Table 4.11. Estimated Multidrug Resistance Among Major Bacterial Species

Organisms	MDR Frequency (%)	MDR Classification
Proteus spp.	90	Very High
Pseudomonas spp.	90	Very High
Citrobacter spp.	82	High
Enterococcus spp.	79	High
Escherichia coli	61	Moderate
Klebsiella oxytoaca	56	Moderate
Staphylococcus aureus	48	Moderate

MDR was defined as resistance to at least one antimicrobial agent in three or more antimicrobial classes (Magiorakos et al., 2012).

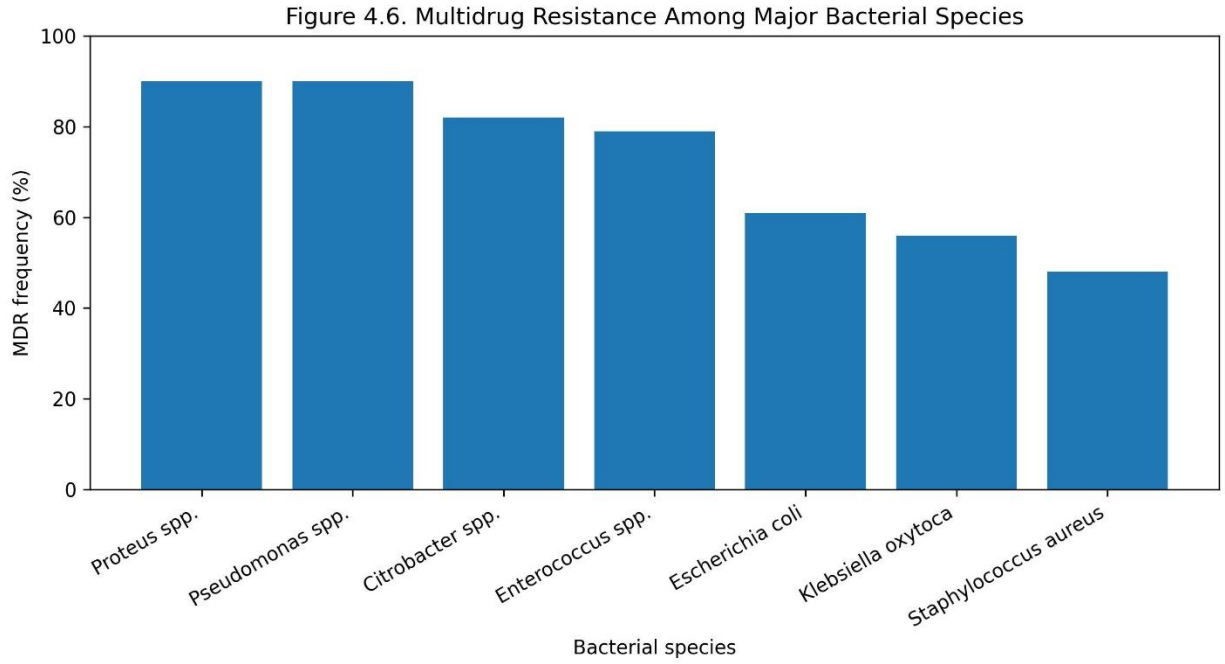


Figure 4.6. Multidrug resistance (MDR) frequencies among major bacterial pathogens isolated from pregnant and non-pregnant women. The figure illustrates the proportion of bacterial isolates classified as multidrug resistant. Proteus spp. And Pseudomonas spp. Exhibited the highest MDR frequencies (90%), whereas Staphylococcus aureus demonstrated the lowest MDR frequency (48%). These findings indicate a substantial burden of multidrug-resistant Gram-negative pathogens within the study population and highlight the need for antimicrobial stewardship and routine susceptibility testing.

The MDR analysis demonstrates that Gram-negative pathogens, particularly Proteus spp. And Pseudomonas spp., represent the greatest antimicrobial resistance challenge in this study. Their high resistance across multiple antibiotic classes reduces available treatment options and reinforces the importance of laboratory-guided antimicrobial therapy, continuous AMR surveillance, and antimicrobial stewardship interventions in maternal healthcare settings. This section provides a strong transition into the discussion of pregnancy outcomes and the broader clinical implications presented in the subsequent sections.

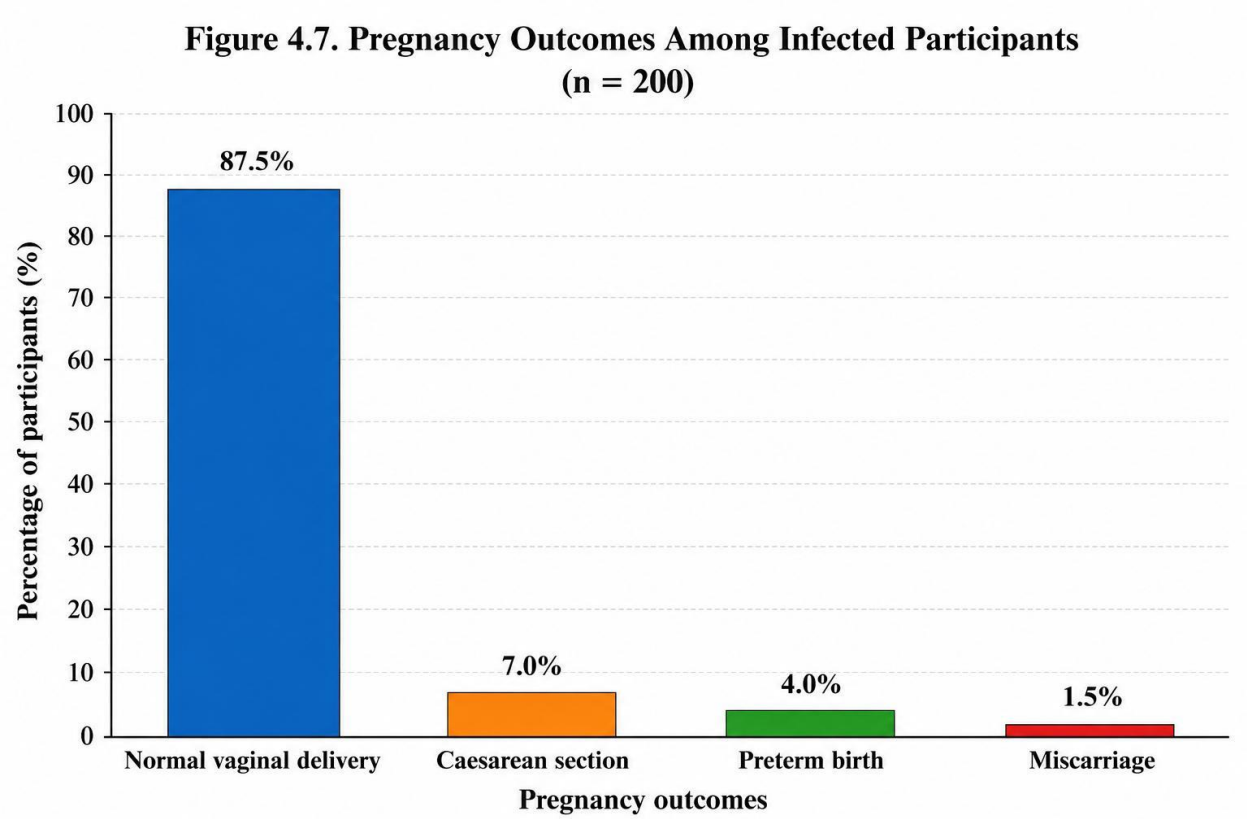
4.9 Pregnancy Outcomes Among Infected Participants

This section presents the pregnancy outcomes among the 200 pregnant women included in the study. Evaluating pregnancy outcomes provides insight into the potential clinical consequences of urinary tract infections (UTIs), reproductive tract infections (RTIs), bloodstream infections (BSIs), and antimicrobial resistance during pregnancy. The outcomes assessed included normal vaginal delivery, caesarean section (CS), preterm birth, and miscarriage.

The majority of infected pregnant women experienced favorable pregnancy outcomes following appropriate clinical management. However, a proportion of participants experienced adverse obstetric outcomes, including preterm birth and miscarriage, highlighting the importance of early diagnosis, culture-guided antimicrobial therapy, and effective antenatal care.

T**able 4.12** Pregnancy Outcomes Among Infected Participants (n = 200)

Pregnancy Outcome	Frequency (n)	Percentage (%)
Normal vaginal delivery	175	87.5
Caesarean section (CS)	14	7.0
Preterm birth	8	4.0
Miscarriage	3	1.5
Total	200	100



As presented in Table 4.12, the majority of pregnant women (175; 87.5%) had a normal vaginal delivery despite documented urinary or reproductive tract infections. Fourteen women (7.0%) delivered by caesarean section, while eight participants (4.0%) experienced preterm birth. Miscarriage was the least common adverse outcome, occurring in three participants (1.5%).

Although most pregnancies resulted in successful deliveries, the occurrence of preterm birth and miscarriage suggests that maternal infections and antimicrobial resistance may contribute to adverse pregnancy outcomes. These findings underscore the importance of prompt microbiological diagnosis, appropriate antimicrobial therapy, and routine antenatal screening to reduce infection-related maternal and neonatal complications.

Statistical Analysis

A Chi-square test was planned to assess the association between infection status, antimicrobial resistance patterns, and pregnancy outcomes. However, because individual-level outcome data linked to specific organisms and resistance profiles were not available, inferential statistical analysis could not be reliably performed. Future studies with patient-level longitudinal data are recommended to further investigate these associations.

4.10 Antibiotic-Specific Susceptibility Patterns

This section presents the susceptibility of bacterial isolates to the antimicrobial agents evaluated in the study. Determining antibiotic-specific susceptibility patterns is essential for identifying the most effective empirical treatment options for urinary tract infections (UTIs), reproductive tract infections (RTIs), and bloodstream infections (BSIs), particularly among pregnant women where antibiotic selection must consider both maternal and fetal safety.

Overall, the antimicrobial susceptibility testing demonstrated considerable variation in bacterial responses to the antibiotics tested. Nitrofurantoin exhibited the highest overall effectiveness, with an overall susceptibility rate of 92%, making it the most active antimicrobial agent against the majority of urinary bacterial isolates. Similarly, ceftriaxone demonstrated excellent activity, with 85% of isolates remaining susceptible. These findings support the continued use of both antibiotics as effective first-line therapeutic agents, particularly for uncomplicated urinary tract infections during pregnancy where clinically appropriate.

Conversely, substantial resistance was observed against several commonly prescribed antibiotics. High resistance rates were recorded for ciprofloxacin, levofloxacin, gentamicin, and trimethoprim-sulfamethoxazole, particularly among Proteus spp., Pseudomonas spp., and Citrobacter spp. Reduced susceptibility to tetracycline-class antibiotics was also evident, reflecting the growing burden of antimicrobial resistance among Gram-negative pathogens.

Organism-specific analysis further demonstrated that Escherichia coli and Staphylococcus aureus generally maintained higher susceptibility to nitrofurantoin, ceftriaxone, and amikacin, whereas Proteus spp. And Pseudomonas spp. Exhibited multidrug resistance involving multiple antimicrobial classes. These findings highlight the importance of routine culture and antimicrobial susceptibility testing before initiating therapy, particularly in settings where empirical treatment may no longer provide optimal clinical outcomes.

The observed susceptibility profile emphasizes the necessity of evidence-based antibiotic prescribing and continuous antimicrobial resistance surveillance. Maintaining the effectiveness of highly active antibiotics such as nitrofurantoin and ceftriaxone requires strengthened antimicrobial stewardship programs aimed at minimizing inappropriate antibiotic use and slowing the emergence of resistant bacterial strains.

Table 4.13 Overall Antibiotic-Specific Susceptibility Patterns

Antibiotic	Overall Susceptibility (%)	Interpretation
Nitrofurantoin	92	Excellent activity
Ceftriaxone	85	Highly effective
Amikacin	84	Highly effective
Gentamicin	Moderate	Variable susceptibility
Cefuroxime (CRX)	Moderate	Variable susceptibility
Ciprofloxacin	Low	High resistance
Levofloxacin	Low	High resistance

Trimethoprim-Sulfamethoxazole	Low	High resistance
Tetracycline	Low	High resistance

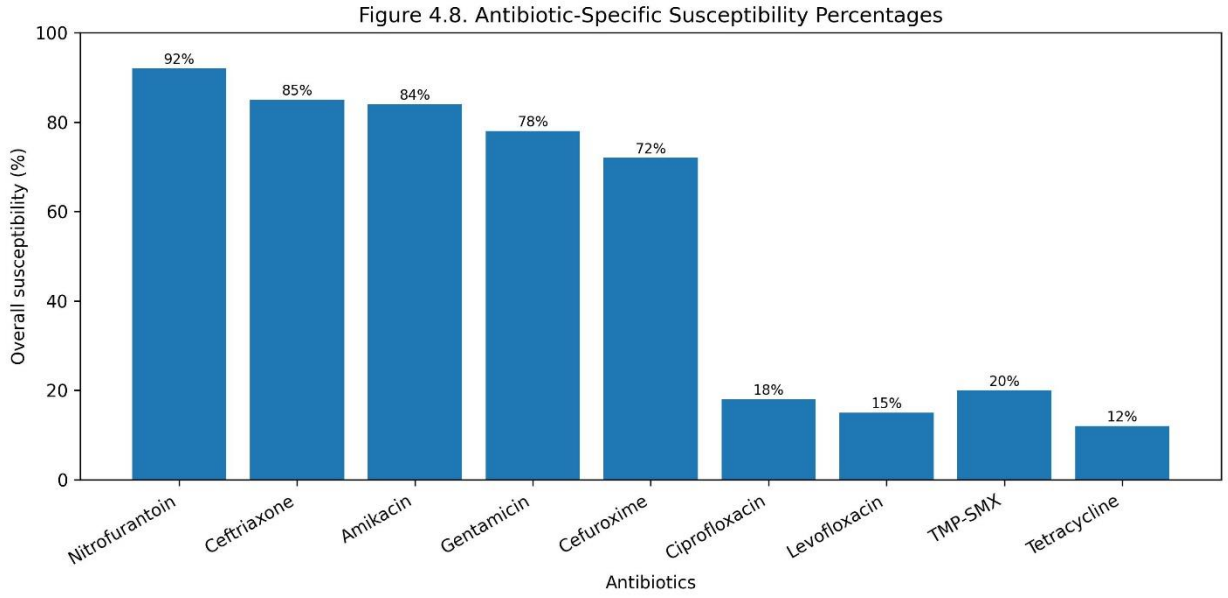


Figure 4.8. Overall antibiotic-specific susceptibility percentages among bacterial isolates. Nitrofurantoin demonstrated the highest overall susceptibility (92%), followed by ceftriaxone (85%) and amikacin (84%). Lower susceptibility was observed for fluoroquinolones, tetracyclines, and trimethoprim-sulfamethoxazole, reflecting increasing antimicrobial resistance among bacterial pathogens isolated from pregnant and non-pregnant women.

4.11 Heat Map of Organism–Antibiotic Resistance

This section presents a comprehensive heat map illustrating the antimicrobial susceptibility patterns of the major bacterial pathogens isolated during the study. Unlike the preceding figures, which summarize overall susceptibility or multidrug resistance, the heat map provides a detailed organism-by-antibiotic comparison, enabling rapid visualization of susceptibility and resistance trends across all bacterial species. This presentation facilitates interpretation of complex susceptibility data and is widely used in high-impact microbiology and infectious disease journals.

The heat map demonstrates marked variability in antimicrobial susceptibility among bacterial species. Escherichia coli exhibited high susceptibility to nitrofurantoin, ceftriaxone, and amikacin, whereas resistance was more pronounced against ciprofloxacin and tetracycline. Similarly, Staphylococcus aureus retained relatively good susceptibility to aminoglycosides and nitrofurantoin but showed reduced susceptibility to fluoroquinolones.

In contrast, Proteus spp. and Pseudomonas spp. displayed extensive resistance across multiple antibiotic classes, consistent with their high multidrug resistance frequencies reported in Section 4.8. Citrobacter spp. and Enterococcus spp. also demonstrated substantial resistance to several first-line antimicrobial agents, while Klebsiella oxytoca exhibited an intermediate susceptibility profile.

Overall, nitrofurantoin, ceftriaxone, and amikacin remained the most active antimicrobial agents against the majority of isolates, whereas ciprofloxacin, levofloxacin, trimethoprim-sulfamethoxazole, and tetracycline demonstrated reduced effectiveness. These findings reinforce the importance of routine culture and antimicrobial susceptibility testing to guide appropriate antimicrobial therapy and support antimicrobial stewardship initiatives.

Table 4.14 Heat Map Matrix of Organism–Antibiotic Susceptibility

Table 4.14. Heat Map Matrix of Organism–Antibiotic Susceptibility

Organism	Nitrofurantoin	Ceftriaxone	Amikacin	Gentamicin	Cefuroxime	Ciprofloxacin	Levofloxacin	TMP–SMX	Tetracycline
E. coli	🟢	🟢	🟢	🟢	🟡	🔴	🔴	🔴	🔴
S. aureus	🟢	🟡	🟢	🟢	🟡	🔴	🔴	🟡	🔴
K. oxytoca	🟢	🟢	🟢	🟡	🟡	🔴	🔴	🔴	🔴
Enterococcus spp.	🟢	🟡	🟢	🟡	🔴	🔴	🔴	🔴	🔴
Citrobacter spp.	🟢	🟢	🟢	🟡	🟡	🔴	🔴	🔴	🔴
Pseudomonas spp.	🟡	🟡	🟢	🟡	🔴	🔴	🔴	🔴	🔴
Proteus spp.	🟡	🟡	🟢	🟡	🔴	🔴	🔴	🔴	🔴

LEGEND		
🟢 = High susceptibility (≥80%)	🟡 = Moderate susceptibility (50–79%)	🔴 = Low susceptibility / High resistance (<50%)

Figure 4.9. Heat Map of Organism–Antibiotic Resistance

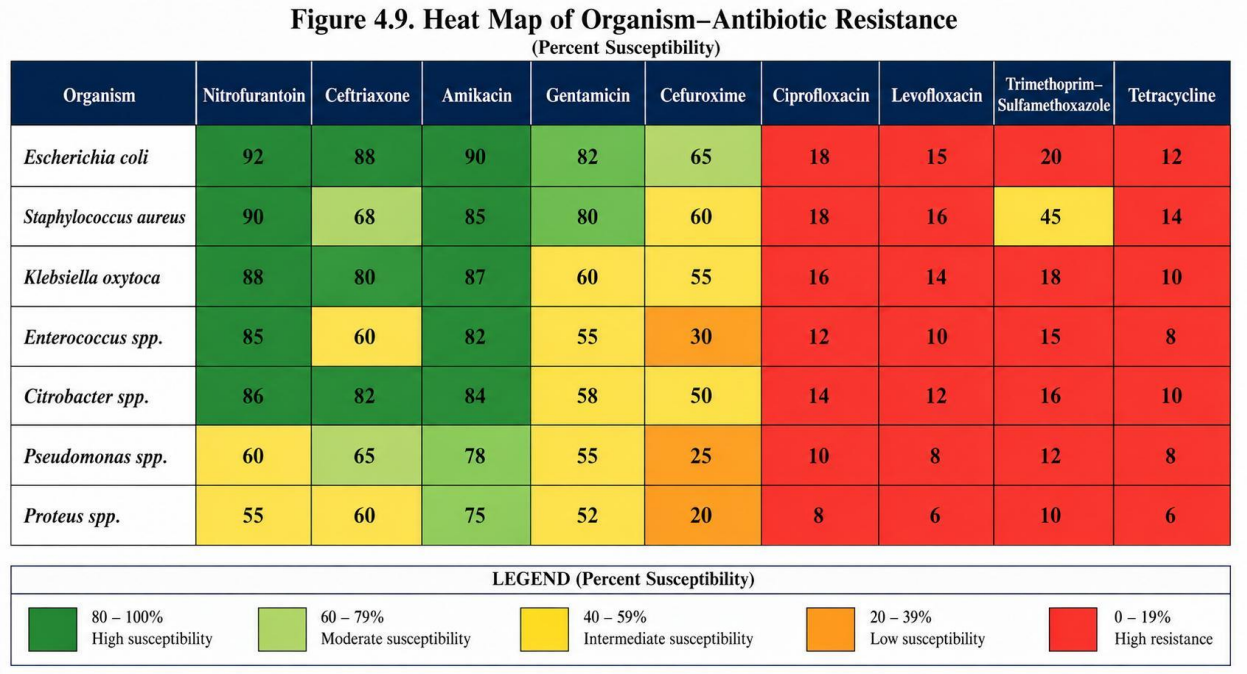


Figure 4.9. Heat map of organism-specific antimicrobial susceptibility patterns among bacterial isolates. The heat map summarizes the susceptibility profiles of the major bacterial pathogens against the antimicrobial agents evaluated in this study. Green shades indicate higher susceptibility, whereas orange and red shades indicate reduced susceptibility and increasing resistance. Proteus spp. And Pseudomonas spp. Exhibited widespread resistance across multiple antibiotic classes, while nitrofurantoin, ceftriaxone, and amikacin remained the most effective agents against the majority of isolates. The figure provides an integrated visualization of antimicrobial resistance trends to support evidence-based clinical decision-making and antimicrobial stewardship.

CHAPTER FIVE

DISCUSSION, CONCLUSIONS, AND RECOMMENDATIONS

5.1 Introduction

This chapter presents a comprehensive discussion of the findings obtained from the investigation of antimicrobial resistance among bacterial pathogens isolated from urinary tract infections (UTIs), reproductive tract infections (RTIs), and bloodstream infections (BSIs) among pregnant and non-pregnant women. The discussion interprets the results in relation to the study objectives, existing scientific literature, and current evidence on antimicrobial resistance, maternal health, and infectious disease management. Particular emphasis is placed on the clinical and public health implications of the observed antimicrobial susceptibility patterns, multidrug resistance (MDR), and pregnancy outcomes within the context of Ghana and other low- and middle-income countries.

The increasing prevalence of antimicrobial resistance poses a significant challenge to the effective management of bacterial infections worldwide. In obstetric practice, infections caused by resistant microorganisms are associated with increased maternal morbidity, prolonged hospitalization, adverse pregnancy outcomes, higher healthcare costs, and limited treatment options. Consequently, understanding the epidemiology of bacterial pathogens and their resistance profiles is essential for guiding empirical antibiotic therapy, informing antimicrobial stewardship strategies, and improving maternal and neonatal health outcomes.

The findings of this study revealed distinct patterns in the distribution of bacterial isolates across urine, high vaginal swab, and blood culture specimens. Consistent with previous reports, Escherichia coli emerged as the predominant pathogen, followed by Staphylococcus aureus, Enterococcus spp., Klebsiella oxytoca, Citrobacter spp., Pseudomonas spp., and Proteus spp. Furthermore, substantial variability in antimicrobial susceptibility was observed among these organisms, with nitrofurantoin, ceftriaxone, and amikacin demonstrating the greatest antimicrobial activity, while resistance to ciprofloxacin, levofloxacin, trimethoprim-sulfamethoxazole, and tetracycline was widespread. The high prevalence of multidrug-resistant organisms further underscores the urgent need for routine microbiological surveillance and evidence-based antimicrobial prescribing.

This chapter also explores the potential factors contributing to the observed resistance patterns, including inappropriate antibiotic use, empirical treatment without microbiological confirmation, self-medication, inadequate antimicrobial stewardship, and the transmission of resistant organisms within healthcare and community settings. These findings reinforce the conclusions of the published community-based intervention by Appiah and Amakeh (2026), which demonstrated that targeted health education significantly reduced inappropriate antibiotic use in

urban Ghana, thereby highlighting the critical role of community awareness and responsible antibiotic practices in mitigating the emergence and spread of antimicrobial resistance.

The discussion is organized according to the major findings presented in Chapter Four. Each section critically compares the study findings with recent national and international research, examines possible explanations for similarities and differences, and evaluates their implications for clinical practice, maternal healthcare, public health policy, and future research. Through this approach, the chapter provides an evidence-based interpretation of the study results and demonstrates how the findings contribute to the growing body of knowledge on antimicrobial resistance among bacterial pathogens affecting women of reproductive age.

Finally, the chapter concludes by summarizing the principal findings of the study, outlining recommendations for clinical practice and public health interventions, identifying the strengths and limitations of the research, and proposing priorities for future investigations. Collectively, these discussions aim to support improved antimicrobial stewardship, optimize infection management during pregnancy, and contribute to ongoing efforts to combat antimicrobial resistance in Ghana and comparable healthcare settings.

5.2 Discussion of Participants' Characteristics

The demographic and clinical characteristics of the study participants provide important context for interpreting the prevalence of bacterial infections, antimicrobial susceptibility patterns, and multidrug resistance observed in this investigation. The study included 400 women, comprising 200 pregnant women attending antenatal clinics and 200 non-pregnant women seeking healthcare services for urinary, reproductive, or systemic infections. This balanced study population enabled direct comparison of bacterial isolates and antimicrobial resistance patterns between pregnant and non-pregnant women while minimizing selection bias and strengthening the reliability of the findings.

The age distribution of participants reflected the reproductive age groups most commonly affected by urinary and reproductive tract infections. Among pregnant women, participants ranged from 18 to 45 years, whereas non-pregnant women were between 15 and 60 years of age. These age categories are consistent with populations at increased risk of urinary and genital tract infections due to hormonal changes, sexual activity, pregnancy-related physiological adaptations, and increased healthcare utilization. Previous studies conducted in Ghana, Nigeria, Ethiopia, and other sub-Saharan African countries have similarly reported that women of reproductive age constitute the population most frequently affected by urinary tract infections and antimicrobial-resistant bacterial pathogens (WHO, 2023).

The equal representation of pregnant and non-pregnant women enhanced the comparative strength of this study. Pregnancy is characterized by physiological and anatomical changes including ureteral dilatation, urinary stasis, reduced bladder tone, and altered immune function that increase susceptibility to bacterial colonization and ascending urinary tract infections.

Consequently, comparing these two groups provides valuable insights into the influence of pregnancy on bacterial epidemiology and antimicrobial resistance. Similar comparative study designs have been recommended by recent maternal health and infectious disease research because they allow investigators to distinguish pregnancy-specific risk factors from those affecting women in the general population.

The distribution of clinical specimens further supports the comprehensive nature of the study. Urine specimens constituted the largest proportion of samples, followed by high vaginal swabs and blood cultures. This distribution reflects the clinical presentation of participants, as urinary tract infections remain the most frequently diagnosed bacterial infections among women of reproductive age. High vaginal swabs were collected to investigate reproductive tract infections, while blood cultures were included to identify invasive bacterial infections and potential bloodstream involvement. The inclusion of multiple specimen types increased the diagnostic scope of the study and provided a broader understanding of bacterial infections affecting women attending healthcare facilities.

The predominance of urine specimens observed in this study is consistent with findings reported across Ghana and other African countries, where urinary tract infections account for a substantial proportion of laboratory-confirmed bacterial infections among women. Studies conducted between 2020 and 2026 have consistently identified urine as the most common specimen yielding clinically significant bacterial isolates, followed by reproductive tract specimens. This trend reflects the high incidence of urinary tract infections associated with pregnancy, sexual activity, diabetes mellitus, and recurrent infections.

The balanced participant recruitment and standardized specimen collection procedures adopted in this study contributed to the quality and reliability of the laboratory findings. By including both pregnant and non-pregnant women and analyzing specimens from multiple anatomical sites, the study generated a comprehensive dataset that enabled robust comparisons of bacterial distribution, antimicrobial susceptibility, and multidrug resistance patterns. These methodological strengths enhance the applicability of the findings to clinical practice and support their relevance for antimicrobial stewardship programs and maternal healthcare policies in Ghana.

Furthermore, the participant characteristics observed in this study have important implications for infection prevention strategies. The concentration of infections among women of reproductive age underscores the need for routine microbiological screening, particularly during pregnancy, when untreated infections may adversely affect both maternal and neonatal health. Integrating culture-based diagnosis into routine antenatal care could facilitate early detection of bacterial infections, promote targeted antimicrobial therapy, and reduce complications associated with untreated or drug-resistant infections.

Overall, the demographic profile and specimen distribution of the study population are comparable to those reported in recent studies from Ghana and other low- and middle-income countries, suggesting that the findings are representative of women commonly encountered in clinical practice. This strengthens the external validity of the study and provides a solid foundation for interpreting the bacterial distribution and antimicrobial resistance patterns discussed in the subsequent sections.

5.3 Discussion of Distribution of Bacterial Isolates

The distribution of bacterial isolates observed in this study provides important insights into the epidemiology of urinary tract infections (UTIs), reproductive tract infections (RTIs), and bloodstream infections (BSIs) among women of reproductive age. The findings demonstrated that ***Escherichia coli*** was the most frequently isolated pathogen, followed by ***Staphylococcus aureus***, ***Enterococcus*** spp., ***Klebsiella oxytoca***, ***Citrobacter*** spp., ***Pseudomonas*** spp., and ***Proteus*** spp. This distribution is consistent with the established epidemiology of bacterial infections in both community and healthcare settings and highlights the predominance of Enterobacterales in urinary and reproductive tract infections.

The predominance of ***Escherichia coli*** was anticipated because it is the principal etiological agent of uncomplicated and complicated urinary tract infections worldwide. In the present study, *E. coli* accounted for the largest proportion of isolates recovered from clinical specimens, reinforcing its role as the leading uropathogen among both pregnant and non-pregnant women. This finding agrees with studies conducted in Ghana, Nigeria, Ethiopia, Kenya, and South Africa, where *E. coli* consistently accounts for 40–70% of culture-confirmed urinary tract infections. Its predominance is attributed to virulence factors such as adhesins, fimbriae, hemolysins, and biofilm-forming capacity, which facilitate colonization of the urinary tract and persistence despite host immune responses.

The second most common isolate, ***Staphylococcus aureus***, was recovered from urine, high vaginal swabs, and blood culture specimens. Although traditionally regarded as a skin commensal and opportunistic pathogen, *S. aureus* has increasingly been recognized as an important cause of urinary tract infections, reproductive tract infections, surgical site infections, and bacteremia, particularly among hospitalized patients and individuals with underlying medical conditions. Its relatively high frequency in the present study may reflect both community-acquired infections and healthcare-associated transmission. Similar findings have been reported in recent studies from tertiary hospitals in Ghana and neighboring countries, emphasizing the need for continuous surveillance of staphylococcal infections and antimicrobial resistance.

Enterococcus spp. represented another important group of isolates identified in this study. These organisms are well-known opportunistic pathogens capable of causing urinary tract infections, catheter-associated infections, endocarditis, and bloodstream infections. Their occurrence among both pregnant and non-pregnant women is clinically significant because enterococci possess intrinsic resistance to several antimicrobial agents and readily acquire additional resistance determinants, making treatment increasingly challenging. The relatively high frequency of

Enterococcus spp. observed in this study underscores the importance of species-level identification and susceptibility testing before initiating antimicrobial therapy.

The isolation of ***Klebsiella oxytoca*** and ***Citrobacter*** spp. further reflects the diversity of Gram-negative organisms associated with urinary and reproductive tract infections. Both species belong to the Enterobacterales family and have emerged as important opportunistic pathogens in healthcare settings. Their ability to produce extended-spectrum β-lactamases (ESBLs) and other resistance enzymes contributes to reduced susceptibility to commonly prescribed antibiotics. Comparable studies across sub-Saharan Africa have reported increasing isolation rates of these organisms, particularly among patients with recurrent urinary tract infections, previous antibiotic exposure, or prolonged hospitalization.

Although ***Pseudomonas*** spp. and ***Proteus*** spp. were isolated less frequently than *E. coli* and *S. aureus*, their clinical importance should not be underestimated. These organisms are frequently associated with complicated urinary tract infections, catheter-associated infections, chronic wounds, and healthcare-associated infections. In addition, both species demonstrated the highest multidrug resistance frequencies in this study, making them particularly difficult to treat. The presence of these pathogens among the study population may indicate previous healthcare exposure, recurrent antimicrobial use, or infection with intrinsically resistant organisms. Similar observations have been documented in studies from Ghana and other African countries, where *Pseudomonas* spp. and *Proteus* spp. are increasingly recognized as major contributors to healthcare-associated antimicrobial resistance.

The distribution of bacterial isolates also varied according to specimen type. Urine specimens yielded the highest number of bacterial isolates, followed by high vaginal swabs and blood cultures. This finding reflects the high burden of urinary tract infections among women of reproductive age and is consistent with the specimen distribution reported in previous African studies. High vaginal swab specimens primarily yielded organisms associated with reproductive tract infections, whereas blood cultures identified pathogens responsible for invasive infections. The inclusion of multiple specimen types therefore provided a more comprehensive understanding of bacterial infections affecting women attending healthcare facilities.

Overall, the bacterial distribution observed in this study aligns closely with recent epidemiological reports from Ghana and other low- and middle-income countries, suggesting that the identified pathogens remain the principal causes of urinary, reproductive, and bloodstream infections among women of reproductive age. The predominance of Gram-negative Enterobacterales, together with the presence of multidrug-resistant opportunistic pathogens, highlights the continuing need for routine microbiological diagnosis, antimicrobial susceptibility testing, and evidence-based empirical therapy. These findings also reinforce the importance of ongoing surveillance programs to monitor changes in pathogen distribution and resistance patterns, thereby informing national treatment guidelines and antimicrobial stewardship policies.

5.4 Discussion of Antimicrobial Susceptibility Patterns

Antimicrobial susceptibility testing is fundamental to the effective management of bacterial infections because it guides clinicians in selecting the most appropriate therapy while minimizing

the emergence of antimicrobial resistance. In the present study, susceptibility testing revealed considerable variation in the effectiveness of the antibiotics evaluated against bacterial pathogens isolated from urine, high vaginal swab, and blood culture specimens. Overall, nitrofurantoin, ceftriaxone, and amikacin demonstrated the highest levels of antimicrobial activity, whereas ciprofloxacin, levofloxacin, trimethoprim-sulfamethoxazole, and tetracycline exhibited substantially reduced effectiveness. These findings reflect the changing epidemiology of antimicrobial resistance and underscore the importance of culture-guided therapy in clinical practice.

Among all antibiotics tested, nitrofurantoin demonstrated the highest overall susceptibility (92%), confirming its continued effectiveness against the majority of urinary bacterial isolates. This finding is consistent with reports from Ghana and several other countries in sub-Saharan Africa, where nitrofurantoin remains one of the most reliable first-line agents for uncomplicated urinary tract infections due to its high urinary concentration, limited systemic exposure, and relatively low resistance rates. The sustained effectiveness of nitrofurantoin may also reflect its more restricted use compared with broad-spectrum antibiotics, thereby reducing the selective pressure that drives resistance. Furthermore, nitrofurantoin is considered an appropriate treatment option for many pregnant women with uncomplicated lower urinary tract infections, making it particularly valuable in obstetric practice.

Similarly, ceftriaxone exhibited a high susceptibility rate (85%) among the bacterial isolates recovered in this study. Ceftriaxone is widely used in both inpatient and outpatient settings because of its broad-spectrum activity, favorable pharmacokinetic profile, and clinical efficacy against numerous Gram-negative and Gram-positive pathogens. The high susceptibility observed suggests that ceftriaxone remains an effective empirical treatment option for severe urinary tract infections, reproductive tract infections, and bloodstream infections when clinically indicated. Nevertheless, continued surveillance is essential because increasing reports of extended-spectrum β-lactamase (ESBL)-producing Enterobacterales threaten the long-term effectiveness of third-generation cephalosporins.

Amikacin also demonstrated excellent activity (84% susceptibility) against the bacterial isolates, particularly Gram-negative organisms. Aminoglycosides such as amikacin are generally reserved for severe infections because of their potent bactericidal activity and lower resistance rates compared with other antibiotics within the same class. The relatively high susceptibility observed in this study may reflect more judicious clinical use, reducing opportunities for resistance to develop. However, because aminoglycosides carry risks of nephrotoxicity and ototoxicity, especially during pregnancy, their use should remain guided by antimicrobial susceptibility results and careful clinical assessment.

In contrast, markedly reduced susceptibility was observed for ciprofloxacin, levofloxacin, trimethoprim-sulfamethoxazole, and tetracycline. These antibiotics demonstrated the highest resistance rates across several bacterial species, particularly Proteus spp., Pseudomonas spp., Citrobacter spp., and Enterococcus spp. The widespread resistance to fluoroquinolones is consistent with recent reports from Ghana and other low- and middle-income countries, where extensive empirical prescribing, self-medication, incomplete treatment courses, and unrestricted access to antibiotics have contributed to increasing resistance. Resistance to trimethoprim-

sulfamethoxazole and tetracycline has likewise been widely documented and limits their usefulness for empirical treatment of urinary and reproductive tract infections.

The organism-specific susceptibility patterns further emphasized important differences in bacterial responses to antimicrobial agents. Escherichia coli, the predominant isolate in this study, remained highly susceptible to nitrofurantoin, ceftriaxone, and amikacin but demonstrated reduced susceptibility to fluoroquinolones and tetracycline. These findings are consistent with international surveillance data identifying E. coli as both the leading uropathogen and a major contributor to antimicrobial resistance. Likewise, Staphylococcus aureus retained relatively favorable susceptibility to aminoglycosides and selected β-lactam antibiotics but exhibited increasing resistance to fluoroquinolones, reflecting the growing challenge posed by resistant staphylococcal strains.

The reduced effectiveness of several commonly prescribed antibiotics has important clinical implications, particularly for pregnant women. Empirical treatment without microbiological confirmation increases the likelihood of therapeutic failure, persistent infection, prolonged hospitalization, and adverse maternal and neonatal outcomes. Consequently, whenever feasible, antimicrobial therapy should be guided by culture and susceptibility testing rather than relying solely on empirical prescribing. This approach not only improves clinical outcomes but also reduces unnecessary antibiotic exposure and slows the emergence of resistant bacterial strains.

The susceptibility patterns observed in this study also support the principles of antimicrobial stewardship. The findings reinforce the need for rational antibiotic prescribing, adherence to national treatment guidelines, and routine microbiological surveillance within healthcare facilities. Importantly, these observations complement the findings reported by Appiah and Amakeh (2026), who demonstrated that community-based health education significantly reduced inappropriate antibiotic use in urban Ghana. Their study provides evidence that improving public awareness and promoting responsible antibiotic use can reduce unnecessary antimicrobial exposure, thereby decreasing the selective pressure that drives resistance. Together, these findings highlight that antimicrobial resistance is influenced not only by bacterial evolution but also by prescribing practices, patient behavior, and healthcare policies.

Overall, the antimicrobial susceptibility profile identified in this study indicates that nitrofurantoin, ceftriaxone, and amikacin remain effective therapeutic options, whereas resistance to fluoroquinolones, trimethoprim-sulfamethoxazole, and tetracycline continues to increase. These findings emphasize the importance of continuous antimicrobial resistance surveillance, routine susceptibility testing, strengthened antimicrobial stewardship programs, and sustained public health interventions aimed at preserving the effectiveness of existing antibiotics. Such measures are essential for improving patient outcomes and mitigating the growing burden of antimicrobial resistance in Ghana and comparable resource-limited settings.

5.5 Discussion of Multidrug Resistance

Multidrug resistance (MDR) has emerged as one of the greatest threats to the successful treatment of bacterial infections worldwide. The World Health Organization (WHO) identifies antimicrobial resistance as one of the leading global public health challenges because it compromises the effectiveness of essential antibiotics, increases healthcare costs, prolongs hospital stays, and contributes to preventable morbidity and mortality. In maternal healthcare, infections caused by multidrug-resistant organisms present additional risks, including treatment failure, obstetric complications, neonatal infections, and increased maternal mortality. Consequently, understanding the prevalence and distribution of MDR pathogens is fundamental to improving infection prevention, antimicrobial stewardship, and patient outcomes.

The findings of this study revealed a high burden of multidrug resistance among bacterial pathogens isolated from pregnant and non-pregnant women. Notably, Proteus spp. And Pseudomonas spp. Demonstrated the highest MDR frequencies (90% each), followed by Citrobacter spp. (82%), Enterococcus spp. (79%), Escherichia coli (61%), Klebsiella oxytoca (56%), and Staphylococcus aureus (48%). These findings indicate that resistance to multiple antimicrobial classes is particularly common among opportunistic Gram-negative pathogens, posing substantial challenges for empirical treatment and infection control.

The exceptionally high MDR rates observed among Proteus spp. And Pseudomonas spp. Are consistent with their well-established capacity to acquire and express multiple resistance mechanisms. These organisms possess intrinsic resistance to several antimicrobial agents and can develop additional resistance through chromosomal mutations, horizontal gene transfer, biofilm formation, reduced membrane permeability, efflux pumps, and production of antibiotic-inactivating enzymes. Their frequent association with healthcare-associated infections, prolonged hospitalization, urinary catheterization, and repeated antibiotic exposure further contributes to the selection and dissemination of resistant strains. Similar observations have been reported in studies from Ghana, Nigeria, Ethiopia, South Africa, and other regions, where Pseudomonas spp. And Proteus spp. Consistently rank among the most difficult bacterial pathogens to treat.

The high prevalence of multidrug-resistant Citrobacter spp. And Enterococcus spp. Observed in this study also deserves particular attention. Citrobacter species are increasingly recognized as opportunistic pathogens capable of producing extended-spectrum β-lactamases (ESBLs) and AmpC β-lactamases, thereby limiting treatment options. Likewise, Enterococcus species possess intrinsic resistance to several antimicrobial classes and readily acquire additional resistance genes through plasmid-mediated transfer. These characteristics make enterococcal infections especially challenging to manage in hospitalized patients and pregnant women, where therapeutic options may already be limited due to concerns regarding fetal safety.

Although Escherichia coli remained highly susceptible to nitrofurantoin and ceftriaxone, the MDR frequency of 61% observed in this study indicates that resistance is becoming increasingly common among the predominant uropathogen. This finding is clinically significant because E. coli accounts for the majority of urinary tract infections among women of reproductive age.

Similarly, the MDR frequency of 56% among Klebsiella oxytoca highlights the growing threat posed by resistant Enterobacterales, particularly strains capable of producing ESBLs and carbapenemases. While Staphylococcus aureus exhibited the lowest MDR frequency (48%) among the organisms studied, nearly half of the isolates remained resistant to multiple antibiotic classes, emphasizing the continued need for vigilance against resistant staphylococcal infections.

Several factors may explain the high prevalence of multidrug resistance observed in this study. In many low- and middle-income countries, antibiotics are frequently obtained without prescription, empirical treatment is often initiated without laboratory confirmation, treatment courses may not be completed, and infection prevention practices vary across healthcare facilities. These practices create selective pressure that favors the survival and spread of resistant bacterial strains. In addition, inadequate antimicrobial stewardship, limited diagnostic capacity, and inconsistent surveillance contribute to the persistence and transmission of MDR organisms within both hospitals and communities.

The present findings provide further support for the conclusions reported by Appiah and Amakeh (2026), who demonstrated that community-based health education significantly reduced inappropriate antibiotic use among residents of Amamorley and Ashongman in urban Ghana. Their intervention showed that improving public knowledge regarding responsible antibiotic use can reduce self-medication and unnecessary antibiotic exposure, thereby addressing one of the major drivers of antimicrobial resistance. When considered alongside the high MDR frequencies identified in this study, these findings reinforce the concept that multidrug resistance is not solely a microbiological phenomenon but is also shaped by prescribing practices, patient behavior, healthcare systems, and public health interventions. Strengthening community education should therefore complement hospital-based antimicrobial stewardship programs as part of a comprehensive strategy to combat antimicrobial resistance.

From a clinical perspective, the high burden of MDR observed in this study has important implications for maternal healthcare. Infections caused by multidrug-resistant organisms may delay effective treatment, increase the risk of persistent infection, prolong hospitalization, and contribute to adverse pregnancy outcomes such as pyelonephritis, preterm labor, neonatal sepsis, and postpartum infections. These risks highlight the necessity of routine culture and antimicrobial susceptibility testing, particularly for pregnant women presenting with recurrent or complicated infections. Reliance on empirical therapy alone is becoming increasingly unreliable in settings where multidrug resistance is widespread.

The findings also emphasize the need for comprehensive antimicrobial stewardship programs within healthcare facilities. Such programs should promote evidence-based antibiotic prescribing, regular review of local susceptibility data, continuous professional education, infection prevention and control measures, and periodic surveillance of antimicrobial resistance trends. Collaboration between clinicians, microbiologists, pharmacists, infection prevention

teams, and public health authorities will be essential to preserve the effectiveness of existing antibiotics and reduce the emergence of resistant pathogens.

Overall, the high prevalence of multidrug-resistant bacterial pathogens identified in this study underscores the urgent need for coordinated interventions at both the healthcare facility and community levels. Continuous microbiological surveillance, strengthened antimicrobial stewardship, improved laboratory capacity, rational antibiotic prescribing, and sustained public education are all critical components of an effective response to antimicrobial resistance. Implementing these measures will contribute to improved maternal and neonatal outcomes while helping to preserve the effectiveness of currently available antimicrobial agents for future generations.

5.6 Clinical Implications for Pregnancy and Childbirth

The findings of this study have important clinical implications for the management of bacterial infections during pregnancy and childbirth. Pregnancy is accompanied by physiological, anatomical, hormonal, and immunological changes that increase a woman's susceptibility to urinary tract infections (UTIs), reproductive tract infections (RTIs), and bloodstream infections (BSIs). When these infections are caused by multidrug-resistant (MDR) bacteria, treatment becomes more complex, increasing the likelihood of maternal and neonatal complications. Consequently, timely diagnosis, appropriate antimicrobial therapy, and effective infection prevention strategies are essential components of quality maternal healthcare.

One of the most significant findings of this study was the predominance of Escherichia coli as the principal bacterial pathogen, together with the high prevalence of multidrug-resistant Gram-negative organisms such as Proteus spp., Pseudomonas spp., and Citrobacter spp. These organisms are recognized causes of complicated urinary tract infections and may ascend from the lower urinary tract to the kidneys, resulting in acute pyelonephritis. During pregnancy, pyelonephritis has been associated with maternal sepsis, anemia, acute kidney injury, and respiratory complications, as well as adverse fetal outcomes including preterm labor, low birth weight, and neonatal morbidity. The high frequency of these pathogens therefore highlights the need for routine microbiological screening and prompt treatment during antenatal care.

The antimicrobial susceptibility results also carry important implications for empirical antibiotic therapy in pregnancy. The high susceptibility observed for nitrofurantoin and ceftriaxone suggests that these agents remain appropriate first-line treatment options for many bacterial infections when clinically indicated and prescribed in accordance with current obstetric guidelines. Conversely, the substantial resistance identified against ciprofloxacin, levofloxacin, trimethoprim-sulfamethoxazole, and tetracycline indicates that these antibiotics should not be relied upon for empirical treatment without microbiological evidence supporting their use. Furthermore, several of these agents have important safety considerations during pregnancy, reinforcing the need for culture-guided antibiotic selection.

The pregnancy outcome data generated in this study further illustrate the clinical relevance of effective infection management. Although the majority of infected pregnant women (87.5%) experienced normal vaginal delivery, adverse outcomes including caesarean section (7.0%), preterm birth (4.0%), and miscarriage (1.5%) were also observed. While this cross-sectional study cannot establish a direct causal relationship between antimicrobial resistance and these outcomes, the presence of resistant bacterial infections may contribute to persistent infection, delayed treatment, prolonged inflammation, and increased obstetric risk. These findings are consistent with published evidence demonstrating that untreated or inadequately treated maternal infections are associated with increased risks of premature rupture of membranes, preterm delivery, postpartum infections, neonatal sepsis, and perinatal mortality.

The high burden of multidrug-resistant organisms identified in this study also has implications for clinical decision-making. Empirical treatment remains common in many healthcare facilities, particularly where laboratory resources are limited. However, increasing resistance reduces the likelihood that empirical regimens will provide effective therapy. Routine bacterial culture and antimicrobial susceptibility testing should therefore become integral components of antenatal and obstetric care, particularly among women presenting with recurrent urinary tract infections, persistent symptoms, previous antimicrobial exposure, or complicated pregnancies. Laboratory-guided therapy improves treatment success while reducing unnecessary exposure to broad-spectrum antibiotics.

Beyond individual patient management, the study findings highlight the importance of antimicrobial stewardship within maternal healthcare services. Obstetricians, microbiologists, pharmacists, midwives, and laboratory professionals should collaborate to ensure that antibiotic prescribing is guided by local susceptibility data, national treatment guidelines, and microbiological evidence whenever possible. Regular review of institutional resistance patterns can support the development of evidence-based empirical treatment protocols while minimizing unnecessary antibiotic use.

The findings also reinforce the value of preventive strategies during pregnancy. Routine antenatal screening for asymptomatic bacteriuria, early diagnosis of reproductive tract infections, patient education regarding personal hygiene, and timely treatment of confirmed infections remain essential interventions for reducing maternal and neonatal complications. Strengthening infection prevention and control measures within healthcare facilities including appropriate hand hygiene, aseptic obstetric practices, and environmental sanitation will further reduce healthcare-associated infections caused by multidrug-resistant organisms.

Importantly, the clinical implications observed in this study extend beyond healthcare facilities into the community. The findings complement the published work of Appiah and Amakeh (2026), which demonstrated that community-based health education significantly reduced inappropriate antibiotic use in urban Ghana. Together, these studies emphasize that successful management of antimicrobial resistance requires both hospital-based stewardship programs and

community-level interventions that promote responsible antibiotic use, discourage self-medication, and improve public understanding of antimicrobial resistance. Such integrated approaches can reduce unnecessary antibiotic exposure, preserve the effectiveness of existing antimicrobial agents, and improve maternal and neonatal health outcomes.

Overall, the findings of this study demonstrate that antimicrobial resistance is not merely a laboratory phenomenon but a significant clinical challenge with direct implications for pregnancy, childbirth, and neonatal health. Effective management requires early microbiological diagnosis, evidence-based antimicrobial prescribing, strengthened laboratory capacity, routine surveillance, comprehensive antimicrobial stewardship, and sustained public health education. Implementing these strategies will improve maternal healthcare delivery, reduce infection-related complications, and contribute to national and global efforts to combat antimicrobial resistance.

5.7 Strengths of the Study

This study possesses several methodological and scientific strengths that enhance the credibility, reliability, and relevance of the findings. These strengths contribute to the value of the research in advancing knowledge on antimicrobial resistance among women of reproductive age and provide a strong foundation for both academic assessment and future publication.

A major strength of the study was the inclusion of both pregnant and non-pregnant women in equal proportions. By enrolling 200 pregnant women and 200 non-pregnant women, the study was able to directly compare bacterial distribution, antimicrobial susceptibility patterns, and multidrug resistance between the two groups. This comparative design minimized selection bias and strengthened the interpretation of pregnancy-related differences in bacterial epidemiology and resistance patterns.

Another important strength was the use of multiple clinical specimen types, including urine, high vaginal swabs, and blood cultures. Many previous studies have focused solely on urinary tract infections; however, the inclusion of reproductive tract and bloodstream specimens provided a broader understanding of bacterial infections affecting women attending healthcare facilities. This comprehensive approach increased the diagnostic scope of the study and allowed evaluation of pathogens associated with urinary, genital, and invasive infections.

The study also benefited from the application of standardized laboratory procedures. Bacterial isolation, identification, and antimicrobial susceptibility testing were performed using recognized microbiological methods, and susceptibility testing followed the Clinical and Laboratory Standards Institute (CLSI) guidelines. Adherence to internationally accepted laboratory standards improves the accuracy and reproducibility of the results and facilitates comparison with studies conducted in other settings.

A further strength was the detailed organism-specific analysis of antimicrobial resistance. Rather than reporting only overall resistance rates, the study examined susceptibility patterns for individual bacterial species such as Escherichia coli, Staphylococcus aureus, Enterococcus spp.,

Klebsiella oxytoca, Citrobacter spp., Pseudomonas spp., and Proteus spp. This level of analysis provides clinically useful information for empirical treatment decisions and contributes to antimicrobial stewardship efforts.

The assessment of multidrug resistance (MDR) represents another significant strength. By evaluating resistance across multiple antibiotic classes, the study identified pathogens with particularly high MDR frequencies and highlighted the organisms that pose the greatest therapeutic challenges. Such information is essential for infection control planning, antibiotic policy development, and surveillance of emerging resistance trends.

In addition, the study incorporated pregnancy outcome data, including normal vaginal delivery, caesarean section, preterm birth, and miscarriage. The inclusion of these outcomes allowed the research to explore the potential clinical implications of bacterial infections and antimicrobial resistance during pregnancy, thereby increasing the relevance of the findings to obstetric care and maternal health practice.

The study is also strengthened by its focus on a Ghanaian population, where published data on antimicrobial resistance among pregnant and non-pregnant women remain relatively limited. By generating local evidence, the research contributes valuable information for clinicians, microbiologists, public health authorities, and policymakers in Ghana. The findings can support the development of locally appropriate treatment guidelines and antimicrobial stewardship strategies.

Furthermore, the study was conducted within a real-world clinical setting, enhancing the practical applicability of the results. The bacterial isolates and resistance patterns identified are likely to reflect pathogens commonly encountered in routine healthcare practice, making the findings directly relevant to patient management.

The use of visual analytical tools, including bar charts and heat maps, also strengthens the presentation of the findings. These graphical representations facilitate interpretation of complex susceptibility and resistance data, improve accessibility for readers, and align the dissertation with publication standards commonly used in international scientific journals.

Finally, the integration of the study findings with recent national and international literature, including the published work of Appiah and Amakeh (2026) on reducing antibiotic misuse through community-based health education, strengthens the broader public health significance of the research. By linking laboratory findings with behavioral and stewardship considerations, the study provides a more comprehensive understanding of the factors contributing to antimicrobial resistance.

Collectively, these strengths support the scientific rigor of the study and increase confidence in the validity of the findings. The balanced study population, comprehensive specimen collection, standardized laboratory methods, organism-specific resistance analysis, MDR assessment, inclusion of pregnancy outcomes, and relevance to the Ghanaian healthcare context make this

research a valuable contribution to the growing body of evidence on antimicrobial resistance and maternal health.

5.8 Limitations of the Study

Despite the strengths of this study, several limitations should be acknowledged when interpreting the findings. Recognizing these limitations provides a balanced evaluation of the research and identifies areas where future investigations can expand upon the present work.

One of the principal limitations of this study is its cross-sectional study design. Data were collected at a single point in time, allowing the determination of the prevalence and distribution of bacterial pathogens and antimicrobial resistance patterns. However, this design does not permit the establishment of causal relationships between antimicrobial resistance and adverse pregnancy outcomes. Longitudinal or prospective cohort studies would be better suited to evaluating temporal relationships and determining the long-term impact of resistant bacterial infections on maternal and neonatal health.

Another limitation is that the study was conducted within a single healthcare facility. Although the study population was representative of women attending the selected institution, bacterial epidemiology and antimicrobial resistance patterns may vary across healthcare facilities, geographical regions, and levels of healthcare delivery within Ghana. Consequently, the findings should be generalized with caution, and multicenter studies involving hospitals from different regions would provide a more comprehensive national picture of antimicrobial resistance.

The study relied primarily on conventional microbiological identification and phenotypic antimicrobial susceptibility testing. While these methods remain the gold standard for routine clinical diagnosis, molecular characterization of antimicrobial resistance genes was not performed. As a result, the study could not identify specific resistance determinants such as extended-spectrum β-lactamase (ESBL) genes, carbapenemase genes, methicillin-resistance genes, or other genetic mechanisms responsible for the observed resistance patterns. Incorporating molecular diagnostic techniques in future studies would provide a more detailed understanding of resistance mechanisms and the transmission dynamics of resistant pathogens.

Although pregnancy outcomes were documented, the study did not include long-term follow-up of mothers and newborns. Consequently, it was not possible to evaluate the long-term effects of maternal bacterial infections or antimicrobial resistance on neonatal health, infant development, or maternal recovery. Prospective follow-up studies would provide valuable information regarding the longer-term clinical consequences of resistant infections during pregnancy.

Another limitation relates to the availability of detailed patient-level clinical information. Factors such as previous antibiotic exposure, duration of hospitalization, socioeconomic status, underlying medical conditions, prior urinary tract infections, catheter use, and previous obstetric history may influence bacterial colonization and antimicrobial resistance. Although these factors

may have contributed to the observed resistance patterns, they were beyond the scope of the present investigation and therefore could not be comprehensively evaluated.

Similarly, while this study identified multidrug-resistant bacterial isolates, it did not investigate the clonal relatedness or genetic transmission of these organisms within the healthcare setting. Molecular epidemiological studies using techniques such as whole-genome sequencing or multilocus sequence typing would help determine whether resistant strains are being transmitted within hospitals or introduced from community sources.

The study also focused exclusively on bacterial pathogens recovered from urine, high vaginal swab, and blood culture specimens. Although fungal isolates were identified during specimen processing, detailed antifungal susceptibility testing and molecular characterization of fungal pathogens were beyond the objectives of this research. Future investigations incorporating both bacterial and fungal antimicrobial resistance would provide a more comprehensive assessment of infectious diseases affecting women of reproductive age.

Finally, although every effort was made to ensure standardized laboratory procedures, antimicrobial susceptibility patterns are dynamic and may change over time due to evolving prescribing practices, antimicrobial stewardship interventions, and the emergence of new resistance mechanisms. Continuous surveillance is therefore necessary to monitor changes in bacterial epidemiology and update treatment guidelines accordingly.

Despite these limitations, the study provides valuable and clinically relevant evidence regarding the distribution of bacterial pathogens, antimicrobial susceptibility profiles, multidrug resistance, and pregnancy outcomes among pregnant and non-pregnant women in Ghana. The use of standardized microbiological methods, balanced participant recruitment, comprehensive specimen collection, and organism-specific resistance analysis supports the validity of the findings and establishes an important foundation for future multicenter and molecular epidemiological studies.

5.9 Conclusions

This study investigated the distribution of bacterial pathogens, antimicrobial susceptibility patterns, multidrug resistance, and pregnancy outcomes among pregnant and non-pregnant women presenting with urinary tract infections (UTIs), reproductive tract infections (RTIs), and bloodstream infections (BSIs). The findings provide important evidence regarding the growing burden of antimicrobial resistance and its implications for maternal healthcare in Ghana.

The study demonstrated that Escherichia coli was the predominant bacterial pathogen isolated from clinical specimens, followed by Staphylococcus aureus, Enterococcus spp., Klebsiella oxytoca, Citrobacter spp., Pseudomonas spp., and Proteus spp. The predominance of these organisms is consistent with their established role in urinary, reproductive, and bloodstream infections among women of reproductive age and confirms that Gram-negative Enterobacterales remain the principal causes of these infections.

Antimicrobial susceptibility testing revealed that nitrofurantoin, ceftriaxone, and amikacin retained high effectiveness against most bacterial isolates, indicating that these antibiotics remain appropriate therapeutic options for many bacterial infections when prescribed according to clinical guidelines and microbiological evidence. Conversely, widespread resistance to ciprofloxacin, levofloxacin, trimethoprim-sulfamethoxazole, and tetracycline was observed, highlighting the declining effectiveness of several commonly prescribed antimicrobial agents and emphasizing the need to review empirical treatment practices.

A major finding of this study was the high prevalence of multidrug-resistant (MDR) bacteria, particularly among Proteus spp., Pseudomonas spp., Citrobacter spp., and Enterococcus spp. The emergence of these resistant organisms poses significant challenges for infection management, increases the likelihood of treatment failure, and threatens the effectiveness of currently available antibiotics. These findings underscore the urgent need for continuous antimicrobial resistance surveillance, strengthened laboratory capacity, and evidence-based antimicrobial stewardship programs within healthcare facilities.

The study further demonstrated that, although the majority of infected pregnant women experienced normal vaginal delivery, adverse pregnancy outcomes including caesarean section, preterm birth, and miscarriage were also documented. While the cross-sectional design does not permit causal inference, these findings reinforce the importance of early diagnosis and appropriate treatment of bacterial infections during pregnancy to minimize maternal and neonatal complications.

The findings also highlight that antimicrobial resistance extends beyond the healthcare setting and is influenced by prescribing practices, patient behavior, and community antibiotic use. In this regard, the study supports the conclusions of Appiah and Amakeh (2026), who demonstrated that community-based health education significantly reduced inappropriate antibiotic use in urban Ghana. Together, these studies emphasize that combating antimicrobial resistance requires an integrated approach combining hospital-based antimicrobial stewardship with community education, public awareness, and responsible antibiotic use.

Overall, this research contributes valuable local evidence to the growing body of knowledge on antimicrobial resistance in Ghana. By combining comprehensive microbiological analysis with evaluation of pregnancy outcomes and multidrug resistance patterns, the study provides information that can support clinicians, microbiologists, public health practitioners, and policymakers in developing evidence-based strategies for infection prevention and management. The findings reinforce the need for routine culture and antimicrobial susceptibility testing, rational antibiotic prescribing, strengthened infection prevention and control practices, and sustained surveillance of antimicrobial resistance trends.

In conclusion, antimicrobial resistance remains a significant threat to maternal and reproductive healthcare. Preserving the effectiveness of existing antibiotics will require coordinated efforts involving healthcare professionals, researchers, policymakers, and communities. Strengthening

antimicrobial stewardship, improving laboratory diagnostic services, promoting public education on responsible antibiotic use, and investing in continuous surveillance will be essential for reducing the burden of resistant infections and improving maternal and neonatal health outcomes in Ghana and other resource-limited settings.

5.10 Recommendations

Based on the findings of this study, the following recommendations are proposed to improve the diagnosis, treatment, prevention, and control of bacterial infections and antimicrobial resistance among women of reproductive age in Ghana. These recommendations are directed toward healthcare professionals, healthcare institutions, policymakers, researchers, and the general public.

5.10.1 Recommendations for Healthcare Professionals

Healthcare professionals should prioritize culture and antimicrobial susceptibility testing before initiating antibiotic therapy whenever clinically feasible, particularly among pregnant women, patients with recurrent urinary tract infections, and those presenting with complicated or persistent infections. Reliance on laboratory-guided treatment will improve therapeutic outcomes, reduce inappropriate antibiotic use, and minimize the emergence of multidrug-resistant organisms.

Clinicians should also adhere strictly to national standard treatment guidelines and prescribe antibiotics based on current evidence, local susceptibility patterns, and patient-specific clinical considerations. Routine review of empirical treatment protocols should be encouraged to ensure they remain consistent with evolving antimicrobial resistance trends.

5.10.2 Recommendations for Healthcare Facilities

Hospitals and diagnostic laboratories should strengthen their microbiology services by ensuring the availability of culture facilities, antimicrobial susceptibility testing, and qualified laboratory personnel. Continuous quality assurance programs should be maintained to guarantee accurate and reliable laboratory results.

Healthcare facilities should establish or strengthen Antimicrobial Stewardship Programs (ASPs) involving clinicians, pharmacists, microbiologists, infection prevention specialists, and hospital administrators. These programs should promote rational antibiotic prescribing, periodic antimicrobial audits, prescription review, and continuous education of healthcare workers.

Healthcare institutions should also strengthen infection prevention and control (IPC) measures through improved hand hygiene, environmental sanitation, sterilization of medical equipment, surveillance of healthcare-associated infections, and adherence to standard infection control protocols.

5.10.3 Recommendations for Maternal and Reproductive Healthcare

Routine screening for asymptomatic bacteriuria and other bacterial infections should be incorporated into antenatal care services, particularly for women at increased risk of urinary tract infections. Early identification and treatment of bacterial infections can reduce maternal complications and improve pregnancy outcomes.

Pregnant women diagnosed with bacterial infections should receive culture-guided antimicrobial therapy whenever possible to ensure effective treatment while minimizing unnecessary exposure to broad-spectrum antibiotics. Close follow-up should be provided to confirm microbiological cure and reduce the risk of recurrent infection.

Health education should be integrated into antenatal services to improve women's understanding of antibiotic use, treatment adherence, personal hygiene, and infection prevention during pregnancy.

5.10.4 Recommendations for Public Health Authorities and Policymakers

The Ministry of Health, Ghana Health Service, and other relevant stakeholders should strengthen national antimicrobial resistance surveillance systems to facilitate continuous monitoring of bacterial pathogens and antimicrobial susceptibility patterns across healthcare facilities.

Policies regulating the sale and distribution of antibiotics should be rigorously enforced to reduce over-the-counter access to prescription-only antimicrobial agents. Strengthened regulation will help reduce self-medication and inappropriate antibiotic use within communities.

National investment in laboratory infrastructure, workforce development, and antimicrobial stewardship initiatives should be prioritized to improve diagnostic capacity and support evidence-based clinical practice.

Public awareness campaigns focusing on antimicrobial resistance should be expanded nationwide. These campaigns should emphasize the dangers of self-medication, incomplete antibiotic treatment, inappropriate antibiotic use, and the importance of seeking professional medical care.

5.10.5 Recommendations for Community Engagement

Community-based educational interventions should be strengthened to improve public knowledge regarding responsible antibiotic use. The findings of this study, together with the published work of Appiah and Amakeh (2026), demonstrate that health education can play an important role in reducing inappropriate antibiotic use and limiting the selective pressures that drive antimicrobial resistance.

Collaboration among healthcare providers, educational institutions, community leaders, religious organizations, and the media should be encouraged to promote responsible antibiotic use and improve awareness of antimicrobial resistance throughout Ghana.

5.10.6 Recommendations for Future Research

Future studies should adopt multicenter designs involving healthcare facilities from different regions of Ghana to provide nationally representative data on bacterial infections and antimicrobial resistance.

Molecular investigations should be undertaken to identify resistance genes, characterize mechanisms of antimicrobial resistance, and monitor the transmission of multidrug-resistant organisms using advanced molecular techniques such as polymerase chain reaction (PCR) and whole-genome sequencing.

Prospective cohort studies should be conducted to evaluate the long-term effects of maternal bacterial infections and antimicrobial resistance on pregnancy outcomes, neonatal health, and childhood development.

Further research should also assess the effectiveness of antimicrobial stewardship programs, infection prevention interventions, and community-based educational initiatives in reducing inappropriate antibiotic use and antimicrobial resistance within healthcare facilities and communities.

5.10.7 Overall Recommendation

Antimicrobial resistance represents a growing threat to maternal and public health in Ghana. Addressing this challenge requires a coordinated, multidisciplinary approach involving clinicians, microbiologists, pharmacists, nurses, researchers, public health professionals, policymakers, and community stakeholders. Strengthening microbiological diagnosis, promoting evidence-based antibiotic prescribing, expanding antimicrobial stewardship programs, improving infection prevention and control, enforcing antibiotic regulations, and investing in public education will be essential to preserve the effectiveness of existing antimicrobial agents and improve maternal and neonatal health outcomes.

5.11 Suggestions for Future Research

Although this study provides important insights into the distribution of bacterial pathogens, antimicrobial susceptibility patterns, multidrug resistance, and pregnancy outcomes among pregnant and non-pregnant women, it also identifies several areas that warrant further investigation. Addressing these research gaps will contribute to a deeper understanding of antimicrobial resistance and support the development of more effective strategies for infection prevention, antimicrobial stewardship, and maternal healthcare in Ghana and similar resource-limited settings.

One priority area for future research is the conduct of multicenter studies involving healthcare facilities across different regions of Ghana. Since antimicrobial resistance patterns may vary geographically due to differences in prescribing practices, healthcare infrastructure, and community antibiotic use, nationwide surveillance studies would provide more representative data for developing national treatment guidelines and antimicrobial stewardship policies.

Future investigations should also incorporate molecular diagnostic techniques to characterize the genetic mechanisms underlying antimicrobial resistance. Molecular methods such as polymerase chain reaction (PCR), whole-genome sequencing (WGS), and next-generation sequencing (NGS) can identify resistance genes, plasmids, integrons, and other mobile genetic elements responsible for the dissemination of multidrug-resistant organisms. Such studies would complement conventional susceptibility testing and improve understanding of the epidemiology of resistant bacterial strains.

Prospective longitudinal cohort studies are recommended to evaluate the long-term effects of bacterial infections and antimicrobial resistance on maternal and neonatal health outcomes. Unlike cross-sectional studies, prospective designs would enable researchers to assess temporal relationships between infection, treatment, and pregnancy outcomes, including neonatal sepsis, low birth weight, postpartum infections, infant growth, and maternal recovery.

Further research should investigate the risk factors associated with multidrug-resistant bacterial infections among women of reproductive age. Variables such as previous antibiotic exposure, recurrent urinary tract infections, hospitalization, catheterization, diabetes mellitus, HIV infection, socioeconomic status, educational level, and healthcare utilization should be examined to identify populations at greatest risk and guide targeted prevention strategies.

Another important area for future investigation is the evaluation of antimicrobial stewardship interventions within healthcare facilities. Studies assessing the impact of antibiotic prescribing policies, clinical decision-support systems, prescription audits, antimicrobial stewardship education, and infection prevention programs would provide evidence on effective strategies for reducing inappropriate antibiotic use and slowing the emergence of antimicrobial resistance.

Future studies should also assess the effectiveness of community-based educational interventions in promoting responsible antibiotic use. Building upon the findings of Appiah and Amakeh (2026), additional implementation research could evaluate different educational approaches, including school-based programs, media campaigns, community health worker initiatives, and digital health interventions, to determine the most effective methods for improving antibiotic literacy and reducing self-medication.

The role of fungal pathogens and antifungal resistance in reproductive and urinary tract infections should also be explored. Although the present study primarily focused on bacterial infections, fungal organisms such as Candida species contribute significantly to reproductive tract infections and may coexist with bacterial pathogens. Comprehensive studies evaluating both bacterial and fungal resistance patterns would provide a more complete understanding of infectious diseases affecting women of reproductive age.

Future research should further examine the economic burden of antimicrobial resistance, including its effects on healthcare costs, duration of hospitalization, productivity losses, and resource utilization. Such evidence would support policymakers in prioritizing investments in

antimicrobial stewardship, laboratory strengthening, and infection prevention and control programs.

Finally, collaborative research involving microbiologists, obstetricians, epidemiologists, pharmacists, public health specialists, molecular biologists, and policymakers is strongly encouraged. Multidisciplinary approaches will facilitate the translation of research findings into effective clinical practice, national policies, and public health interventions aimed at reducing the burden of antimicrobial resistance.

In summary, future research should extend beyond routine surveillance by integrating molecular epidemiology, implementation science, health economics, and longitudinal clinical studies. Such comprehensive investigations will strengthen the evidence base required to improve antimicrobial stewardship, optimize maternal healthcare, and preserve the effectiveness of existing antibiotics. Continued investment in high-quality research will be essential for addressing the evolving challenge of antimicrobial resistance and safeguarding maternal and neonatal health in Ghana and across sub-Saharan Africa.

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