MICROBIAL PROFILE AND ANTIMICROBIAL SENSITIVITY PATTERNS IN PATIENTS HOSPITALISED IN THE SIX REGIONAL/PROVINCIAL HOSPITALS IN THE FREE STATE AND NORTHERN CAPE

FROM 2018 TO 2022

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DECLARATION OF ORIGINAL WORK

I, Thabiso Khulile Mkhatshwa (Student number: ________) hereby declare that all the work submitted in this project report titled "Microbial profile and antimicrobial sensitivity patterns in patients hospitalised in the six regional/provincial hospitals in the Free State and Northern Cape from 2018 to 2022" is my original and independent academic effort that was carried out under the able supervision of scientists: Prof P.M. Makhoahle and Dr B. Malope-Kgokong and it is hereby submitted to the CUT for the fulfilment of the degree: Master of Health Sciences – Biomedical Technology. I confirm that I know the meaning of plagiarism, and this work has never been presented or submitted to another institution for any other degree or part of a qualification, by me or by any other person.

30 September 2025

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Signature

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Date

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This treatise is dedicated to my family members for the love and support that they have given me throughout this journey. I would like to express my appreciation to my supervisors as this study would have not been possible without their support. Lastly, I would like to appreciate the Central University of Technology for their support in funding my research and the National Health Laboratory Service for allowing me to use their data as part of my research.

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AARMS – Academic Affairs and Research Management System

AIDS – Acquired immunodeficiency syndrome

AMR – Antimicrobial resistance

ART – Antiretroviral therapy

ARV – Antiretroviral

ASBL-E – Extended Spectrum Beta-Lactamase producing *Enterobacteriaceae*

BSI – Bloodstream infection

BAL – Bronchoalveolar lavage

C. difficile – *Clostridium difficile*

cART – Combination of antiretroviral therapy

CDW – Central Data Warehouse

CLD – Chronic Lung Disease

CLSI – Clinical and Laboratory Standard Institute

COPD – Chronic obstructive pulmonary disease

CRAB – Carbapenem-resistant *Acinetobacter baumannii*

CRE – Carbapenem Resistant *Enterobacteriaceae*

CUT – Central University of Technology

DM – Diabetes mellitus

E. faecalis – *Enterobacter faecalis*

E. faecium – *Enterobacter faecium*

E. cloacae – *Enterobacter cloacae*

E. coli – *Escherichia coli*

GNB – Gram negative bacteria

HAART – Highly active antiretroviral therapy

HAT – Hospital-acquired infection

H. infuenzae – *Haemophilus influenza*

HIV – Human immunodeficiency virus

hMPV – Human metapneumovirus

ICU – Intensive Care Unit

K. pneumoniae – *Klebsiella pneumoniae*
LRTI – Lower respiratory tract infection
MCS – Microscopy Culture Sensitivity
MDR – Multidrug resistant
MRDE – Multidrug-resistant *Enterobacteriaceae*
MRSA – Methicillin-resistant *Staphylococcus aureus*
MTB – *Mycobacterium tuberculosis*
NHLS – National Health Laboratory Service
NP – Nasopharyngeal
P. aeruginosa – *Pseudomonas aeruginosa*
PI – Principal investigator
PLWH – People living with HIV
PDR – Pandrug resistant
RBC – Red blood cell
REDCap – Research Electronic Data Capture
RIF – Rifampicin
SAB – *Staphylococcus aureus* bacteraemia
SABI – *Staphylococcus* bloodstream infection
S. aureus – *Staphylococcus aureus*
S. pneumoniae – *Staphylococcus pneumoniae*
S. pyogenes – *Streptococcus pyogenes*
S. viridans – *Streptococcus viridans*
TB – Tuberculosis
UTI – Urinary Tract Infection
WBC – White blood cell
WHO – World Health Organisation
XDR – Extensively drug resistant
ZN – Ziehl-Neelsen

ABSTRACT

Background: Bacterial infections are the major cause of morbidity and mortality in an immune-compromised subset of patients. Over 1.4 million people worldwide suffer from nosocomial infections that are associated with microorganisms. Hospital-acquired infections are an increasing problem across Sub-Saharan Africa, while bacterial contamination of indoor hospitals, particularly in Intensive-Care Units is a serious global health hazard with high morbidity and mortality rates. Many patient factors influence the acquisition of microbial infections in patients. This includes age, immune status, pre-existing disease and diagnostic or therapeutic interventions. Patients with chronic diseases such as HIV or TB are vulnerable to infections, especially to opportunistic organisms. Only the bacteria that are sensitive to antibiotics are suppressed or killed, while the resistant strains survive and become endemic and spread easily within the hospital environment.

Objectives

1. Determine microbial profile prevalence in immunocompromised patients who were hospitalized in the different hospitals having TB or are HIV positive.
2. Determine the risk factors that are associated with microbial infections in immunocompromised patients.
3. Compare the microbial prevalence rate in HIV-positive patients compared to HIV-negative patients.
4. Determine the antibiotic susceptibility pattern of the identified microorganisms.
5. Assess the impact of microbial infections on the mortality rate of immunocompromised patients from other studies globally.

Methods: This was a retrospective, cross-sectional study. The data included in the study was from 1 January 2018 to 31 December 2022. All patients who were admitted at the selected sites having underlying diseases such as TB and HIV from 1 January 2018 to 31 December 2022 were selected.

Results: The study consisted of 48 597 participants and most of the participants in the study were from the Frances Baard District Municipality in Kimberley in the Northern Cape Province (58.4%), followed by the Mangaung Metropolitan Municipality in the Free State Province (37.9%). The majority of the patients in the study (58.4%) were treated at the Robert Mangaliso Sobukwe Provincial Hospital (Northern Cape Province), followed by 20.9% patients treated at the Universitas Academic hospital (Free State Province). The highest age group percentage in the study was 27.1%, which fell between 28 and 37 years, followed by 26.4% between the ages of 38 and 47 years, with the lowest population (0.8%) was found between 78 and 87 years. The study showed that fewer patients were admitted to hospital from the age of 58 years and above and most participants in the study were recorded to be female 49.9%). There was a slight difference among male (49.4%). The study also recorded that 0.7% of the patients' gender was unknown.

The study showed that 89.4% of patients tested negatively for TB across all six hospitals. 6.8% patients tested positively for TB, while 1.6% and 1.8% patients' TB results were unknown or not tested, respectively. The National District Hospital recorded the highest number of patients who tested positively for TB at a rate of n=169 (9.7%), followed by Bongani Regional Hospital at a rate of n=119 (8.3%). Robert Mangaliso Sobukwe Provincial Hospital had n=2 226 (7.8%) TB-positive cases, Mofumahafi Manapo Mopeli Regional Hospital recorded n=23 (7.1%) TB-positive cases, Pelonomi Regional Hospital had n=409 (6.3%) positive cases and Universitas Academic hospital recorded n=362 (3.6%) TB-positive cases, which is the lowest. The majority of the participants in the patients in the study were not tested for HIV using the HIV-1/2 rapid screen test and of those who were tested, only 1.2% were reported to be HIV positive and 4.2% were negative. 70.9% of the patients did not have HIV-1/2 AB/AG screen results, while 24.4% tested negative and 4.3% tested positive. The data show that only 0.6% of the patients had equivocal HIV results.

The study showed that 7.9% (n=3 862/48 597) patients' HIV viral load were undetectable, which means that the patients were compliant with Antiretroviral Therapy (ART) treatment. The undetectable HIV viral load was <20-50 copies/mL, 6.9% patients had a low HIV viral load of 50-10 000 copies/mL and a population of n=3 299 (6.8%) was found to have a high HIV viral load >100 000 copies/mL. The study showed that 74.9% patients were not tested for HIV viral load. 68.9% of patients in this study did not have CD4 ARV results, so their immune systems were not monitored. 23.4% of the patients displayed a low immune system (<350 cells/mm$^{3)}$, which means that they were not complying with ART treatment. 3.6% of the patients had mild immunosuppression (350–499 cells/mm$^{3)}$ and 4.2% of the patients had a strong immune system, which means that they are complying with to ART treatment.

The study also evaluated the prevalence testing method for all the specimens submitted to the laboratory for microbes and antimicrobial testing. Automated culture was the method mostly used in the laboratory and it was reported to be at the rate of 42.8%, followed by culture urine (25.4%), culture pus (23.3%). Culture catheter tip was the least frequently used test method, displaying a rate of 8.5%. 48 597 specimens were reported to have been tested in the laboratory. In the study, the type of specimen collected from patients and sent to the laboratory for testing was also analysed. 48 597 specimens were collected. Blood culture (38.4%) was the most frequently collected specimen as the patients might have been suspected of having a bloodstream infection and urine was the second-most frequently collected specimen (16.5%), as the patients might have been suspected for having UTI. The study observed a prevalence of microorganisms in hospitals that are located in urban facilities, compared to facilities located in rural areas and the top 10 prevalent microorganisms from the sample isolates were *Escherichia Coli* (16.9%), *staphylococcus aureus* (14.5%), Coagulase Negative *staphylococcus* (11.9%), *Klebsiella Pneumoniae* subsp Pneumonia (9.4%), *Staphylococcus Epidermidis* (5.2%), *Streptococcus Pneumoniae* (4%), *Proteus Mirabilis* (4%), *Acinetobacter Baumannii* (3.7%), *Pseudomonas Aeruginosa* (3.2%), *Enterobacter Cloacae* subsp. Cloacae (2.9%). The study showed that Trimethoprim-sulfamethoxazole antibiotic showed high resistance to both gram-negative and gram-positive bacteria, 68.3% and 42.2%, respectively. Gentamicin showed high antibiotic resistance in gram-positive bacteria *Enterococcus faecalis* at 31.8% and *Enterococcus Faecium* at 69.8%). The study showed that *Streptococcus Pneumoniae* had high sensitivity (50.7%) to Ceftriaxone antibiotic.

The study proved that the ward type where patients were admitted to plays a huge risk factor in antibiotic treatment. Most patients who were admitted to Medical wards showed a very high prevalence of antimicrobial resistance. Resistance was observed in all the antibiotics. The same trend was observed in both ICUs, in the A6 Intensive Care Unit and Multidisciplinary unit. Nitrofurantoin antibiotic displayed high sensitivity

in most wards. A systematic review of previous studies found that opportunistic microorganisms cause a high mortality rate in immunocompromised patients.

Conclusion: Majority of patients had a high HIV viral load and low CD4 count, which show non-compliance with ART. The majority of male patients had a detectable viral load and a low CD4 count, which is a risk factor for acquiring microbial infections. There was a high prevalence of antimicrobial resistance from different wards in the study and Trimethoprim-sulfamethoxazole antibiotic showed high resistance to both gram-negative and gram-positive bacteria, 68.3% and 42.2%, respectively.

CHAPTER 1: INTRODUCTION

Over the years bacterial infections, reinfections, drug resistance and multidrug resistance have deteriorated health systems and caused morbidity and mortality globally. Bacterial infections are the major cause of morbidity and mortality in an immune-compromised subset of patients (Singh et al., 2014). Over 1.4 million people worldwide suffer from nosocomial infections that are associated with microorganisms (Xia et al., 2016). Patients' long stay in hospital exposes them to these microbes through different pathways, which can be contaminated hospital equipment, bedding articles or aerosols (Xia et al., 2016). In addition, cross-contamination between patients can be spread through contact with hospital staff members. The research has shown that most common diseases are associated with respiratory tract infections that mostly occur in patients receiving mechanical ventilation, followed by a high rate of bloodstream infection, urinary tract infection and wound infection (Blot, 2008). Microorganisms are responsible for most human infections of varying severity. Among them, bacteria account for the majority of cases, while fungi, viruses and parasites also contribute significantly, depending on the clinical context (Katarzyna Góralska & Błaszkowska, 2015; Nazeerah et al., 2022). Microorganisms such as *Staphylococcus aureus, Enterobacteriaceae* species (*Escherichia, Salmonella, Citrobacter, Shigella), Acinetobacter baumannii, Klebsiella pneumoniae, Enterococci* and *Pseudomonas* spp are the most common pathogens associated with infections in hospitalized patients. Only the bacteria that are sensitive to antibiotics are suppressed or killed, while the resistant strains survive and become endemic and spread easily within the hospital environment (Xia et al., 2016). The present available antibiotics are becoming less effective on microbes and it is important to develop new strategies to manage them (Cerini et al., 2023). Bacterial species that produce antibiotics have antibiotic-resistant genes that are chromosomally encoded and are responsible for different physiological functions such as self-protection, metabolism, biosynthesis and signalling (Chadha, 2014). The rapid increase by microorganisms posed health challenges globally and South Africa's challenges of healthcare to be specific are associated with nosocomial infections caused by multidrug-resistant organisms. These include Methicillin-resistant *Staphylococcus aureus* (MRSA), Carbapenem-resistant *Acinetobacter baumannii (*CRAB) and Carbapenem-resistant *Enterobacterales* (CRE), which show resistance to most available antibiotics and lead to a high mortality rate. It has previously been reported that some hospitals (2% to 49%) in developing countries lack general infection prevention measures, prevention of cross-transmission and a policy of restricted antimicrobial use (Blot, 2008; Mbim, Mboto & Agbo, 2016). The rate of microbial infections differs from region to another, along with time variations (Nimer, 2022). An important factor in achieving a high index of appropriate antimicrobial therapy is rapid reporting of microbial results, species identification and sensitivity testing. In this way an observed regimen that is not appropriate for the causative pathogen can be corrected within the clinically important time frame of 48 hours (Blot, 2008). The pressure on clinical diagnostic laboratories to produce rapid identification and antibiotic susceptibility profiles has resulted in increasing use of automated microbiology systems (Moodley et al., 2013). Patients identified should be given adequate doses of antimicrobial agents and the source of infection such as contaminated devices or intra-abominated collections or leakages should be eliminated. Healthcare setting and patient population also has a huge impact on the prevalence of infections caused by micro-organisms (Szabó et al., 2022). The prevalence of microbial infections has been observed to be increasing in hospitals caring for a large number of patients. An increasing antibiotic resistance has also been observed (Szabó et al., 2022). Longer hospital stay, high morbidity rate and mortality are some of the consequences that are associated with microbial infections in hospitalised patients. These consequences affect the cost of patient healthcare services and reduce the reliability of available resources in developing countries (Nimer, 2022). There are many patient risk factors that influence the acquisition of nosocomial infections, such as age, immune status, pre-existing disease and diagnostic or therapeutic interventions (Nair et al., 2018). Patients with chronic diseases such as cancer, diabetes mellitus, renal failure TB or HIV are vulnerable to infections, especially to opportunistic organisms (Nair et al., 2018). Modern diagnostic and therapeutic procedures such as biopsies, endoscopic examinations, catheterisation, ventilation and surgical procedures have also been reported to increase the risk of contracting nosocomial infections (Nair et al., 2018). Other contributing risk factors are crowded conditions within the hospital, frequent transfers of admitted hospital patients from one unit to another, and a concentration of patients highly susceptible to infection. These include neonates, burn patients and patients in intensive-care units in one area (Nair et al., 2018).

1.1 PROBLEM STATEMENT

South Africa is one of the developing countries with many people suffering from TB (87%) and HIV (7.9 million) (Matakanye et al*.,* 2021; Inbarani et al., 2022). Micro-organisms such as bacteria, fungi, viruses and parasites have been reported as opportunistic infections among immunocompromised people, which resulted in a huge challenge to patient care, with an increase in morbidities, mortalities and cost of healthcare (Nazeerah et al., 2022). Early diagnosis and treatments of microorganisms in immunocompromised patients are important to reducing morbidity and mortality rate. Little information is known about the prevalence of microorganisms that attack hospitalized patients and their antibiotic susceptibility in the different regional/provincial hospitals of the Free State and Northern Cape Province. There is not much information on the risk factors that are associated with microbial infections in immunocompromised patients.

1.2 AIM

The study aimed to do microbial profiling and antimicrobial sensitivity patterns in patients hospitalized in the six regional/provincial hospitals in the Free State and Northern Cape from 2018 to 2022.

The following sites were included in the study.

- Bongani Regional Hospital (Welkom),
- Mofumahadi Manapo Mopeli Regional Hospital (Qwaqwa),
- National District Hospital (Bloemfontein),
- Pelonomi Regional Hospital (Bloemfontein),
- Universitas Academic Hospital (Bloemfontein)
- Robert Mangaliso Sobukwe Provincial Hospital (Kimberley).

CHAPTER 2: LITERATURE REVIEW

Hospital-acquired infections are an increasing problem across Sub-Saharan Africa, while bacterial contamination of indoor hospitals, particularly in Intensive-Care Units is a serious global health hazard with high morbidity and mortality rates (Archary et al., 2017; Temesgen et al., 2023). There is a wide range of microorganisms that can cause severe harm to the body and become lethal (Sarmah et al., 2018). Even though research and development in the treatment and prevention procedures have advanced, infectious diseases remain the topmost cause of death in the world, especially in developing countries (Sarmah et al., 2018). Critically ill patients in Intensive-Care Units (ICUs) have a five to seven higher risk of nosocomial infection, with ICU infections reported to contribute to 20% to 25% of all hospital nosocomial infections (Javeri et al., 2012). Many patient factors influence the acquisition of microbial infections in patients. This includes age, immune status, pre-existing disease and diagnostic or therapeutic interventions (Nair et al., 2018). Patients with chronic diseases such as HIV or TB are vulnerable to infections, especially to opportunistic organisms (Nair et al., 2018). Microbial contamination can occur because of healthcare professionals and patients' hands, or direct shedding of microorganisms that can live for long periods on dry surfaces (Temesgen et al., 2023). Multidrug-resistant bacteria can cross-contaminate medical devices and inanimate surfaces. Modern diagnostic and therapeutic procedures such as biopsies, endoscopic examinations, catheterisation, ventilation and surgical procedures have also been reported to increase the risk of contracting nosocomial infections (Nair et al., 2018). Other contributing risk factors are crowded conditions within the hospital, frequent transfer of patients from one unit to another and a concentration of patients who are highly susceptible to infection, such as neonates, patients in ICU and burn patients (Nair et al., 2018). Microorganisms such as Coagulase-negative *Staphylococc*i (CoNS), *Enterobacteriaceae, Staphylococcus aureus, Pseudomonas spp, Haemophilus influenzae, Klebsiella pneumoniae, Enterococci* and *Acinetobacter* spp. are the most common microbes responsible for about 90% of infections. They can be found in patients, attendants, contaminated instruments and the environment, and they are able to persist for a very long period of time in the hospital environment (Temesgen et al., 2023). These microbes also have developed resistance to disinfectants, while protozoa, fungi and viruses are less attributed to nosocomial infection (Temesgen et al., 2023). Clinical signs and symptoms suggestive of infections are fever >38 °C, leucocytosis >10 000/mm³, new infiltrates on chest X-ray, persistent tracheal aspirates, turbid urine, suprapubic tenderness, abdominal pain and microorganisms in peritoneal dialysis fluid (Javeri et al., 2012). Depending on a patient’s symptoms and clinical suspicion, laboratory samples such as urine, sputum, pus, body fluids, blood and stool are collected from the patient for further investigation (Javeri et al., 2012). Legal costs are also involved in the present environment of litigation, as the nosocomial infections are often attributed to negligence or substandard healthcare (Nair et al., 2018).

Critically ill patients in ICU have a higher chance to acquire bacterial infections in the bloodstream (Dewi et al., 2023). Bacteraemia is a bacterial infection in the bloodstream and can reflect the presence of blood infection in a patient (Dewi et al., 2023). Bacteraemia is more common in patients that are undergoing surgical procedures or invasive medical devices such as central venous catheters, where microbes can enter the patient’s bloodstream (Dewi et al., 2023). Bloodstream infections that are caused by bacteria can be life-threatening infections, especially in immunocompromised patients (Dewi et al., 2023). Microorganisms can also indirectly get through an infected surgical wound (Dewi et al., 2023). In most of the cases, there is a need to initiate empirical antimicrobial treatment before obtaining microbial results. However, the situation is complicated by the emergence of multiple beta-lactamase producers and multidrug-resistant pathogens (Goel et al., 2009). Most of the admitted patients are treated with empirical prescribed antibiotics; however, this commonly leads to antimicrobial resistance (AMR) and the emergence of multidrug resistance (MDR) as well as death of patients (Temesgen et al., 2023). It is imperative that empirical antibiotic therapy for suspected nosocomial infection in patients be sufficiently broad spectrum to cover likely pathogens. However, this must be backed up with adequate diagnostic microbiology facilities to ensure the recognition and sensitivity testing of the responsible microorganism, further aiding the switch to targeted therapy (Archary et al., 2017). Multidrug-resistant bacteria are usually encountered among immunocompromised patients (Bhat et al., 2021). The ability of bacteria to develop resistance to antimicrobial agents has made treating bacterial infections more difficult in recent years (Temesgen et al., 2023). The emergence of resistance to antibiotic agents is a global public-health problem, particularly in microbes causing nosocomial infections that contribute to morbidity, mortality, increased healthcare costs resulting from treatment failures and longer hospital stays from invasive procedures, high antibiotic usage and transmission of bacteria among patients due to inadequate infection control measures (Temesgen et al., 2023). A study regarding the prevalence in pathogenic bacteria in patients with bacteraemia from 1996 to 2016 in hospitals found an increase in the prevalence of multidrug-resistant (MDR) bacteria from 6.2% in 1997 to 2000 to 15.8% in 2013 to 2016 (Dewi et al., 2023). The increase includes Extended Spectrum b-lactamase (ESBL)-producing bacteria, Carbapenem-resistant *Enterobacteriaceae*, *Psedomonas aeruginosa* and *Acinetobacter baumannii* (Dewi et al., 2023). Data on microbial profiles and antibiotic sensitivity can be used to determine the effectiveness of blood-infection control measures in hospitals (Dewi et al., 2023). Specific pathogens with susceptibility patterns can differ from one hospital to another (Dewi et al., 2023). Thorough research on the prevalence in bacterial profiles and patterns of antimicrobial sensitivity in blood-culture specimen isolates from patients experiencing bacteraemia can provide information that can be used in basic diagnostic approaches and treatment strategies for patients (Dewi et al., 2023). The understanding of research outcomes will aid in personalizing treatment, improving prognosis and reducing the cost of healthcare (Bhat et al., 2021). The management of the infections is based on the use of appropriate empirical antimicrobial therapy with a comprehensive understanding of the encountered pathogens and antibiotic sensitivity (Bhat et al., 2021).

The Human immunodeficiency virus affects and weakens the immune system of the infected individual, leaving it exposed to opportunistic diseases (Kamara et al., 2024). In 2019, about 38 million people were thought to be living with HIV globally. 25.6 million of these people live in Sub-Saharan Africa and South Africa contains the highest number of people living with HIV (Okon et al., 2023). HIV destroys the white blood cell lymphocyte subpopulations of CD4 T-cells and B-cells; therefore, this results in the body to lose its ability to defend itself against opportunistic pathogens (Okon et al., 2023). HIV infection results in continuous depletion of CD4 T-cells as well as an impairment of cellular and humoral immunity through a dysfunction of the T and B cells; therefore, a dysfunction of T cells results in abnormal cellular responses, while a dysfunction of B cells results in a lack of antibody responses to infections (Lubega et al., 2023). HIV infection causes changes in several lines of the host defences in the respiratory tract, which contribute to an increased risk for pulmonary infection and its attending difficulties (Seyi et al., 2019). The alveolar macrophages from HIV-positive people have been shown to be deficient in pathogen recognition. Furthermore, HIV also results in chronic stimulation and activation of inflammatory cells inside the alveolar space (Seyi et al., 2019). HIV infections have various effects on cellular and humoral immunity; therefore, results in qualitative and quantitative neutrophil deficits. Skin and mucous membrane defects predispose people who are HIV positive to develop bacterial infections more regularly than HIV-negative patients (Franceschini et al., 2020).

HIV and its related immunodeficiency increase the risk and mortality of bacterial infections (Archary et al., 2017), and bacterial infections in HIV-positive patients could be severe, leading to prolonged hospital stay, admittance to Intensive-Care Units (ICUs), or even result in mortality (Franceschini et al., 2020). The HIV epidemic still remains a major cause of morbidity and mortality globally, especially in Sub-Saharan Africa, due to co-infection with opportunistic infection (Okon et al., 2023). Opportunistic infections are the leading cause of illness and death in HIV-positive people (Kamara et al., 2024). HIV-positive people are at an increased risk of hospital-acquired infections due to their regular contact with the healthcare system through regular clinic visits and hospital admissions (Lubega et al., 2023). The continuous attack and elimination of the alveolar macrophages and CD4 cells by the virus in HIV-positive people make respiratory tract infection common among HIV-infected patients and a wide range of opportunistic pathogens (bacteria, fungi, parasites and viruses), armed with variance virulent factors have been found to co-exist with one another (Seyi et al., 2019). The most prevalent symptoms for which HIV-positive people seek medical attention is a cough and pneumonia*,* which are the most common respiratory illnesses among HIV-positive people (Kamara et al., 2024). *Streptococcus pneumoniae* and *Mycobacterium tuberculosis* are the most dangerous bacterial pathogens of respiratory-tract infection in HIV-positive patients and their prevalence depends on geographical region and the CD4 cell count in HIV patients (Seyi et al., 2019). Tilahun et al. (2023) conducted a study to assess the bacteriology of community-acquired pneumonia at six healthcare facilities in Ethiopia. The study observed 64% bacterial growth in rural facilities and 40.8% bacterial growth in urban facilities and according to them, etiological differences are due to environmental contamination (Tilahun et al., 2023).

People living with HIV (PLWH) have had an improved quality of life since Antiretroviral therapy (ART) was introduced (Lubega et al., 2023). However, even in the era of a combination of antiretroviral therapy (cART), respiratory-tract infections are the major cause of morbidity and mortality among HIV-positive patients (Kamara et al., 2024), and when it comes to patients with HIV seropositivity, the infection rate differs from 3.9 to 20 infections per 100 people per year (Kamara et al., 2024). About 70% of illness in HIV-positive people are respiratory-tract infections (Lubega et al., 2023) and factors associated with these infections are low CD4 counts (<200 cells/mm^3) and detectable viral loads (Lubega et al., 2023). The outcome of immune dysfunction, regulation and decrease of CD4 lymphocytes causes a high susceptibility of infections and risk of other complications like resistant pathogens (Lubega et al., 2023). When HIV infection is untreated in a patient, the patient experiences immune-system deficits that result in deadly opportunistic infections like lower-respiratory-tract infections. However, when a patient initiates ART, the ART reduces the incidence of opportunistic infections by increasing the CD4 count to a normal range. Furthermore, clinicians use CD4 cells to monitor the effectiveness of antiretroviral treatment (ART) (Okon et al., 2023). Lower-respiratory-tract infections are also the most common bacterial infections in immunocompromised patients who are in Intensive-Care Units, occurring in 10–25% of all ICU patients and resulting in a high overall mortality, which may range from 22–71% (Goel et al., 2009). LRTI are usually the first clinical manifestations of HIV infections (Alem, 2021). It is the most prevalent illness among HIV-positive people in Sub-Saharan African nations (Kamara et al., 2024). Diagnosing LRTI is done using GeneXpert MTB/RIF or sputum microscopy-culture sensitivity (MCS) and the right diagnosis or identification of the pathogens causing LRTI, and their antimicrobial susceptibility provides a great direction to healthcare workers for better management of the HIV patient (Okon et al., 2023). Bacterial, fungal, viral, mycobacterial and parasitic infections are all included in the broad spectrum of HIV-associated opportunistic lower-respiratory-tract infections (LRTI) (Kamara et al., 2024). LRTI is responsible for about 3 million deaths annually among all ages over the world and is the leading cause of mortality in low-income countries (Carrim et al., 2023). The most common bacterial agents in lower-respiratory-tract infection are *Pseudomonas,* *Acinetobacter, Klebsiella, Citrobacter, Escherichia coli* (Goel et al., 2009). In the study that was conducted by Okon et al. (2023) on sputum samples of HIV-positive patients, the rate of LRTI was higher among patients with CD4 cells of 201–300 cells/mm^3 (64.3%), while patients with CD4 cells above 301–400 cells/mm^3 (2:16.7%) had the lowest LRTI rate (Okon et al., 2023). Patients with a viral load above 1 000 copies/mL (45.1%) had the highest LRTI prevalence rate when compared with those who had a viral load below 1 000 copies/mL (1:10%) (Okon et al., 2023). The study further showed that gram-positive and gram-negative bacteria were mostly sensitive to Imipenem, 93.3% and 77.8%, respectively (Okon et al., 2023). In the study, they further stated that Trimethoprim-sulfamethoxazole (40%) and Ceftriaxone (51.7%) were the antibiotics to which gram-positive bacteria showed high resistance, furthermore, Gentamicin (44.4%), Azithromycin (33.3%) and Trimethoprim-sulfamethoxazole (33.3%) were also the antibiotics which gram-positive bacteria showed high resistance (Okon et al., 2023).

Respiratory diseases are responsible for more than 50% of all HIV-related mortality in Sub-Saharan Africa and studies in Malawi, Zimbabwe and South Africa estimate about a 30% prevalence of Chronic Lung Disease (CLD) (Abotsi et al., 2021), which is a contributing factor for HIV-positive persons to be admitted to an ICU (Abotsi et al., 2021). Bacteria implicated in forms of HIV-associated CLDs such as bronchiectasis in people living with HIV include *Streptococcus pneumoniae, Streptococcus aureus, Haemophilus influenzae* and *Moraxella catarrhalis* (Abotsi et al., 2021). *Streptococcus pneumoniae* is the leading bacterial cause of community-acquired LRTI and the carriage is assumed to be a source of pneumococcal disease transmission through close contacts. This is important in high human HIV-prevalence settings, because HIV-positive people have high chances of developing severe pneumonia and have a higher mortality rate due to pneumonia, compared to HIV-negative people (Carrim et al., 2023). *Streptococcus pneumoniae* is responsible for about 60% of bacterial pneumonia of adults who require hospitalization. Typical symptoms include cough, fever, chest pain and sputum production (Seyi et al., 2019). The bacterial pneumonia infection rate ranges from 3.9 to 20 cases per 100 persons per year in HIV-seropositive patients (Alem, 2021). In immunocompromised patients, especially those who are HIV positive, pneumonia is a common opportunistic infection (Alem, 2021) and the most common bacterial opportunistic pathogens in the development of bacterial pneumonia are *Streptococcus pneumoniae, Haemophilus influenzae, Staphylococcus aureus* and *Mycobacterium tuberculosis* (Alem, 2021).

Pneumococcal disease may occur at any time during the course of HIV-1 infection, even though pneumococcal disease can be an early presentation of HIV-1 infection and its incidence spread as HIV-1 disease progresses (Seyi et al., 2019). The incidence of pneumococcal disease is 50 times higher in children <2 years of age. In adults it is >65 years (Alem, 2021). A male:female ratio of 1.5–2:1 has been seen in 80% of cases of bacterial pneumonia occurring with a CD4 count, 400 cells per mm^3 and in recurrent pneumonia with a CD4 count of 300 cells per mm^3 (Alem, 2021). This study includes patients from the ages of 18 years and above. However, we also looked at the study that was conducted by Abotsi et al. (2021), where they investigated the prevalence of these bacteria and their antibiotics susceptibility in children living with HIV recovered from nasopharyngeal (NP) swabs and sputa. The study discovered that in the CLD-positive group, 67% of the swabs had at least one of the four bacteria species, while the CLD-negative group had 39% (Abotsi et al., 2021). Kamara et al. (2024), conducted a study in Uganda to check for bacterial isolates in the sputum of HIV-positive patients with cough symptoms. Bacterial growth was observed in 56/180 participants (31.1%) and the most prevalent organisms isolated in the study were *Staphylococcus aureus* (35.7%), followed by *Pseudomonas aeruginosa* (19.6%), *Streptococcus pneumoniae* (17.9%), *Klebsiella pneumoniae* (12.5%) and *Enterobacter* species (8.9%). Research has shown that that *Staphylococcus aureus* was observed to be sensitive to Imipenem, Ceftriaxone and Chloramphenicol; however, it was resistant to Piperacillin-tazobactam (Kamara et al., 2024). Furthermore, *Pseudomonas aeruginosa* was sensitive to Imipenem, Ceftriaxone and Ciprofloxacin, while *Enterobacter* species were sensitive to Gentamicin and Cefepime, but resistant to Ampicillin. Lastly, *Klebsiella pneumoniae* was sensitive to Imipenem, but resistant to Azithromycin (Kamara et al., 2024). Factors that were associated with sputum culture positive among HIV-positive patients in the study were age, education, viral load and peripheral oxygen saturation. Therefore, an unsuppressed viral load ≥200 copies per millilitre of blood and low peripheral oxygen saturation of ≤94% at room air were independently linked with a sputum culture-positive cough, which means that a patient with an unsuppressed viral load was 2.315 times more likely to have a sputum culture-positive cough when compared to the patients whose viral load was fully suppressed (Kamara et al*.,* 2024). A patient with low peripheral oxygen saturation was 2.448 times likely to have a sputum culture-positive cough when compared to the patients with normal peripheral oxygen saturation (Kamara et al., 2024). Lubega et al. (2023) conducted a study to check the susceptibility pattern of microbes isolated from respiratory samples taken from HIV-positive patients in Uganda. In their study, the isolated bacteria were *Moraxella* species (27.4%), *Streptococcus pneumoniae* (25.4%), Haemophilus *influenzae* (22.4%), *Mycobacterium* species (4.5%), *Pseudomonas* species (4%), *Staphylococcus aureus* (4%), *Escherichia coli* (1%) and other bacteria (10.4%) out of 201 samples that had bacterial growth. Most bacterial growth in their study was highly sensitive to Amoxicillin + Clavulanic acid and Ceftriaxone with *Moraxella* spp*.* and *Streptococcus pneumoniae* having 100% sensitivity to both antibiotics (Lubega et al., 2023). A100% sensitivity to Gentamicin was observed in *Pseudomonas*, while *H. influenzae* had a 100% sensitivity to Ceftriaxone and 88.6% sensitivity to Amoxicillin + Clavulanic acid (Lubega et al., 2023). Other bacteria showed high sensitivity to Ceftriaxone and Gentamycin at a rate of 85.7% (Lubega et al., 2023). All microorganisms had low sensitivity to Cotrimoxazole (<17%), while *Moroxella* spp*., H. influenza* and *Pseudomonas* showed zero sensitivity to Cotrimoxazole (Lubega et al., 2023). The study further had low sensitivity towards erythromycin that was observed from *Moraxella* spp. (28.8%), *H. influenzae* (31.6%), *S. aureus* (42.9%) and other bacteria (42.9%) (Lubega et al., 2023). Ciprofloxacin showed low sensitivity in *H. influenzae* (50%) and other bacteria (69.2%) (Lubega et al., 2023).

In more resource-limited areas, late-stage diagnosis of HIV with associated opportunistic infections remain a common reason for ICU admission in developing countries (Ueckermann et al., 2022). The need for ICU admission and ventilation increases the mortality risk (Ueckermann et al., 2022). The mortality rates of HIV-positive patients in Sub-Saharan Africa show a huge variability in the practice and outcome among different hospitals (Ueckermann et al., 2022). The risk factors for bloodstream infections in HIV-positive people are high HIV-RNA, low CD4 cell counts and concomitant AIDS-defining conditions (Franceschini et al., 2020). However, some studies have proven that severe bacterial infections still occurred at a high rate even in the absence of severe CD4 cell depletion (Shahcheraghi et al., 2016). In the post-combination antiretroviral treatment (cART) period, Persons Living With HIV (PLWH) are more often admitted to an ICU due to Blood-Stream Infection (BSIs) than *Pneumocytostis jiroveci pneumonia* (Franceschini et al., 2020). Recent studies have shown that clinical manifestations of BSIs in PLWH are the same with those in HIV-seronegative patients. However, the BSIs prevalence and mortality rate are often higher in the HIV-positive population (Franceschini et al., 2020). In the study conducted by Franceschini et al. (2020), they describe the BSI epidemiology in PLWH. They discovered that 34% of patients had more than one bacterial episode. They further discovered that 48% of the cases were community-acquired BSI, while 52% of the cases were hospital-acquired and 9% were polymicrobial (Franceschini et al., 2020). The study further elaborated that 82.8% of the cases were collected in the Internal Medicine Wards, 8% in ICUs and 8.8% in surgical wards (Franceschini et al., 2020), while 27.4% of the BSI originated from the central in-dwelling caterers (4/9 in ICU, 40%) (Franceschini et al., 2020). Gram-positive bacteria have been reported to be more in ICU and medical wards, while gram-negative bacteria were prevalent in surgical wards (Franceschini et al., 2020).

The incidence of bacterial pneumonia in HIV-positive people is higher than in people who are HIV negative (Alem, 2021). As mentioned earlier, the most prevalent pathogens that cause bacterial pneumoniae in HIV-positive patients include *Streptococcus pneumoniae, Haemophilus influenzae, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus* and *Escherichia coli.* However, it has been reported that *S. pneumoniae* is the most prevalent cause of pneumonia in HIV-positive persons, accounting for 40 of all bacterial pneumonia (Alem, 2021). *Streptococcus Pneumoniae* is the most common agent in HIV-infected adults, as confirmed in various etiological studies from Africa (Shahcheraghi et al., 2016). It is the most prevalent bacterial pathogen that causes pneumonia in HIV-positive individuals, and implicates around 20% of all bacterial pneumonia, while *H. influenzae* accounts for 10–15% of cases of bacterial pneumonia in HIV-positive patients (Alem, 2021). More than 60% of bacterial pneumonia in adults are caused by *S. pneumoniae* and require hospitalization. In addition, the risk is higher in people whose CD4 lymphocyte counts less than 200 cells/mm^3 (Alem, 2021). In HIV-infected adults, *Pneumococcus* has been investigated to be implicated in 20% of bacterial pneumonia, 40% of pneumonia with identified organisms, and 70% of pneumonia with positive blood cultures (Shahcheraghi et al., 2016). The highest prevalence of pneumoniae was 59.76% in HIV-seropositive patients in a study that was conducted in Tanzania (Alem, 2021). Studies that were conducted previously show that bacterial pneumonia is the most common infection in HIV-seropositive patients, and the frequency of the infection is increased by >10 times than in healthy people (Alem, 2021). The risk factors of pneumonia development are common in both developed and developing countries and bacterial pneumonia may occur in the entire course of HIV infection, but the incidence increases as CD4 cell counts decrease (Alem, 2021). Intravenous drugs and smoking are also risk factors for the development of bacterial pneumonia in HIV-positive patients (Alem, 2021), and smoking cigarettes are associated with a two-to-five-fold increase in the risk, especially in patients with low CD4+ T cell counts (Alem, 2021). Age, gender, detectable viral load and recurrent pneumonia are also identified as risk factors (Alem, 2021).

Bacterial pneumonia in HIV-seropositive patients is commonly persistent, and a persistent pneumonia is an AIDS-defining condition (Alem, 2021). *Escherichia coli* is the most common etiological agents of bacterial gastroenteritis in HIV-infected individuals, whose diseases present with varying severity (Chabala et al., 2020). With the whole PLWH population in the study that was conducted by Franceschini et al. (2020), *Enterobacteriaceae* were the most prevalent microbes at a rate of 29.8%, followed by Coagulase-negative *Staphylococci* at a rate of 21.4% and *Staphylococcus aureus* at a rate of 12.7%. Non-fermenting gram-negative bacteria were reported to be 12.4%, *Streptococci* at a rate of 8% and *Enterococci* at a rate of 7.4% (Franceschini et al., 2020). In the group of *Streptococci, S. pneumoniae* was the most prevalent pathogen at a rate of 54.8%, followed by *S. viridans* at a rate of 20.8% (Franceschini et al., 2020). In the group of *Enterobacteriaceae, E. Coli* was the most prevalent microorganism at a rate of 55.7%, followed by *K. pneumoniae* at 21.6%, and lastly *E. Cloacae* at a rate of 9.1% (Franceschini et al., 2020). *E. Faecalis* was the most prevalent microbe among *Enterococci* at a rate of 11.50%, followed by *E. Faecium* at a rate of 45.5% (Franceschini et al., 2020). In the group of *Staphylococcus* bacteraemia, Congulase-negative *Staphylococci* were the most isolated (62.4%), and *S. aureus* had 37.6% isolates (Franceschini et al., 2020). Archary et al. (2017), conducted a study at the King Edward VIII Hospital in the eThekwini District of KwaZulu-Natal about HIV infection and malnutrition in the paediatric ward. The study discovered that a total of 43 gram-negative bacteria and 8 gram-positive bacteria were isolated from 39 patients, *Klebsiella pneumoniae* was the most prevalent isolate (n=17), followed by *E.coli* (11), *Staphylococcus aureus* (6), *Acinetobacter* species (4) and *Pseudomonas aeruginosa* (3) (Archary et al., 2017). In Archary et al.'s (2017) study, *Acinetobacter* was the second prevalent nosocomial blood culture isolate, while *E.coli* was the second prevalent urinary pathogen. Only one non-typhoidal *Salmonella* species was isolated from the study.

Enteric diseases are part of the primary causes of morbidity and mortality in developing countries (Marbou & Kuete, 2017). Enteric diseases represent the second-most common cause of death after tuberculosis in HIV-positive people in developing countries (Marbou & Kuete, 2017). Most opportunistic diseases are observed when CD4 counts fall below 200 cells/mm³ of blood (Marbou & Kuete, 2017). Enteric pathogens like *Salmonella* and *Shigella* species have been described to be among the causative microbes of diarrhoea in people who are HIV positive or that have AIDS, especially in low-income or developing countries (Belay et al., 2020). About a 90% occurrence of HIV/AIDS in adults and children in low-income countries with constant diarrhoea is associated with II-fold increase in mortality when compared to uninfected people (Belay et al., 2020). *Salmonellosis* is estimated to be about 20 times more often in individuals that have HIV/AIDS, and these patients are also 5 times more likely to develop bacteraemia than those without HIV/AIDS (Belay et al., 2020). Furthermore, in HIV-positive adults, the rates of gram-negative bacteria enteric infections are at least 10-fold higher than in the general population and HIV infection increases the risk of *Salmonella* bacteraemia by 20 to 100-fold and mortality as high as 7-fold when compared to people who are HIV negative (Belay et al., 2020). Longer periods on ART or low viral loads are associated with a reduced carriage for bacterial species (Abotsi et al., 2021). Cotrimoxazole has been used as a prophylactic agent against opportunistic infections in HIV patients worldwide (Marwa et al., 2015) and the current guidelines recommend the test-and-treat strategy. However, late presentation represents a high clinical problem in HIV infection and some microorganisms such as non-typhoidal *Salmonella, Mycobacteria* and *Cryptococci* represent AIDS-defining conditions. They are strictly linked to late presentation (Franceschini et al., 2020). Previous studies have demonstrated a relationship between antibiotic consumption and the incidence of antimicrobial resistance in various bacterial infections (Marwa et al., 2015).

Studies have reported a much higher prevalence of drug-resistant bacteria in HIV-positive patients (79%) compared to HIV-negative patients (30%) (Lubega et al., 2023). Archary et al. (2017), discovered that gram-positive microorganisms were susceptible to most first-line antibiotics and resistance was more prevalent among gram-negative microorganisms. Carbapenems and Amikacin were seen to be the most active antibiotic against gram-negative bacteria. Only two gram-negative bacteria were susceptible to Amoxicillin; and two others were susceptible to Trimethoprim-sulfamethoxazole. There was Ciprofloxacin resistance in 12 isolates across a range of species (Archary et al., 2017). A study that was done in Soweto, South Africa, reported a high resistance of *K. Pneumoniae* and *S. aureus* to Cotrimoxazole among isolates from HIV-infected patients (Marwa et al., 2015). Archary et al. (2017) discovered that all micro-organisms, apart for a single *P. aeruginosa,* were susceptible to Meropenem and Imipenem and no Ertapenem resistance was found. Furthermore, Extended-spectrum ®-lactamase was recognized in 39.5%(17) of persons, including 13 of 19 *Klebsiella* isolates (Archary et al., 2017). Franceschini et al. (2020) report that the majority of the patients in their study were on effective cART (65.3%). However, 34.7% of patients with BSI had a virological failure; 25% and 13% of the patients showed HIV-RNA above 10 000 copies/mL and 100 000 copies/mL, respectively, while the median CD4 count at the moment of the episode was low (207 CD4 cells/mm³) (Franceschini et al., 2020). Franceschini et al. (2020) mention that 48% of patients died during the study, with a median survival duration of 28 days after the last episode of bacteraemia. Furthermore, the 30-day mortality rate after the last episode was 24.2%, while the 90-day mortality rate was 32.4%. The mortality rate of MDR microorganisms were 33.3% and 46.9% at 30 and 90-days after the last bacterial episode, respectively (Franceschini et al., 2020).The mortality for BSI due to MDR microorganisms was higher than observed in people without MDR at a rate of 44.7% versus 24.3%, respectively (Franceschini et al., 2020).

Mycobacterium tuberculosis causes a chronic infection of the lungs called tuberculosis (TB). It is characterized by slight fever, weight loss, sweating at night and chronic cough producing blood-stained sputum (Seyi et al., 2019). Tuberculosis is a deadly disease, despite the novel advances in its diagnostic tools and drug therapy (Gashaw et al., 2021). Pulmonary tuberculosis is a main cause of lower respiratory-tract infection and may present as an acute or chronic disease (Dube et al., 2016). Factors that contribute to the high prevalence of tuberculosis in developing countries and difficulties in its control include co-infection with HIV, the emergence of multidrug-resistant tuberculosis, inadequate treatment, continuing poverty, malnutrition, overcrowding and increasing numbers of displaced persons (Seyi et al., 2019). Almost 10% of new TB cases globally are HIV positive. However, this number varies on a country basis and can be as high as 80% (Seyi et al., 2019). Tuberculosis has been a major co-morbidity in HIV-positive individuals since the beginning of the HIV epidemic (Seyi et al., 2019), and the emergence of HIV in South Africa has resulted in a huge rise in the incidence of tuberculosis (Cohen et al., 2010).

Infection with HIV increases the risk of developing tuberculosis and speeds up its progress (Seyi et al., 2019). The risk of developing TB is 5% to 10% in HIV-negative persons and 50% in HIV-positive people. This results in difficulty for health systems to keep up with the increasing demands for health services for both diseases (Seyi et al., 2019). Populations with latent tuberculosis who acquire HIV infection experience up to a 100-fold higher risk of developing active tuberculosis, while people with HIV-induced immunosuppression are more susceptible to new TB infections and are at high risk of progressing to active tuberculosis (Seyi et al., 2019). TB and HIV co-infection form a lethal combination; each accelerates the other’s progress. Without TB treatment, one in three people infected with HIV will develop TB (Seyi et al., 2019). An HIV-infected person who is infected with TB is 50 times more likely to become sick with TB than someone who is TB positive who is HIV negative (Seyi et al., 2019). TB is difficult to diagnose and progress faster in HIV-positive people, and TB is certain to be rapidly fatal if undiagnosed or untreated (Seyi et al., 2019). The two diseases constitute a deadly combination, as they are extra destructive, other than when a patient is infected with one disease only (Seyi et al., 2019).

A systematic review of previous studies recorded that hospital admissions in HIV-positive patients reported that community-acquired pneumonia and tuberculosis accounted for 57% of in-patient deaths globally (Owusu et al., 2024). In 2010, the number of people who died from TB were about 1.4 million, including 350 000 people with HIV (Seyi et al., 2019). Tuberculosis is mostly implicated in HIV-associated pneumonia; however, information on the role of other bacterial and viral pathogens is not much in many developing countries (Owusu et al., 2024) and the risk of mortality in hospitalized patients is believed to be higher due to limited diagnosis of microbial aetiologies of pneumonia (Owusu et al., 2024). An estimation by the World Health Organization (WHO) is that TB causes about 40% of AIDS deaths in Sub-Saharan Africa and Southeast Asia (Seyi et al., 2019). About 80% of TB cases in South Africa are HIV seropositive (Cohen et al., 2010). Pulmonary infection is the most common immunodeficiency-virus-affiliated illness with complications in the period of antiretroviral therapy (ART) (Owusu et al., 2024). Mixed pulmonary infections with two or more pathogens are common in HIV-positive patients. They often present diagnostic difficulties for doctors and result in potentially serious consequences for the patient if it is unrecognized (Seyi et al., 2019). ART has prompted a reduction of the rate of respiratory disorders, including tuberculosis (Mushunje et al., 2024). In 2019, about 2.8 million children and adolescents were living with HIV globally and 90% was recorded in Sub-Saharan Africa, while respiratory infections remain the major popular manifestation of HIV among children and adolescents (Mushunje et al., 2024). Pulmonary tuberculosis has been reported to be increasing in children that are diagnosed with pneumonia. Furthermore, culture-confirmed TB has been reported in 8% of South African children hospitalized with acute pneumonia with no difference relating to the HIV status of the patient (Dube et al., 2016).

Studies in Sub-Saharan Africa report that nearly 30% of HIV-positive older children experience chronic respiratory symptoms, which include cough and reduced tolerance to exercise, often resulting in presumptive tuberculosis treatment (Mushunje et al., 2024). There are not much published data on the role of other respiratory organisms in patients who are suspected to have TB; however, in Africa, a study conducted in Botswana reported microbiologically confirmed TB in 52%, *Mycoplasma pneumoniae* infection in 17% and *Pneumocystis jirovecii* infection in 3% of PTB adults suspects (Dube et al., 2016). Co-infection with two or more microorganisms is reported in 25% of patients (Dube et al., 2016). Dube et al. (2016) conducted a study to investigate the respiratory pathogen in nasopharynx (NP) of children who were hospitalized with suspected TB. In this study, 16% of the children were TB positive and 13% of the children were HIV infected, with a similar HIV prevalence by TB category (Dube et al., 2016). The most common bacteria detected in NP were *Moxaxella catarrhalis* (64%), *S. Pneumoniae* (42%), *H. influenzae spp* (29%) and *Staphylococcus aureus* (22%) (Dube et al., 2016). However, *Mycoplasma pneumoniae* (9%), *Bordetella pertussis* (7%) and *Chlamydia pneumoniae* (4%) were detected as less prevalent in the study

(Dube et al., 2016). The most-detected viral agents were the human metapneumovirus (hMPV) (19%), rhinovirus (15%), influenzae C virus (9%) adenovirus (7%) and Coronavirus O43 (5.6%) (Dube et al., 2016). Furthermore, seasonal patterns were observed when it comes to hMPV, rhinovirus, enterovirus and influenzae viruses with peak prevalence in late winter (August) and spring (November) (Dube et al., 2016).

The study conducted by Dube et al. (2016) further details that bacteria alone were detected on 40% of samples; viruses alone were detected in 5% of samples; and both bacteria and viruses were detected in 55% of the samples. Furthermore, in children that were diagnosed with TB, both bacterial and viral targets were detected at the rate of 71% (Dube et al., 2016). In the cohort study that was conducted by Ueckermann et al. (2022), pulmonary tuberculosis was diagnosed in 33% (41/117) of patients, while *P. jirovecii* was the associated pathogen in 21.4% (25/117) of patients. In the study, they reported that 22 sputum and BAL cultures revealed other bacteria as the aetiology for pneumonia, which included *Pseudomonas aeruginosa* 45% (9/20), *Streptococcus pneumoniae* 30% (6/20), *Klebsiella pneumoniae* 20% (4/20) and *Staphylococcus aureus* 5% (1/20) (Ueckermann et al., 2022). The study further showed that 52% (61/117) of patients required admission to ICU and the in-hospital mortality rate was 40.2% (47/117) (Ueckermann et al., 2022). Ueckermann et al. (2022) mention that in their study, the mean CD4 count of those with TB was lower than those without TB and some patients diagnosed with HIV during the presenting admission and late diagnosis of HIV have been shown to be a risk factor for admission to the ICU (Ueckermann et al., 2022). Patients on Highly Active Antiretroviral Therapy (HAART) in the study conducted by Ueckermann et al. (2022) were more likely to survive than those who were not; 38.6% of survivors were on HAART compared to 31% of non-survivors. Patients with TB admitted to ICU had a high mortality rate of 33% to 67% and a South African study in patients with TB admitted to ICU showed that 53% of patients were co-infected with HIV with a mortality rate of 59% (Ueckermann et al., 2022).

The co-infection of *S. pneumoniae* and *M. tuberculosis* is regarded as a defining disease of the acquired immunodeficiency syndrome and their establishment in a person depends on whether certain conditions are favourable such as smoking, a crowded environment, use of drugs and use of steroids, as a low CD4 cell count in patients may be indicated by *Streptococcus pneumoniae* and *Mycobacterium* *tuberculosis* co-infection in HIV-positive patients (Seyi et al., 2019). *Streptococcus pneumoniae* and *Mycobacterium tuberculosis* are the two most common causes of co-infection in HIV-seropositive patients in Sub-Saharan Africa and highly contribute to the mortality and morbidity rates of HIV/AIDS globally,. They further have similar clinical features and radiological appearances (Seyi et al., 2019). Seyi et al. (2019) conducted a study on the prevalence of *Streptococcus pneumoniae* and *Mycobacterium tuberculosis* co-infection in HIV-positive adult patients who were on Highly Active Antiretroviral Therapy (HAART) in Nigeria. They report a prevalence rate of 8.8% (*Streptococcus pneumoniae* mono-infection), 21.5% (*Mycobacterium tuberculosis* mono-infection) and 2.7% (*Streptococcus pneumoniae* and *Mycobacterium tuberculosis* co-infection) among 260 patients.

Antimicrobial susceptibility testing is important in prescribing an effective drug regime for TB patients, especially in areas where drug resistance is high (Gashaw et al., 2021). The global mortality rate of TB is reducing by 3% annually. However, the threat of its drug resistance is on the increase (Gashaw et al., 2021). The cumulative effects of treatment interruption like lack of awareness about the nature of the bacteria, shortage and lack of the WHO's recommended diagnostic tools, and a prolonged drug consumption period for treatment increases the risk (Gashaw et al., 2021). Prevalent flora and antimicrobial resistance patterns can sometimes vary from region to region, depending upon the antibiotic pressure in that locality (Agmy et al., 2013). There is a need for local resistance-prevalence data to guide empirical prescription and to identify areas in which a medical need for new agents is greater (Agmy et al., 2013).

As mentioned previously, microbial infections cause a high mortality rate in immunocompromised patients. Therefore the study also looked at the mortality rate caused by opportunistic microorganisms globally. Infections due to *Campylobacter* are one of the most common causes of bacterial enteritis globally and about 1.3 million cases of *Campylobacter* infections are reported each year (Sunnerhagen et al., 2024; Baek et al., 2024). However, the cases reduced in 2020 when social distancing measures were implemented during the new COVID-2019 pandemic in some countries such as the United States and Spain (Baek et al., 2024). *Campylobacter* infections are usually associated with systemic invasive illness (Nielsen et al., 2010). The disease usually comprises abdominal pain, fever and watery or bloody stools (Sunnerhagen et al., 2024). Bloodstream infection with *Campylobacter* species has been reported commonly in immunocompromised patients (Nielsen et al., 2010). The mortality rate associated with *Campylobacter* bacteraemia is estimated to range from 2.5% to 15% (Sunnerhagen et al., 2024). Sunnerhagen et al. (2024) report that a study that was conducted in France observed that *Campylobacter* bacteraemia most often occur in immunocompromised cases, with a 30-day mortality rate of 11.7% (Sunnerhagen et al., 2024). Zayet et al. (2023) report that in France, *Campylobacter fetus* is the most common isolated *Campylobacter* species after *Campylobacter jejuni* and *Campylobacter coli;* therefore, the risk of death from *Campylobacter foetus* systemic infection are a huge concern for clinicians, as the fatality rate is about 15% (Zayet et al., 2023). A study conducted by Baek et al. (2024) shows that in-hospital mortality occurred at a rate of 13% and the risk factors associated with in-hospital mortality were male sex, cancer, liver disease and septic shock. Tinvez et al. (2022) state that hypogammaglobulinemia and human immunodeficiency virus (HIV) infections are also some of the underlying predisposing risk-factor conditions.

Clostridium difficile is among the normal flora of the gastrointestinal tract. However, it becomes pathogenic if the normal intestinal flora are disturbed (Seugendo et al., 2015). It is the most common cause of infectious diarrhoea in North America and Europe (Olanipekun et al., 2016). Other studies have reported an increase in *C. difficile* prevalence, morbidity and mortality (Olanipekun et al., 2016). Few studies have been done on the *Clostridium difficile* prevalence in Sub-Saharan Africa and the prevalence rate of *Clostridium difficile* infection in Sub-Saharan Africa from previous studies has been reported to range between 4% and 43% (Seugendo et al., 2015). Zimbabwe reported a prevalence rate of *C. difficile* infection of 8.6% (Seugendo et al., 2015). Seugendo et al. (2015) further state that HIV-positive individuals are significantly more positive for *C.difficile* than individuals who are HIV negative. It has been reported that the mortality rates from *C. difficile* in the United States increased from 5.7 million in 1999 to 23.7 million in 2004 and the mortality rate in the United Kingdom due to *C. difficile* infection rose from 1 804 cases in 2003 to 8 324 cases in 2007 (Karas et al., 2010). A study conducted by Solanki et al. (2021) shows that the mortality rate was higher in *C. difficile* hospitalization at a rate of 6.1% than the mortality rate due to all other hospitalization (1.9%). Furthermore, *C. difficile* patients have a more than two times higher chances of dying (Solanki et al., 2021).

Escherichia coli is part of the normal commensal gut of microbes in a healthy human being; however, some of the strains can cause intestinal or extraintestinal infections due to specific virulence factors (Daga et al., 2019). *Escherichia coli* is among the most common organisms that are involved in bacteraemia (Surgers et al., 2014). *E. coli* is the leading cause of bloodstream infection with an incidence that ranges between 31.9% to 81.0% in 28 European countries (Tao et al., 2020). The contribution of *E.coli* to patient mortality was found to be low with regard to host factors or portal of entry in a study of *E.coli* bacteraemia in adults (Surgers et al., 2014). Tao et al. (2020) state that in the study they conducted, the mortality rate cohort was 21.3%, which is similar to the mortality rates reported by other researchers at a rate of 10.3 to 33.3%. Daga et al. (2019) state that the mortality associated with bacteraemia due to *E. coli* was 33.3%.

Pseudomonas aeruginosa is the third frequently identified gram-negative microorganism that causes bloodstream infection (BSI) and it carries a very high mortality rate (Ioannou *et al.*, 2023). *P. aeruginosa* bacteraemia are a life-threatening infection in hospitalized patients worldwide with serious underlying conditions (Zhang et al., 2020). The prevalence of *P. aeruginosa* in Europe is 6.1%, i.e. in Spain at the rate of 5.9% (Callejas-Díaz et al., 2019). Previous studies have shown that *P. aeruginosa* bacteraemia could trigger severe septic shock and multiple organ failure, resulting in a high mortality rate and substantial medical costs (Zhang et al., 2020). In some hospital settings, such as in Intensive-Care units, the rate of *Pseudomonas* species isolation as pathogens that cause bloodstream infection are reported to be higher (Ioannou et al., 2023). Gomes et al*.* (2011) note that the high mortality rates in the study they conducted demonstrate the burden of multi-resistant *Pseudomonas aeruginosa* infections in immunocompromised patients. In a study that was conducted in India, 48.2% of 593 blood cultures were determined to be positive for *P. aeruginosa* with 63.6% of which being multidrug resistant (De Matos et al., 2018). *P. aeruginosa* usually causes multi-site infections, of which bacteraemia is fatal, with the mortality rate ranging from 18% to 61% (Zhang et al., 2020). The mortality rate is estimated to be 30% after 30 days from the BSI episode (Ioannou et al., 2023; Callejas-Díaz et al., 2019; Ferreiro et al., 2017). A study conducted by Ioannou et al. (2023) states that mortality at 30 days after occurrence of BSI was very high and if the patients who died had a higher age, they were more likely to have hospital-acquired BSI and more likely to have acquired the BSI during their hospitalization (Ioannou et al., 2023). Callejas-Díaz et al. (2019) state that in their study, the overall mortality was 37.3%, while the mortality directly caused by bacteraemia was 29.1%. Callejas-Díaz et al. (2019) further state that the mortality was higher during the first days after bacteraemia onset. Most studies focusing on *P. aeruginosa* bloodstream infection have only considered mortality up to one month post infection (McCarthy & Paterson, 2017). McCarthy and Paterson (2017) state that a mortality rate of 42% has been described so far, depending on the patient population studied and the time at which the mortality endpoint was determined. The SARS-COV-2 pandemic led to an increase in prolonged times of hospitalization and that resulted in a high rate of hospital-acquired infections (Bongiovanni & Barda, 2023). Before the Covid-19 era, bacterial infections represented one of the leading causes of death (Bongiovanni & Barda, 2023), furthermore, Bongiovanni and Barda (2023) state that the global mortality in 2019 was associated with 33 bacterial pathogens, with *P. aeruginosa* being responsible for more than 50% of the overall cases of death. The estimated comorbidity by the Charlson Comorbidity Index also shows an alliance between increased mortality in patients with Chronic Obstructive Pulmonary Disease (COPD) and respiratory infection by *P. aeruginosa,* as the BODE index similarly indicates (Ferreiro et al., 2017). The influence of a suitable empiric treatment on the mortality of patients with *P. aeruginosa* infections is controversial due to mixed results in various studies in patients with bacteraemia (Ferreiro et al., 2017). Ferreiro et al. (2017) conclude that *P. aeruginosa,* regardless of the presence or absence of associated bacteraemia, shows high mortality at 30 and 90 days of diagnosis (17.7% and 33.9%, respectively). In the study conducted by Zhang et al. (2020), the overall mortality of inpatients in China with *P. aeruginosa* was 28.4%. Furthermore, they state that the poor outcomes of the bacteraemia that is caused by *P. aeruginosa* could be explained by its virulence and the underlying disease of the patients.

Staphylococcus aureus is the second major cause of bloodstream infections (Bello-Chavolla et al., 2018). *S. aureus* has been reported to be responsible for the augmented number of global hospital- and community-acquired infections (Boison et al., 2022). For decades, *S. aureus* has been recognized as a cause of infection, especially in immunocompromised patients and it is associated with major mortality (Kang et al., 2012). *S. aureus* Bacteraemia (SAB) is the most serious case in *S. aureus* infections and is related to mortality rates between 15% and 60% (Li et al., 2021). The general 30-day mortality of MRSA BSIs is between 16% to 44% in the general-hospital population (Li et al., 2021). A person that has a chronic illness may interact with the healthcare system on a more regular basis than those in the general population, and physicians may be more likely to admit a patient that is immunocompromised on suspicion of infection, compared to patients that do not have chronic diseases (Smit et al., 2016). In people infected with the human immunodeficiency virus (HIV), *S. aureus* infection accounts for significant morbidity (Hidron et al., 2010). *S. aureus* has been reported to be the most frequent cause of both community- and hospital-acquired bacteraemia in HIV-positive patients (Hidron et al., 2010). In a study done in Ghana, there have been reports of *S. aureus* and MRSA carriage prevalence, although the prevalence of *S. aureus* and MRSA carriage was found to be 13.9% and 13%, respectively, among inpatients and they were found to be 44.9% and 5.6%, respectively among HIV-infected individuals (Boison et al., 2022). Hidron et al. (2010) report that hospitalized patients with HIV have been reported to be 17 times more likely to have *S. aureus* bacteraemia when compared with HIV-negative patients. People living with HIV had a higher short-term mortality following *S. aureus* compared to individuals without HIV (Jaliff et al., 2014). *S. aureus* has a significant proportion of cases developing severe complications; therefore, the mortality attributable to *S. aureus* bloodstream infection has been estimated to be 30% (Bello-Chavolla et al., 2018). The incidence of *S. aureus* has increased and Methicillin-resistant *S. aureus* (MRSA) has also been an increasing problem (Kang et al., 2012). Immunocompromised HIV-infected patients are recognized as one of the higher risk groups due to increased rates of both MRSA colonization and infections (Hidron et al., 2010). Known risk factors for mortality attributable to *S. aureus* bloodstream infection (SABI) are MRSA infection, inadequate empiric therapy and septic shock, among others (Bello-Chavolla et al., 2018). Immunocompromised cancer patients are highly susceptible to bloodstream infections due to regular hospital admissions, the use of invasive procedures and exposure to broad-spectrum antibiotics (Li et al., 2021). There were about 14 million patients with bloodstream infection in the United States from 2006 to 2014, with gram-positive bacteria found to be the leading causative pathogens at a rate of 27.38% in cancer patients (Li et al., 2021). Kang et al. (2012), report that the mortality rate of *S. aureus* bacteraemia of cancer patients in their study was about 50%. They further conclude that the results in their study indicate that *S. aureus* continues to be a significant cause of invasive infection in cancer patients and Methicillin resistance was found in more than 50% of the cases. A study conducted by Li et al. (2021) on cancer patients reports that the 60-day mortality in adult cancer patients with MRSA BSIs was 12% and the 6-month overall mortality was 43.2%. Cusumano et al. (2020), conducted a study about Covid-19, and *S. aureus* has been described as the primary causative pathogen of secondary bacterial infections; therefore, the onset of secondary bacterial infections with influenza is seen within the first six days of influenza infection when viral shedding is the highest (Cusumano et al., 2020). Bacteria have been associated with mortality rates up to 50% compared to 1.4% in patients with influenza, but without bacteraemia (Cusumano et al., 2020). Cusumano et al. (2020) report that in the study they conducted during Covid-19, the 14-day hospital mortality rate from the first positive blood culture was 54.8%, while the 30-day hospital mortality rate was 66.7%. Kang et al. (2012), suggest that as most documented pathogens occurring in *S. aureus* infection are MRSA, empiric antimicrobial therapy should adequately cover this organism, especially in nosocomial infections. Smit et al. (2016) also state that *S. aureus* bacteraemia has a 30-day mortality that ranges between 20% and 40% in developed countries and patients with Diabetes Mellitus (DM) experience a higher mortality from *S. aureus* bacteraemia compared to patients without Diabetes Mellitus because of their decreased immunity (Smit et al., 2016). Smit et al.'s (2016) study report that a 30-day cumulative mortality was 25.8% in patients with DM and about 24.3% in patients without DM. Therefore, patients with DM experienced no increased risk of dying within 30 days of blood culture compared to patients without DM. Smit et al. (2016) further state that the time to blood-culture sampling and initiation of antibiotic therapy could have been shorter in patients with DM. The study further states that the mentioned surveillance bias could lead to the underestimation of DM-related mortality (Smit et al., 2016). Some cases of *S. aureus* bacteraemia's mortality are missed if the patient has received pre-admission antibiotics, if the patient had been hospitalized outside of the catchment area, or if the patient died before blood culture sampling (Smit et al., 2016).

Enterobacteriaceae are the most-observed, hospital-acquired, drug-resistant gram-negative bacteria (Alkofide *et al.*, 2020) and drug-resistant GNB differs from one hospital to another (Alkofide *et al.*, 2020). Multidrug-resistant *Enterobacteriaceae* (MRDE) infections are associated with poor outcome and high cases of mortality rates, especially in low- and middle-income countries (Ballot et al., 2019). Extended-spectrum beta-lactamases producing *Enterobacteriaceae* (ESBL-E) are of great concern, since infections caused by these resistant strains are affiliated with prolonged hospital stay and raise case fatality rates (Ndir et al., 2016). ESBL-E became a crucial therapeutic challenge across the world in daily clinical practice, since their resistance to additional classes of antibiotics reduces effective therapeutic options (Ndir et al., 2016). Studies that were conducted in Africa showed that the ESBL-E prevalence rate is on the increase. It varies from 0.7% in Malawi to 75.8% in Egypt (Ndir et al., 2016). However, the burden of ESBL-E has not been clearly established in Sub-Saharan African countries (Ndir et al., 2016). Ndir et al. (2016) report that 69 (37.1%) patients with an infection caused by *Enterobacteriaceae* died during their study period. Furthermore, the case fatality rate was higher in ESBL-positive patients at a rate of 47.3% compared to ESBL-negative patients at a rate of 22.4% (Ndir et al., 2016). In the study conducted by (Alkofide et al., 2020), in the total of 227 *Enterobacteriaceae* cultures identified, 130 (57.3%) were MDR and 8 (3.5%) were XDR cultures. No PDR cultures were isolated. In the study done by Alkofide et al. (2020), they report that about a 84.1% (116/138) mortality was reported during the hospital stay. A study was done to evaluate the epidemiology of Carbapenem-resistant *Enterobacteriaceae* (CRE) infections in patients with sepsis and organ dysfunction or septic shock. The researchers further compared the bacteria presenting different resistance phenotypes and CRE infections were the ones with a higher 30-day mortality with the following rates: CRE (63.8%), Carbapenem-resistant, non-fermentative, Gram-negative bacteria (60.7%), ESBL-producing *Enterobacteriaceae* (36.4%), MRSA (33.3%), and other pathogens (31.6%) (Sabino et al., 2019).

2.1 OBJECTIVES

- Determine microbial profile prevalence in immunocompromised patients who are hospitalized in the different hospitals having TB or are HIV positive.
- Determine the risk factors that are associated with microbial infections in immunocompromised patients.
- Compare the microbial prevalence rate in HIV-positive patients compared to HIV-negative patients.

- Determine the antibiotic susceptibility pattern of the identified microorganisms.
- Assess the impact of microbial infections on the mortality rate of immunocompromised patients from other studies globally.

2.2 LABORATORY METHODS

This is a retrospective study that utilized data generated from microbiological results obtained from sputum, blood culture, faeces, urine, pus and swabs obtained from the nose, throat and mouth at the different hospitals. The study comprises the data from the different microorganisms, namely bacteria, virus, fungi and parasites. The following microorganisms were analysed.

2.2.1 Gram-positive bacteria

- *Staphylococcus* (Staphylococcus *aureus, staphylococcus saprophyticus* and Coagulase negative staphylococcus)
- *Streptococcus* (*Streptococcus pneumonia, Streptococcus viridans, Streptococcus pyogenes, Streptococcus agalactiae, Streptococcus bovis, Enterococcus faecalis* and *Enterococcus faecium)*
- *Bacillus cereus*
- *Bacillus subtilis*
- *Bacillus anthracis*
- *Corynebacterium diphtheria*
- *Listeria monocytogenes*
- *Nocardia asteroids*

2.2.2 Gram-negative bacteria

- *Escherichia coli*
- *Klebsiella species*
- *Enterobacter species*
- *Proteus species*

- *Moraxella catarrhalis*
- *Providencia rettgeri*
- *Neisseria gonorrhoeae*
- *Neisseria meningitidis*
- *Morganella morganii*
- *Serratia species*
- *Salmonella typhi*
- *Salmonella enteritidis*
- *Shigella species*
- *Pseudo aeruginosa*
- *Acinetobacter baumannii*
- *Haemophilus species*
- *Vibrio cholera*
- *Campylobacter species*

2.3 MICROSCOPY AND STAINING TECHNIQUES USED TO IDENTIFY THE DATA OBTAINED FOR ANALYSIS

2.3.1 Faeces

Stool samples are observed for the presence of blood, mucus and colour. For diagnosis of gastro-intestinal parasites, the parasites or their eggs/larvae must be recovered from the digestive tract of the human being or from faecal material (Maliwa-Majikijela & Lengau, 2023). The number of parasitic forms in faecal specimens is usually too low to be observed microscopically in direct wet mounts or stained smear preparations (Maliwa-Majikijela & Lengau, 2023); therefore, concentration procedures must be used to detect them. The two most-used techniques are sedimentation and flotation.

2.3.2 Staining technique for Cryptosporidium

Cryptosporidium, Isospora and Cyclospora species are recognized when the patient has severe diarrhoea (Maliwa-Majikijela & Lengau, 2023). Oocysts in clinical specimens are mostly difficult to detect without special staining that is called Modified acid-fast stains, and the procedure is as follows. Firstly, make a thin smear from the stool sample and allow the slide to air dry. Then place the slide in a staining rack, and flood with 100% methanol for 30 seconds. After 30 seconds, tilt the slide to discard methanol and flood the slide with Carbol fuchsin. Gently heat the slide until steam rises (but do not boil) and stain for 5 minutes. Rinse the slide with tap water and thereafter flood the slide with 5% H2SO4 and leave for 30 seconds. Rinse the slide with tap water and then flood the slide with Methylene blue for 30 seconds. Lastly, gently rinse with tap water and allow the slide to air dry. Examine the slide under a 100X objective lens for parasites (Wollbrandt, 2021).

2.3.3 Urine

Urine specimens contain different numbers of parasites (*Trichomonas vaginalis* and *Schistosoma haematobium*); therefore, centrifugation aids in the detection of scanty parasites (Maliwa-Majikijela & Lengau, 2023). The procedure for identification of microbes in urine is as follows. Firstly, mix specimen in a specimen jar by rotation and centrifuge the specimen at 3 000 rpm for 5–10 minutes. After centrifuging the urine, decant supernatant and place a drop of the urine sediment on a microscope slide. Place a cover slip on top of the urine drop and observe the specimen at 40X magnification (Wollbrandt, 2021). The urine sample is observed for the presence of red blood cells, white blood cells, epithelial cells, cysts, bacteria and parasites. When analysing a urine, the person also checks for red cell cast, white cell cast, granular casts, hyaline cast and different crystals (Triple phosphate, calcium oxalate, uric acid). The presence of helminth larvae, eggs and some protozoa is also observed (Maliwa-Majikijela & Lengau, 2023).

2.3.4 STAINING TECHNIQUES FOR TB SMEARS

The Ziehl-Neelsen Procedure (Hot stain) is as follows; firstly, prepare a smear of the sample. Next. heat-fix the cells on a glass microscope slide and flood the slide with carbol fuchsin stain. Heat the slide gently until it steams (5 min). Thereafter, pour off the carbol fuchsin on top of the slide and wash the slide thoroughly with water. After washing the slide with water, decolourize the slide with 3% acid-alcohol (5 min); thereafter, wash the slide thoroughly with water (Wollbrandt, 2021). Flood the slide with methylene blue counterstain for 1 min and wash with water. Lastly, air dry or dry the slide in the oven (Maliwa-Majikijela & Lengau, 2023).

2.3.5 Processing of sputum

Firstly, the macroscopic appearance of the sputum is described by determining whether the sputum is purulent, mucopurulent, mucoid, salivary or bloodstained (Maliwa-Majikijela & Lengau, 2023). The second procedure is to examine the sputum microscopically after doing a Ziehl-Neelsen/Auramine staining procedure for AFB (Wollbrandt, 2021). The third procedure is to culture the specimen, and the purulent part of the sputum is used (Maliwa-Majikijela & Lengau, 2023). Sputum culturing is done on blood agar and then add an optochin disc between the first and second streaking. The optochin disc is used to identify *S. pneumoniae* pathogen, which is sensitive to optochin. When *S. pneumoniae* is sensitive to optochin, a 14-mm zone size will appear around the disc on the plate. Chocolate agar and MacConkey agar are also used to culture sputum (Maliwa-Majikijela & Lengau, 2023). Both blood agar and chocolate agar are incubated anaerobically at 35–37 °C for 18-24 hours, while MacConkey agar is Incubated aerobically at 35–37 °C for 18-24 hours (Wollbrandt, 2021). Colony growth on the plates is examined and reported the following day, and further, antimicrobial sensitivity testing is performed. The organism's identification and antimicrobial susceptibility are done on the Vitek 2 bioMérieux machine (Ballot et al., 2019), and the Vitek 2 breakpoint interpretation is based on the Clinical and Laboratory Standard Institute (CLSI) guidelines (Ballot et al., 2019).

2.3.6 Processing of Nose, Throat and Mouth Specimens

The specimen is firstly examined macroscopically. The specimen is then cultured in blood agar, and on the blood agar, bacitracin disc is added between the first and second streaking (Wollbrandt, 2021). Bacitracin is used to identify pathogens such as *S. pyogenes,* which are bacitracin sensitive. Chocolate agar is also used to culture the specimen (Maliwa-Majikijela & Lengau, 2023). For nose swabs, only blood agar is used, and no disc is required to detect MRSA (Maliwa-Majikijela & Lengau, 2023). Both the blood and chocolate agar are incubated anaerobically at 35–37 °C for 18–24 hours (Maliwa-Majikijela & Lengau, 2023; Wollbrandt, 2021). The specimen is sub-cultured onto agar plates to obtain bacteria colonies that are identified using biochemical testing (Archary et al., 2017). The organism's identification and antimicrobial susceptibility are done on the Vitek 2 bioMérieux machine (Ballot et al., 2019).

2.3.7 Processing of pus

The pus sample is firstly analysed macroscopically, and the appearance of the specimen is reported (Wollbrandt, 2021). The pus is also examined microscopically to check for gram-negative and gram-positive bacteria (Maliwa-Majikijela & Lengau, 2023). A ZN smear is also prepared to check for TB in the pus (Maliwa-Majikijela & Lengau, 2023). The pus specimen is cultured on blood agar, chocolate agar and CNA. These plates are incubated at 35–37 °C in anaerobic conditions for 18–24 hours (Maliwa-Majikijela & Lengau, 2023). The pus is also cultured in MacConkey agar and incubated aerobically at 35–37 °C for 18–24 hours (Wollbrandt, 2021). The following day, the plates are examined for any colony growth and reported, and antimicrobial sensitivity testing is done. The organism's identification and antimicrobial susceptibility are done on the Vitek 2 bioMérieux machine (Ballot et al., 2019).

2.3.8 Processing of stool

Firstly, a macroscopic examination is done on the stool sample, where they check the colour, check whether the stool sample is formed, semi-formed, unformed, watery, and also check for the presence of blood, mucus, pus and the presence of worms (Maliwa-Majikijela & Lengau, 2023). Microscopic examination is the second step done on the sample, where they check for parasites, white blood cells, red blood cells and yeast (Maliwa-Majikijela & Lengau, 2023). Microscopic examination happens on a microscopic slide; approximately 1–2 mg of stool is blended in a drop of normal saline (0.85% NaCl) on the left side of the slide. On the right side of the slide, the stool is blended with Lugol's iodine (Belay et al., 2020). A coverslip is placed on top of the slide and then the slide is scanned under 10x and 40x objective lenses of a light microscope (Belay et al., 2020). A ZN or Auramine stain is also done to check for *Cryptosporidium, Isospora* and *Cyclospora* (Maliwa-Majikijela & Lengau, 2023). XLD, MacConkey with crystal violet plates is used to culture the specimen and these plates are incubated at 35–37 °C in anaerobic conditions for 18–24 hours (Maliwa-Majikijela & Lengau, 2023; Wollbrandt, 2021). Campy agar and Sorbitol MacConkey are also used to culture the sample, Campy agar is incubated at 35–37 °C microaerophilic conditions for 48 hours, while Sorbitol MacConkey is incubated at 35–37 °C in aerobically conditions for 18–24 hours (Wollbrandt, 2021). The following day, the cultures are examined and reported, and antimicrobial sensitivity testing is done (Wollbrandt, 2021). The organism's identification and antimicrobial susceptibility is done on the Vitek 2 bioMérieux machine (Ballot et al., 2019).

2.3.9 Processing of urines

The urine specimen is firstly examined macroscopically and reports the colour of the urine and whether it is clear or cloudy (Wollbrandt, 2021). A wet prep is also done to check for White Blood Cells (WBCs), epithelial cells, Red Blood Cells (RBCs), casts, yeast cells, bacteria and crystals under a microscope (Maliwa-Majikijela & Lengau, 2023). The specimen is then cultured in CLED/Chromogenic media and Muller Hinton agar with *Bacillus* subtilis to check for antimicrobial substances that are present in the urine (Maliwa-Majikijela & Lengau, 2023). The plates are then incubated at 35°C–37 °C in aerobic conditions for 18–24 hours (Wollbrandt, 2021). The following day, the plates are examined for any microbial growth . On the antimicrobial plate, a zone of inhibition around the blank disk indicates the presence of antimicrobial substances, while no zone indicates the absence of antimicrobial substances (Maliwa-Majikijela & Lengau, 2023).

2.3.10 Processing of blood cultures

Clinicians submit blood cultures that are collected in two separate bottles (anaerobic and aerobic) (Furuno et al., 2011). The blood cultures are then placed in a continuous automated detection incubator called (BacTAlert, bioMérieux) (Furuno et al., 2011). When a blood culture is detected as positive by the machine, the bottle is removed from the machine and a gram staining is performed for presumptive identification (Archary et al., 2017). The positive blood culture is then plated on media agar as per the Standard Laboratory Protocol (Furuno et al., 2011). The specimen is cultured on chocolate and blood agar, and the plates are then incubated at 35-37 °C in anaerobic conditions for 18–24 hours (Wollbrandt, 2021). The specimen is also cultured in

MacConkey agar and then incubated at 35–37 °C in aerobic conditions for 18–24 hours (Wollbrandt, 2021). The following day, the plates are examined for any colony growth and reported; antimicrobial sensitivity testing is also done (Maliwa-Majikijela & Lengau, 2023). The organism’s identification and antimicrobial susceptibility are done on the Vitek 2 bioMérieux machine (Ballot et al., 2019).

2.4 DIAGNOSIS OF PULMONARY TUBERCULOSIS

A molecular method called GeneXpert MTB/RIF Ultra assay is mostly used by laboratories to diagnose TB in a patient (Maliwa-Majikijela & Lengau, 2023). The Xpert® MTB/RIF assay is a cartridge-based, automated diagnostic test that can simultaneously identify *Mycobacterium tuberculosis* complex bacteria (MTB) and resistance to rifampicin (RIF) in less than two hours, using the GeneXpert® assay (Maliwa-Majikijela & Lengau, 2023).

CHAPTER 3:
METHODOLOGY AND RESEARCH DESIGN

3.1 RESEARCH PHILOSOPHY

The research philosophy that was applied in this study was positivism. Positivism leads to the observation and recording of clear relationships between events in the external world and people's knowledge of them (Iovino and Tsitsianis., 2020). Positivism is not affected by the nature of the research; therefore, the research has to be independent and use objective methods (Iovino and Tsitsianis., 2020).

With positivist research philosophy, statistical analysis and a regression model can be used to test the impact of:

- Microbial profile prevalence in immunocompromised patients who are hospitalized having TB or are HIV positive in the different hospitals.
- Risk factors that are associated with microbial infections in immunocompromised patients.
- Microbial prevalence rate in HIV-positive patients compared to HIV-negative patients.
- Antibiotic susceptibility pattern of the identified microorganisms.

3.2 RESEARCH APPROACH

In this study, deductivism was the research methodology that was used because measurements were made, analysis was then applied and lastly, a conclusion was drawn (Watson, 2015). With the deductive method, we were able to start a structure that supports the research study's theory and then use regression models to analyse and prove the credibility of these assumptions. Deductive research proceeds from theory to findings (Iovino and Tsitsianis., 2020). This research approach allowed the researchers to produce data that could be interpreted first so that a conclusion could be drawn from the data (Watson, 2015). The data were stored and analysed using an electronic database or statistical package that permitted more sophisticated analysis (Watson, 2015). This method aimed to establish the cause-and-effect relationship between two variables (Ahmad et al., 2019).

3.3 STUDY DESIGN AND SETTING

This was a retrospective, cross-sectional study (Ballot et al., 2019). A cross-sectional study allows the researcher to gather a large amount of data to describe samples and population (Watson, 2015). The data were gathered once and referred to a point of time (Iovino and Tsitsianis., 2020). In this study, the data were from 1 January 2018 to 31 December 2022. All patients who were admitted at the selected sites having underlying diseases such as TB and HIV from 1 January 2018 to 31 December 2022 were selected. The study measured the presence of exposure and disease at one point in time, including repeat patient admissions. Participants were selected regardless of microbial exposure and outcome/disease status. Data were requested from the National Health Laboratory Service Central Data Warehouse. The application to use these was submitted through the Academic Affairs and Research Management System (AARMS) and the data consisted of patients' laboratory results.

3.4 STUDY POPULATION

The study population consisted of patients who were admitted to hospitals from the age of 18 and above. Laboratory records of all the patients' samples that were sent in the laboratory to be examined were reviewed from the NHLS Central Data Warehouse (CDW) in order to get demographic and laboratory results data. The population, with a minimum of 1 200 samples, with 200 from each hospital was categorized into different age groups. All the patients' laboratory results were requested from CDW. Patients' data for this study were included if they met the inclusion criteria and did not meet the exclusion criteria (Li et al., 2021)

The inclusion criteria of the data were that data generated should be from:

- HIV-positive patients with no TB.
- Patients who are HIV negative with TB only.
- Patients who were diagnosed with both TB and HIV.
- All patients who had laboratory results of microorganisms and antimicrobial susceptibility.

The exclusion criteria were:

- Antimicrobial susceptibility was not done on that sample.
- Patients below the age of 18 years.
- Results of patients that were admitted before 1 January 2018 and after 31 December 2022.

3.5 DATA COLLECTION

Data were requested from the NHLS CDW. The data consisted of patients' laboratory results. An application for that was submitted through AARMS. Data on socio-demographic variables (in-depended variable) included:

- Age.
- Sex.
- Diagnosis (TB or HIV).

Associated risk factors included the following:

- Sex.
- Hospital type (district, regional or tertiary).
- ICU patients compared to patients in other wards.
- HIV-positive patients compared to TB patients.
- HIV status (negative compared to positive).
- HIV patients (CD4 count and Viral load)

For every hospital, the following information was investigated**:**

- Prevalence of nosocomial infections according to patient characteristics (sex, age group and diagnosis).
- Risk factors for nosocomial infections.
- Antimicrobial susceptibility to the identified microbes.

Table 3.1: Demographic characteristics of patients with nosocomial infections

Variable	Variable type	Possible values
Age	Binary	18 years and above
Sex	Categorical-binary	Male
		Female
Diagnosis	Categorical-binary **TB Positive**	Yes
		No
	HIV Positive	Yes
		No
	Both TB and HIV Positive	Yes
		No

Table 3.2: Demographic characteristics of patients with nosocomial infections

		Immunocompromised TB positive (n=number of TB-positive patients/N=total number of patients) (%) (n/N)%	***Immunocompromised HIV positive = (n=number of HIV-positive patients/N=total number of patients) (%) (n/N)%***	***Both TB and HIV positive patients***	***All patients***
Age	***18– 27***				
	28– 37				
	38– 47				
	48– 57				
	58– above				
Sex					
Diagnosis					
Ward type					
Hospital type					

Patient in ICU				
HIV status				
TB status				
If HIV Positive (CD4 count)				
If HIV positive (Viral load)				

Table 3.3: risks factors of nosocomial infection.

Variable	Variable type	Possible values
Sex	Categorical-binary	Male
		Female
Hospital type	Categorical-binary	District
		Regional
		Tertiary (including Academic and Provincial)
Patient in ICU	Categorical-binary	Yes
		No
HIV status	Categorical-binary	Positive
		Negative
TB status	Categorical-binary	Positive
		Negative
CD4 count	Categorical-ordinal	Low <200 cells/mm
		Medium 200-500 cells/mm
		High >500 cells/mm
Viral load	Categorical-ordinal	Low <50 copies/mL (undetectable)
		Medium 20-1000 copies/mL (suppressed)
		High >1000 copies/mL

3.6 DOCUMENTATION AND METADATA

The Research Electronic Data Capture (REDCap) website was used to capture and analyse the data as it was a secure web application that meets all the security policies It is password protected with a password only known by the research team members. Data were requested in CSV file format to ensure integrity. Furthermore, from RedCap, the analysis was done in Excel files that were password protected on the completely de-identified data and stored with a reference to a folder different from that with the de-identified and pseudo-anonymous information, although the data were then anonymous. The number was stored in a different file that does not have the metadata of the original study data and identifier. The anonymous data were analysed in Excel to create documents with initials of the principal investigator, the date created, and protected with passwords.

3.7 DATA ANALYSIS

Laboratory data were obtained from the NHLS CDW. The data were analysed through STATA version 13 statistical software for Windows and the results of total microbial profile and antimicrobial susceptibility for each hospital were presented in a table. A summary of the statistical data was made where normally distributed data were summarized using mean and standard deviation. Data that were not normally distributed were then described using medians and interquartile ranges. Categorical variables were summarized using frequencies and proportions. Crosstabulation was used to describe the interaction between each independent variable by each category of dependent variable.

3.8 DATA STORAGE

Data were kept confidential on the principal investigator’s laptop with a secure password and limited access. Data were not shared with anyone outside the research group. The data were de-identified to avoid traceability to any patient before being shared among the research team and only the information required for the research was supplied. Data were captured on Excel and managed through RedCap. The devices were extensively scanned for malware using reputable antivirus software that could interfere with the RedCap system and regular backups were done to ensure safe storage of data. The data will be stored for five years and thereafter destroyed. Should I leave the NHLS/CUT, data under my protection will be deleted and final control will be with the supervisor/CUT or an employee appointed in the event that the supervisor is no longer available.

3.9 ETHICAL CONSIDERATION

According to the Protection of Personal Information Act (POPIA) (RSA, 2013) for researchers, any research involving human participants requires ethical approval from a recognized or constituted research ethics committee. That information is to be protected in accordance with sections 14, 15, and 17 of the National Health Act 61 of 2003 (RSA, 2003) with regard to confidentiality, access to health records and protection of health records. The study obtained ethical clearance from the Ethics committee of the Faculty of Health Sciences, University of Free State, UFS-HSD2024/1404/2801. Permission to use data from the CDW was requested from the National Health Laboratory Service, and the application was submitted through AARMS, Reference Number: PR2455098. Patient information and identities were not used and only information on organisms and mentioned data were utilised. Data were kept confidential with security password and access limited.

3.10 DATA SHARING AND ACCOUNTABILITY

Data supplied by the NHLS were used ethically and solely for the purpose of this research. Confidentiality measures were maintained at a participant and institutional level with no disclosure of personal or confidential information as described by the NHLS policy and POPIA. The data were de-identified to avoid traceability to any patient. Only the information required for the research was supplied. The data used in this study were obtained from routine clinical-care investigations and no further investigations will be required.

Data were not shared with anyone else outside the research group. The principal investigator was responsible for obtaining, storing and protecting the research data according to the POPIA code of conduct and was liable for any non-compliance.

Data will be stored for 5 years and thereafter destroyed. Should the principal investigator (PI) leave the NHLS/CUT, the data will be deleted, and final control will be with the supervisor/CUT or an employee appointed in the event that the supervisor is no longer available.

3.11 EXPECTED OUTCOMES

The study is expected to generate new knowledge of microbial profiles that are prevalent in the different selected hospitals. Results obtained in this study are intended to contribute to the body of knowledge in the health sector, depending on the data outcomes. This study focuses on assessing and outlining any possible risk factors associated with microbial infections in patients receiving treatment in the public health sector.

CHAPTER 4: RESULTS

4.1 DESCRIPTIVE STATISTICS

This section presents the patients' demographic profiles from the six sampled hospitals from 1 January 2018 to 31 December 2022. Frequency tables demonstrate the demographic profiles of the patients, including district name, facility name, age and gender of the patients.

Table 4.1: Frequency distribution per district name

Frequency distribution per district name		
DISTRICT NAME	**Frequency**	**Percentage%**
Frances Baard	28 395	58.4
Lejweleputswa	1 437	3
Mangaung Metro	18 440	37.9
Thabo Mofutsanyana	325	0.7
Total	48 597	100

Table 4.1 above shows a descriptive statistic indicating that the data collected for the study were from the Frances Baard District Municipality in Kimberley in the Northern Cape Province (58.4%). This is followed by the Mangaung Metropolitan Municipality in the Free State Province with 37.9%, Lejweleputswa District Municipality in the Free State Province with 3% and lastly, Thabo Mofutsanyana District Municipality in the Free State Province with 0.7%.

Table 4.2: Frequency distribution per hospital

Frequency distribution per Hospital		
FACILITY NAME	**Frequency**	**Percentage%**
Robert Mangaliso Sobukwe Provincial hospital	28 395	58.4
Bongani Regional Hospital	1 437	3
National District Hospital	1746	3.6
Mofumahadi Manapo Mopeli Regional Hospital	325	0.7
Pelonomi Regional Hospital	6 541	13.5
Universitas Academic hospital	10 153	20.9
Total	48 597	100

Table 4.2 shows the distribution per facilities sampled for this study. The majority of the patients (58.4%) were treated at the Robert Mangaliso Sobukwe provincial Hospital, followed by 20.9% of patients reported to have received treatment at the Universitas Academic hospital, and 13.5% patients who received treatment at the Pelonomi Regional Hospital.

Table 4.3: Frequency distribution per age categories

Frequency distribution per age categories		
AGE TESTED IN YEARS	**Frequency**	**Percentage%**
18–27	9 151	18.8
28–37	13 190	27.1
38–47	12 831	26.4
48–57	7 138	14.7
58–67	3 830	7.9
68–77	1 872	3.9
78–87	409	0.84
88+	103	0.21
Unspecified	73	0.15
Total	48 597	100

Table 4.3 shows the patients' age grouped into categories. The results show that 27.1% of the patients were aged 28–37 years, followed by 26.4% aged 38–47 years and 18.8% of patients aged 18–27 years. Aged 48 and above accounted for 27.7% collectively, including unspecified ages.

Table 4.4: Frequency distribution per gender

Frequency distribution per gender		
GENDER	**Frequency**	**Percentage%**
Male	24 018	49.4
Female	24 257	49.9
Unknown	322	0.7
Total	48 597	100

Table 4.4 shows that 49.4% of the patients in the study were males, while 49.4% of respondents were female. A very small percentage (0.7%) was not classified.

4.2 ADDITIONAL DESCRIPTIVE STATISTICS

The subset of the dataset was further tested for HIV and TB.

Table 4.5: Frequency distribution per TB test outcomes

Frequency distribution per TB test outcomes		
GeneXpert Ultra results	**Frequency**	**Percentage%**
None	755	1.6
Negative TB	43 427	89.4
Positive TB	3 308	6.8
Unknown	851	1.8
Error	256	0.5
Total	48 597	100

Table 4.5 represents patients that were tested for tuberculosis using the GeneXpert Ultra assay, administered at intake. The majority of patients (89.4%) tested negatively for TB, 6.8% tested positively for TB, while 1.8% and 1.6% of patients were either unknown or were not tested, respectively. 0.5% of the patients received test results with errors.

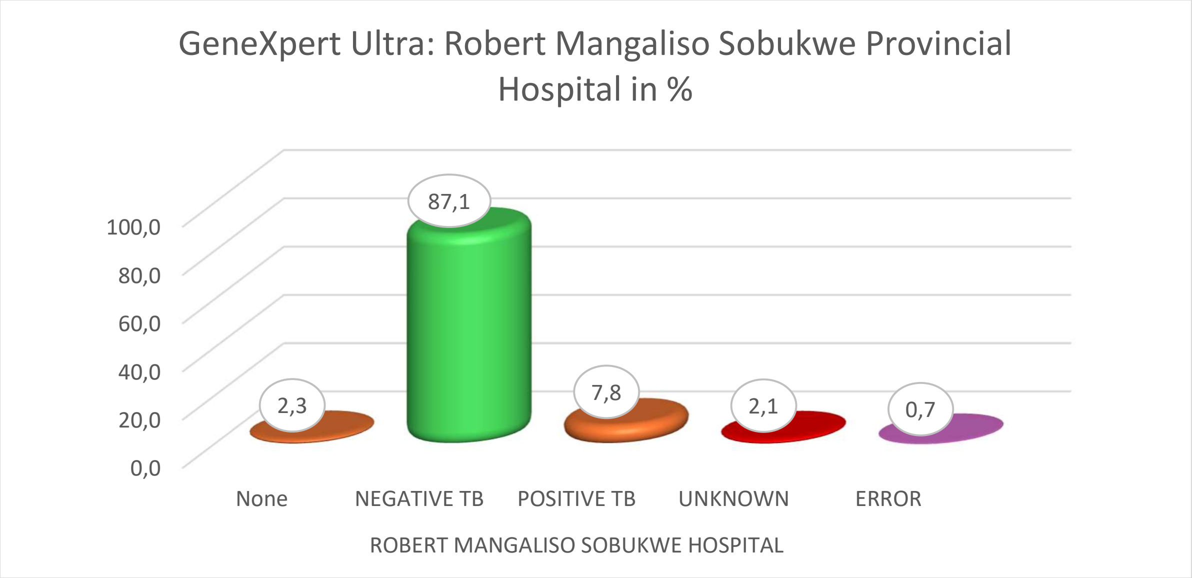
Table 4.6: Frequency distribution of TB GeneXpert Ultra results per hospital

Frequency distribution of TB GeneXpert Ultra results per hospital			
Facility Name	**Status**	**Frequency**	**Percentage%**
Robert Mangaliso Sobukwe Provincial hospital	**None**	650	2.3
	Negative TB	24 726	87.1
	Positive TB	2 226	7.8
	Unknown	606	2.1
	Error	187	0.7
	Total	28 395	100
Bongani Regional Hospital	**None**	1	0.1
	Negative TB	1 259	87.6
	Positive TB	119	8.3
	Unknown	44	3.1
	Error	14	1
	Total	1 437	100

National District Hospital	**None**	13	0.7
	Negative TB	1 538	88.1
	Positive TB	169	9.7
	Unknown	23	1.3
	Error	3	0.2
	Total	1 746	100
Mofumahadi Manapo Mopeli Regional Hospital	**Negative TB**	298	91.7
	Positive TB	23	7.1
	Unknown	3	0.9
	Error	1	0.3
	Total	325	100
Pelonomi Regional Hospital	**None**	85	1.3
	Negative TB	5 931	90.7
	Positive TB	409	6.3
	Unknown	87	1.3
	Error	29	0.4
	Total	6 541	100
Universitas Academic hospital	**None**	6	0.1
	Negative TB	9675	95.3
	Positive TB	362	3.6
	Unknown	88	0.9
	Error	22	0.2
	Total	10153	100

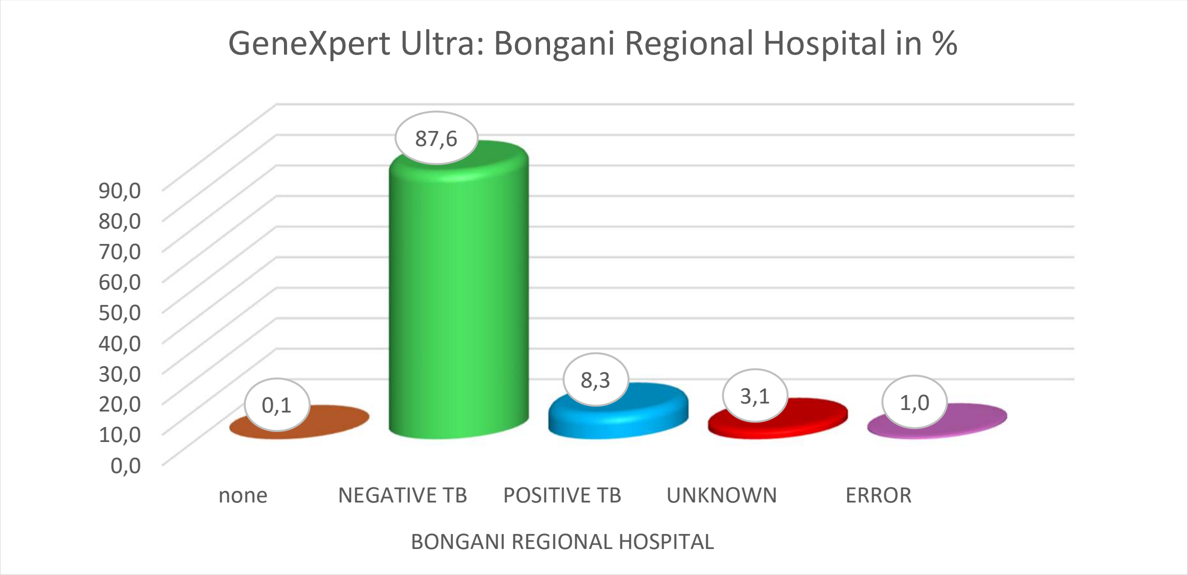
Table 4.6 presents the number of confirmed TB cases as reported by each hospital. 6 541 participants in the study had TB results across the six different hospitals. The table shows that most patients who were admitted to the sampled hospitals tested negatively for TB.

Graph 4.1: Frequency of Robert Mangaliso Sobukwe Provincial Hospital GeneXpert ultra results



The results in Graph 4.1 above report the results generated from data from the Robert Mangaliso Sobukwe Provincial hospital from 1 January 2018 to 31 December 2022. According to Table 4.6 and Graph 4.1, the majority of patients from the Robert Mangaliso Sobukwe Provincial hospital (24 726) tested negatively for TB (87.1%), while 2 226 of the patients tested positively for TB (7.8%). The GeneXpert ultra assay had an error of n=187 (0.7%) patient samples, which means that the samples for those patients had to be tested again N=606 (2.1%) and n=650 (2.3%) patients' TB results were unknown or not available, respectively, upon admission to the hospital.

Graph 4.2: Frequency of Bongani Regional Hospital GeneXpert ultra results



The results in Table 4.6 and Graph 4.2 show that the Bongani Regional Hospital reported 1 259 (87.6%) negative TB cases, in comparison to the 119 (8.3%) positive TB cases from 1 January 2018 to 31 December 2022. The GeneXpert ultra assay had an error in n=14 (1%) patients' samples, which means that the samples for those patients had to be tested again. N=1 (0.1%) and n=44 (2.3%) patients' TB results were not available or unknown, respectively.

Graph 4.3: Frequency of National District Hospital GeneXpert ultra results

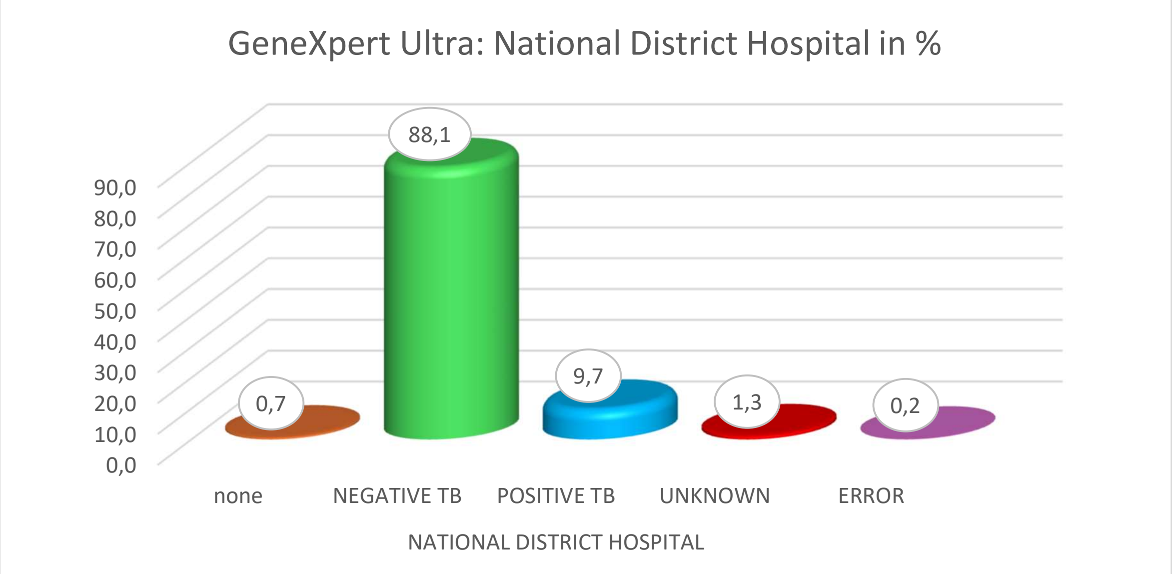
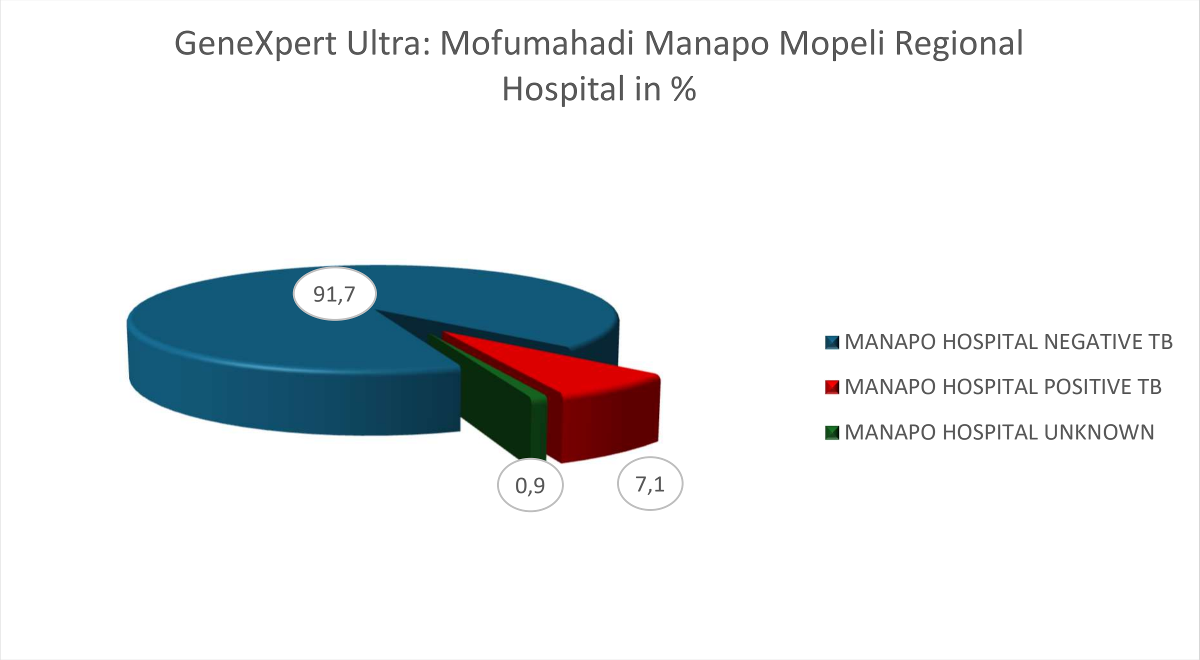


Table 4.6 and Graph 4.3 indicate that the National District Hospital reported 1 538 (88.1%) negative TB cases and 169 (9.7%) positive TB cases of the sampled patients. The GeneXpert ultra assay had an error in n=3 (0.2%) patients' results, which means that the TB test had to be repeated. N=13 (0.7%) and n=23 (1.3%) TB patients' results were either not available or unknown, respectively.

Graph 4.4: Frequency of Mofumahadi Manapo Mopeli Regional Hospital GeneXpert Ultra results



The results in Table 4.6 and Graph 4.4 show that the Mofumahadi Manapo Mopeli Regional Hospital reported 298 (91.7%) TB-negative cases and n=23 (7.1%) TB-positive cases. N=3 (0.9%) patients' TB status were unknown. The GeneXpert Ultra assay had an error of n=1 (0.3%) samples, which means that the samples had to be tested again.

Graph 4.5: Frequency of Pelonomi Regional Hospital GeneXpert Ultra results

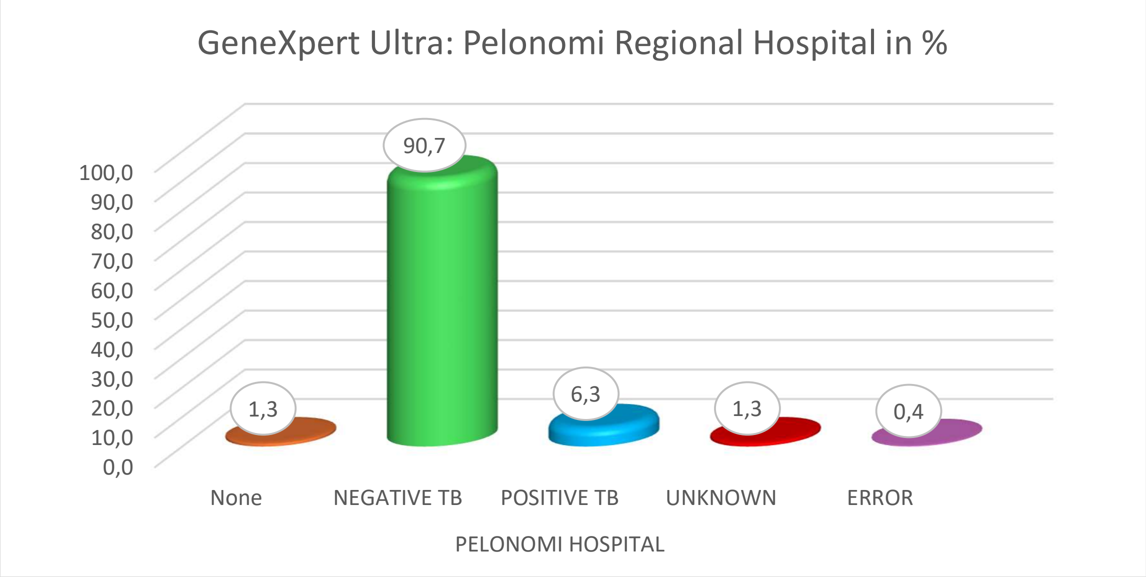
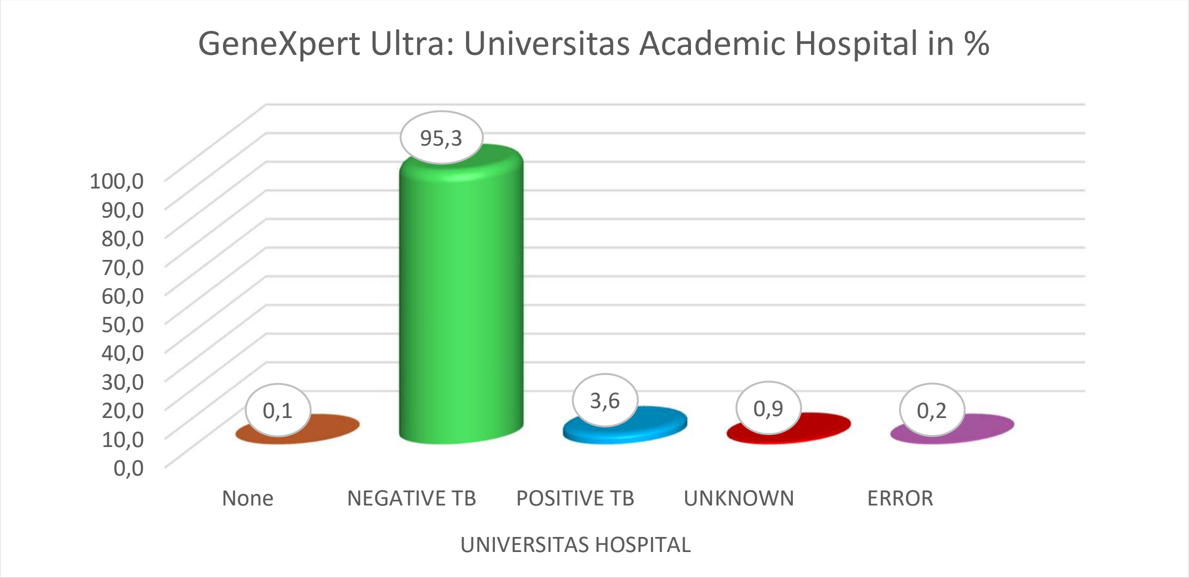


Table 4.6 and Graph 4.5 above indicate that Pelonomi Regional Hospital reported n=5931 (90.7%) TB-negative cases, while n=409 (6.3%) patients tested positively for TB. The GeneXpert ultra assay had an error in n=29 (0.4%) patients' results, which

means that the TB test had to be repeated. N=85 (1.3%) and n=87 (1.3) TB patients' results were either not available or unknown, respectively.

Graph 4.6:Frequency of Pelonomi Regional Hospital GeneXpert Ultra results



The results in Table 4.6 and Graph 4.6 indicate that Universitas Academic hospital reported n=362 (3.6%) TB-positive cases and n=9675 (95.3%) TB-negative cases. The GeneXpert ultra assay had an error in n=22 (0.2%) patients' results, which means that the TB test had to be repeated. N=6 (0.1%) and n=88 (0.8%) TB patients' results were either not available or unknown, respectively.

Table 4.7: Frequency of HIV-½ Rapid (Screen) results

Frequency of HIV-½ RAPID (SCREEN)		
HIV-½ rapid results	**Frequency**	**Percentage%**
None	45 969	94.6
Negative	2 048	4.2
Positive	580	1.2
Total	48 597	100

Table 4.7 above presents the HIV-½ rapid-test results of a subset of the dataset. The table shows that the majority of the patients (94.6%) were not tested for HIV using a rapid-test method, followed by 2% of patients who tested HIV negatively using the rapid-test method, and 1.2% tested HIV positively.

Table 4.8: Frequency of HIV-½ AB/AG (Screen) results

Frequency of HIV-1/2 AB/AG (SCREEN)		
HIV-½ AB/AG results	**Frequency**	**Percentage%**
None	34 347	70.7
Negative	11 869	24.4
Positive	2 090	4.3
Equivocal	291	0.6
Total	48 597	100

Table 4.8 above presents the sampled patients' results for HIV-½ AB/AG tests. Most of the patients (70.7%) were not tested for HIV using the HIV-½ AB/AG test method, while 24.4% tested HIV negative using the HIV-1/2 AB/AG test method. A total of 4.3% tested HIV positive and 0.6% of patients' results were equivocal.

Table 4.9: Frequency of HIV viral load results

Frequency of HIV VIRAL LOAD		
HIV viral load results	**Frequency**	**Percentage%**
None	36 406	74.9
Undetectable < 20–50	3 862	7.9
Low 50 – 10,000	3 347	6.9
Medium 10,001 – 100,000	1 683	3.5
High > 100,000	3 299	6.8
Total	48 597	100

Table 4.9 above presents the patients' viral-load results of the provided dataset. Most of the patients' (74.9%) HIV viral load were not tested, 7.9% had an undetectable viral load, 6.9% had a low HIV viral load, and the remaining 6.8% had a high HIV viral load.

Table 4.10: Frequency of CD4 ARV results

Frequency of CD4 ARV		
CD4 ARV results	**Frequency**	**Percentage %**
None	33 444	68.8
Advanced/severe immunosuppression – <350 cells/mm³	11 346	23.4
Mild immunosuppression – 350–499 cells/mm³	1 766	3.6
No significant immunosuppression – ≥500 cells/mm³	2 041	4.2
Total	48 597	100

Table 4.10 above shows that the majority (68.8%) of the patients' CD4 counts were not tested at intake, 23.4% of patients were reported to have severe immunosuppression with CD4 counts of below 350 cells/mm³, while 4.2% of patients had healthy levels of CD4, with a CD4 count of ≥500 cells/mm³. Only 3.6% of the patients were reported to have mild immunosuppression, with CD4 counts ranging between 350–499 cells/mm^3.

Table 4.11: Frequency of Test Method Name

Frequency of Test Method Name		
Test method name	**Frequency**	**Percentage%**
Culture Urine	12 355	25.4
Automated Culture	20 808	42.8
Culture Catheter Tip	4 124	8.5
Culture Pus	11 310	23.3
Total	48 597	100

Table 4.11 above shows the type of test method that was used to test the specimens collected from patients. Automated cultures were the test method frequently used in the laboratory. It was reported at the rate of 42.8% cases, culture urine and culture pus were used in 25.4% and 23.3% of cases, respectively. Lastly, culture catheter tip was the least frequently used test method, only used in 8.5% of cases.

Table 4.12: Frequency of specimen type collected

Frequency of specimen type		
Specimen type	**Frequency**	**Percentage%**
Abscess (Deep) Aspirate	1	<0.1
Abscess (Superficial) Aspirate	1 887	3.9
Abscess (Superficial) Swab	84	0.2
Arterial Catheter Tip	1 530	3.1
BL, BLC, BLE, PUSW	2	<0.1
Blood Culture	18 668	38.4
Breast Aspiration	2	<0.1
Burn Swab	22	0.5
Catheter Urine	1 416	2.9
CAVP	12	<0.1
Corneal Scraping	6	<0.1
Dialysis Fluid	2	<0.1
Endotracheal Tube	1	<0.1
Fluid / Aspirate	1 323	2.7
Haemodialysis Catheter Tip	101	0.2
Intravenous Catheter Tip	877	1.8
Midstream Urine	2 950	6.1
Peritoneal Dialysis Fluid	380	0.8
Sputum	3	<0.1
Swab (Superficial)	7 580	15.6
Tenckhoff Catheter Tip	1 338	2.8
Tracheal Aspirate	1	<0.1
Urinary Catheter Tip	1	<0.1
Urine	8 036	16.5
Ventricular Catheter Tip, Cerebral	2	<0.1
Ventriculoperitoneal Shunt	110	0.2
Wound Swab	1 598	3.3
Wound Aspirate	83	0.2
Unknown	581	1.2
Total	48 597	100

Table 4.12 shows the profile of specimen types that were collected from the sample population. The table shows that blood cultures accounted for 38.4% of all specimens collected. Abscess (Deep) Aspirate, Endotracheal Tube, Tracheal Aspirate, and Urinary Catheter Tip specimens were reported to be the least collected specimens, accounting for less than 1% each.

Table 4.13: Frequency of the top-10 microorganism's names

Frequency of the top 10 microorganisms name		
Microorganism's name	**Frequency**	**Percentage%**
Escherichia Coli	4 451	16.9
Staphylococcus Aureus	3 836	14.5
Coagulase Negative *Staphylococcus*	3 146	11.9
Klebsiella Pneumoniae* Subsp. *Pneumoniae	2 481	9.4
Staphylococcus Epidermidis	1 372	5.2
Streptococcus Pneumoniae	1 064	4
Proteus Mirabilis	1 062	4
Acinetobacter Baumannii	985	3.7
Pseudomonas Aeruginosa	833	3.2
Enterobacter Cloacae* Subsp. *Cloacae	758	2.9

Table 4.13 above presents the 10 most prevalent microorganisms in the sample population. *Escherichia Coli* was reported in 16.9% cases, while *Staphylococcus aureus* and Coagulase-negative *Staphylococcus* accounted for 14.5% and 11.9% of the cases, respectively.

4.2 CROSSTABULATIONS

Crosstabulations were introduced to investigate the relationship between the variables in this study. Crosstabulation presents the frequency distribution of one variable against another and it offers valuable insights into the potential relationship, patterns and dependencies within the data.

4.3.1 Gender-group comparison

Table 4.14: Crosstabulation of Gender against TB Status (Split by Hospital)

Crosstabulation of Gender against TB Status (Split by Hospital)										
FACILITY NAME	**Gender**	**GENEXPERT ULTRA**						**Total**	**p-value**	**phi**
			None	*TB (-)*	*TB (+)*	*Unknown*	*Error*			
Robert Mangaliso Sobukwe Provincial hospital	**Male**	**N**	358	12 300	1 073	217	76	14 024	0.000	0.055
		%	2.6%	87.7%	7.7%	1.5%	0.5%	100%		
	Female	**N**	284	12 151	1 148	387	109	14 079		
		%	2%	86.3%	8.2%	2.7%	0.8%	100%		
	Unknown	**N**	8	275	5	2	2	292		
		%	2.7%	94.2%	1.7%	0.7%	0.7%	100%		
Bongani Regional Hospital	**Male**	**N**	0	640	26	19	8	693	0.000	0.178
		%	0%	92.4%	3.8%	2.7%	1.2%	100%		
	Female	**N**	1	594	93	25	6	719		
		%	0.1%	82.6%	12.9%	3.5%	0.8%	100%		
	Unknown	**N**	0	25	0	0	0	25		
		%	0%	100%	0%	0%	0%	100%		
National District Hospital	**Male**	**N**	0	743	70	15	2	830	0.016	0.104
		%	0%	89.5%	8.4%	1.8%	0.2%	100%		
	Female	**N**	13	790	99	8	1	911		
		%	1.4%	86.7%	10.9%	0.9%	0.1%	100%		
	Unknown	**N**	0	5	0	0	0	5		
		%	0%	100%	0%	0%	0%	100%		
Mofumahadi Manapo Mopeli Regional Hospital	**Male**	**N**	-	187	15	0	1	203	0.128	0.132
		%	-	92.1%	7.4%	0%	0.5%	100%		
	Female	**N**	-	111	8	3	0	122		
		%	-	91%	6.6%	2.5%	0%	100%		
Pelonomi Regional Hospital	**Male**	**N**	23	3 115	218	54	20	3 430	0.000	0.066
		%	0.7%	90.8%	6.4%	1.6%	0.6%	100%		
	Female	**N**	62	2 816	191	33	9	3 111		
		%	2%	90.5%	6.1%	1.1%	0.3%	100%		
Universitas Academic hospital	**Male**	**N**	0	4 632	123	73	10	4 838	0.000	0.087
		%	0%	95.7%	2.5%	1.5%	0.2%	100%		
	Female	**N**	6	5 043	239	15	12	5 315		
		%	0.1%	94.9%	4.5%	0.3%	0.2%	100%		

The crosstabulation presented in Table 4.14 shows that at all the six above-mentioned hospitals, the majority of the samples had tested negatively for TB at intake, both male, female and those whose genders were unknown.

- From the Robert Mangaliso Sobukwe Provincial Hospital, the report indicates that most patients tested negatively for TB (males: 87.7%, females: 86.3%). Among the patients who were tested, TB prevalence was slightly higher in females (8.2%) than in males (7.7%).
- Furthermore, most patients from the Bongani Regional Hospital tested negatively for TB (males: 92.4%, females: 82.6%). TB prevalence was higher in females (12.9%) compared to males (3.8%).
- Most patients from the National District Hospital tested negatively for TB (males: 89.5%, females: 86.7%). TB prevalence was reported to be higher in females (10.9%) than in males (8.4%).
- From the Mofumahadi Manapo Mopeli Regional Hospital, the majority of patients tested negatively for TB (males: 92.1%, females: 91%). TB prevalence was slightly higher in males (7.4%) than in females (6.6%).
- In addition, most patients from the Pelonomi Regional Hospital tested negatively for TB (males: 90.8%, females: 90.5%). TB prevalence was marginally higher in males (6.4%) compared to females (6.1%).
- Lastly, the majority of patients from the Universitas Academic Hospital tested negatively for TB (males: 95.7%, females: 94.9%) and TB prevalence was higher in females (4.5%) compared to males (2.5%).

Table 4.15: Crosstabulation of Gender against HIV Status (Split by Hospital)

Crosstabulation of Gender against HIV Status (Split by Hospital)

FACILITY NAME	**Gender**		**HIV-1/2 AB/AG (SCREEN)**				**Total**	**p-value**	**phi**
			None	*HIV (-)*	*HIV (+)*	*Equivocal*			
Robert Mangaliso Sobukwe Provincial hospital	Male	N	8584	4817	566	57	14024	000	0.118
		%	61.2%	34.3%	4%	0.4%	100%		
	Female	N	9943	3474	615	47	14079		
		%	70.6%	24.7%	4.4%	0.3%	100%		
	Unknown	N	255	31	2	4	292		
		%	87.3%	10.6%	0.7%	1.4%	100%		
Bongani Regional Hospital	Male	N	596	52	45	-	693	000	0.346
		%	86%	7.5%	6.5%	-	100%		
	Female	N	666	44	9	-	719		
		%	92.6%	6.1%	1.3%	-	100%		
	Unknown	N	7	18	0	-	25		
		%	28%	72%	0%	-	100%		
National District Hospital	Male	N	723	58	46	3	830	000	0.118
		%	87.1%	7%	5.5%	0.4%	100%		
	Female	N	847	22	41	1	911		
		%	93%	2.4%	4.5%	0.1%	100%		
	Unknown	N	5	0	0	0	5		
		%	100%	0%	0%	0%	100%		
Mofumahadi Monapo Mopeli Regional Hospital	Male	N	134	58	9	2	203	006	0.195
		%	66%	28.6%	4.4%	1%	100%		
	Female	N	102	17	3	0	122		
		%	83.6%	13.9%	2.5%	0%	100%		
Pelonomi Regional Hospital	Male	N	2 496	648	241	45	3 430	0.664	016
		%	72.8%	18.9%	7%	1.3%	100%		
	Female	N	2 303	568	199	41	3 111		
		%	74%	18.3%	6.4%	1.3%	100%		
Universitas academic hospital	Male	N	3 671	907	181	79	4 838	000	089
		%	75.9%	18.7%	3.7%	1.6%	100%		
	Female	N	4 015	1 155	133	12	5 315		
		%	75.5%	21.7%	2.5%	0.2%	100%		

- Table 4.15 shows that the highest proportion of both male (61.2%) and female (70.6%) patients from the Robert Mangaliso Sobukwe Provincial hospital had no recorded HIV test result. In those who tested, the HIV prevalence was notably higher in females (4.4%) than in males (4%).

- Most patients from the Bongani Regional Hospital had no recorded HIV test results (males: 86%, females: 92.6%). Among the patients who tested, HIV prevalence was higher in males (6.5%) than in females (1.3%).

- Furthermore, from the National District Hospital, the majority of patients, both male (87.1%) and female (93%), had no recorded HIV test result, while in those who tested, HIV prevalence was higher in males (5.5%) than in females (4.5%).
- Most patients from the Mofumahadi Manapo Mopeli Regional Hospital had no recorded HIV test result, and those who tested for HIV were found at this rate, males: 66%, females: 83.6%. Among the patients who tested, HIV prevalence was higher in males (4.4%) compared to females (2.5%).
- The largest record of both male (72.8%) and female (74%) patients from the Pelonomi Regional Hospital had no recorded HIV test result, while in those who tested, HIV prevalence was slightly higher in males (7%) than in females (6.4%).
- Lastly, most patients from the Universitas Academic hospital had no recorded HIV test result (males: 75.9%, females: 75.5%). Among those who tested, HIV prevalence was higher in males (3.7%) than in females (2.5%).

Table 4.16: Crosstabulation of HIV-1/2 AB/AG (Screen) against HIV viral load (Split by gender)

Crosstabulation of HIV-1/2 AB/AG (SCREEN) against HIV Viral Load (Split by Gender)										
GENDER	**HIV-1/2 AB/AG (SCREEN)**		**HIV VIRAL LOAD**					**Total**	**p-value**	**phi**
			none	*< 20–50*	*50 – 10,000*	*10,001 – 100,000*	*> 100,000*			
Male	**None**	**N**	10 965	1649	1534	835	1221	16204	0.00	0.366
		%	67.7%	10.2%	9.5%	5.2%	7.5%	100%		
	HIV (-)	**N**	6 540	0	0	0	0	6 540		
		%	100%	0%	0%	0%	0%	100%		
	HIV (+)	**N**	1 083	2	0	0	3	1 088		
		%	99.5%	0.2%	0%	0%	0.3%	100%		
	Equivocal	**N**	186	0	0	0	0	186		
		%	100%	0%	0%	0%	0%	100%		
Female	**None**	**N**	11 013	2 202	1 806	832	2 023	17 876	0.00	0.375
		%	61.6%	12.3%	10.1%	4.7%	11.3%	100%		
	HIV (-)	**N**	5 280	0	0	0	0	5 280		
		%	100%	0%	0%	0%	0%	100%		
	HIV (+)	**N**	998	0	0	2	0	1 000		
		%	99.8%	0%	0%	0.2%	0%	100%		

	Equivocal	**N**	101	0	0	0	0	101		
		%	100%	0%	0%	0%	0%	100 %		
Unknown	**None**	**N**	185	9	7	14	52	267	0.31	0.265
		%	69.3%	3.4%	2.6%	5.2%	19.5%	100 %		
	HIV (-)	**N**	49	0	0	0	0	49		
		%	100%	0%	0%	0%	0%	100 %		
	HIV (+)	**N**	2	0	0	0	0	2		
		%	100%	0%	0%	0%	0%	100 %		
	Equivocal	**N**	4	0	0	0	0	4		
		%	100%	0%	0%	0%	0%	100 %		

Table 4.16 reveals that in both gender groups (male and female), the majority of the sample were not tested for HIV using the HIV-1/2 AB/AG test; therefore, producing a status “none”. Among the men who were sampled but were not tested for HIV via the HIV-1/2 AB/AG screen as they were already known HIV-positive patients, 10.2% had viral loads less than 50 copies/mL, indicating viral suppression or undetectable levels, while 7.5% had viral loads exceeding 100 000 copies/mL, indicating high levels of HIV in the blood. Females who were HIV positive, 0.2% had an HIV viral load between 10 001 and 100 000 copies/mL. The majority of patients (99.8%) had no recorded viral load result at intake. Among individuals of unknown gender who were not tested for HIV via the HIV-1/2 AB/AG screen, 19.5% had viral loads greater than 100 ,000 copies/mL, which indicates a high level of HIV in the blood. However, only 3.4% had very low viral loads (<50 copies/mL), which is consistent with viral suppression or undetectable

Table 4.17: Crosstabulation of HIV-1/2 AB/AG (SCREEN) against CD4 ARV (Split by Gender)

Crosstabulation of HIV-1/2 AB/AG (SCREEN) against CD4 ARV (Split by Gender)

GENDER	**HIV-1/2 AB/AG (Screen)**		**CD4 ARV**				**Total**	**p-value**	**phi**
			None	*<350 cells/mm^3*	*350–499 cells/mm^3*	*≥500 cells/m^3*			
Male	**None**	**N**	9 169	5 486	783	765	16 203	000	0.445
		%	56.6%	33.9%	4.8%	4.7%	100%		
	HIV (-)	**N**	6 539	0	1	0	6 540		

		%	100%	0%	02%	0%	100%		
	HIV (+)	**N**	1 075	13	0	0	1 088		
		%	98.8%	1.2%	0%	0%	100%		
	Equivocal	**N**	186	0	0	0	186		
		%	100%	0%	0%	0%	100%		
Female	**None**	**N**	9 943	5 727	958	1 248	17 876	000	0.413
		%	55.6%	32%	5.4%	7%	100%		
	HIV (-)	**N**	5 263	8	0	9	5 280		
		%	99.7%	0.2%	0%	0.2%	100%		
	HIV (+)	**N**	992	7	0	1	1 000		
		%	99.2%	0.7%	0%	0.1%	100%		
	Equivocal	**N**	101	0	0	0	101		
		%	100%	0%	0%	0%	100%		
Unknown	**None**	**N**	121	105	24	17	267	000	0.413
		%	45.3%	39.3%	9%	6.4%	100%		
	HIV (-)	**N**	49	0	0	0	49		
		%	100%	0%	0%	0%	100%		
	HIV (+)	**N**	2	0	0	0	2		
		%	100%	0%	0%	0%	100%		
	Equivocal	**N**	4	0	0	0	4		
		%	100%	0%	0%	0%	100%		

The results in Table 4.17 show that in both gender groups (male and female), the majority of the samples were not tested for ARV compliance as determined by the ARV CD4 count, resulting in a “none” outcome. Among men with an unknown HIV status, in addition to the 56.6% whose CD4 counts were not taken, 33.9% of male patients with an unknown HIV status had CD4 counts of less than 350 cells/mm³, while only 1.2% of HIV-positive men had CD4 counts below 350 cells/mm³. Therefore this could suggest possible non-compliance with antiretroviral treatment (ART). Among HIV-positive females, 0.1% had an ARV CD4 count above 500 cells/mm³; therefore, this indicates compliance with ARV treatment. In contrast, only 0.2% of the female sample tested positively for HIV, but had CD4 counts below 350 cells/mm³. This also indicates a possible non-compliance with ARV treatment. Among the unknown gender category, patients who were not tested for HIV, 39.3% had CD4 counts below 350 cells/mm³, suggesting that ARV treatment was present only in trace amounts in their systems. This is in contrast to another 6.4% in the same group who had an unknown HIV status, but with CD4 counts ≥500 cells/mm³, indicating treatment compliance.

4.3.2 Age-group comparisons

Table 4.18: Facility Name-GeneXpert Ultra results per age group

Facility Name-GeneXpert Ultra results per age group										
	Age Group		*None*	*NEGATIVE TB*	*POSITIVE TB*	*UNKNOWN*	*ERROR*	*Total*	**p-value**	**phi**
Robert Mangaliso Sobukwe Provincial Hospital	**18–27**	**N**	162	5 267	377	143	2	5951	0.000	0.141
		%	2.7%	88.5%	6.3%	2.4%	0%	100%		
	28-37	**N**	175	5 899	s843	225	115	7 257		
		%	2.4%	81.3%	11.6%	3.1%	1.6%	100%		
	38-47	**N**	149	6 744	662	108	37	7 700		
		%	1.9%	87.6%	8.6%	1.4%	0.5%	100%		
	48-57	**N**	108	3 911	182	57	14	4 272		
		%	2.5%	91.5%	4.3%	1.3%	0.3%	100%		
	58-67	**N**	41	1 863	108	68	15	2 095		
		%	2%	88.9%	5.2%	3.2%	0.7%	100%		
	68-77	**N**	15	802	32	3	2	854		
		%	1.8%	93.9%	3.7%	0.4%	0.2%	100%		
	78-87	**N**	0	200	20	2	2	224		
		%	0%	89.3%	8.9%	0.9%	0.9%	100%		
	88+	**N**	0	40	2	0	0	42		
		%	0%	95.2%	4.8%	0%	0%	100%		
Bongani Regional Hospital	**18-27**	**N**	0	260	30	11	0	301	0.000	0.293
		%	0%	86.4%	10%	3.7%	0%	100%		
	28-37	**N**	1	347	46	18	0	412		
		%	0.2%	84.2%	11.2%	4.4%	0%	100%		
	38-47	**N**	0	154	27	9	3	193		
		%	0%	79.8%	14%	4.7%	1.6%	100%		
	48-57	**N**	0	194	9	1	6	210		
		%	0%	92.4%	4.3%	0.5%	2.9%	100%		
	58-67	**N**	0	236	5	2	0	243		
		%	0%	97.1%	2.1%	0.8%	0%	100%		
	68-77	**N**	0	42	1	3	1	47		

		%	0%	89.4%	2.1%	6.4%	2.1%	100%		
	78–87	**N**	0	23	1	0	4	28		
		%	0%	82.1%	3.6%	0%	14.3%	100%		
	88+	**N**	0	2	0	0	0	2		
		%	0%	100%	0%	0%	0%	100%		
	Missing	**N**	0	1	0	0	0	1		
		%	0%	100%	0%	0%	0%	100%		
National District Hospital	**18–27**	**N**	13	192	27	0	0	232	0.000	0.331
		%	5.6%	82.8%	11.6%	0%	0%	100%		
	28–37	**N**	0	388	61	3	1	453		
		%	0%	85.7%	13.5%	0.7%	0.2%	100%		
	38–47	**N**	0	353	39	7	1	400		
		%	0%	88.3%	9.8%	1.8%	0.3%	100%		
	48–57	**N**	0	240	29	2	0	271		
		%	0%	88.6%	10.7%	0.7%	0%	100%		
	58–67	**N**	0	205	8	2	0	215		
		%	0%	95.3%	3.7%	0.9%	0%	100%		
	68–77	**N**	0	124	4	3	1	132		
		%	0%	93.9%	3%	2.3%	0.8%	100%		
	78–87	**N**	0	29	0	6	0	35		
		%	0%	82.9%	0%	17.1%	0%	100%		
	88+	**N**	0	7	1	0	0	8		
		%	0%	87.5%	12.5%	0%	0%	100%		
Mofumahadi Manapo Mopeli Regional Hospital	**18–27**	**N**	-	55	10	0	0	65	0.029	0.328
		%	-	84.6%	15.4%	0%	0%	100%		
	28–37	**N**	-	121	4	0	0	125		
		%	-	96.8%	3.2%	0%	0%	100%		
	38–47	**N**	-	47	4	3	0	54		
		%	-	87%	7.4%	5.6%	0%	100%		
	48–57	**N**	-	38	1	0	1	40		
		%	-	95%	2.5%	0%	2.5%	100%		
	58–67	**N**	-	22	3	0	0	25		
		%	-	88%	12%	0%	0%	100%		
	68–77	**N**	-	8	1	0	0	9		
		%	-	88.9%	11.1%	0%	0%	100%		
	78–87	**N**	-	6	0	0	0	6		
		%	-	100%	0%	0%	0%	100%		

	88+	**N**	-	1	0	0	0	1		
		%	-	100%	0%	0%	0%	100%		
Pelonomi Regional Hospital	**18–27**	**N**	25	1 006	87	32	5	1 155	000	0.164
		%	2.2%	87.1%	7.5%	2.8%	0.4%	100%		
	28–37	**N**	9	2 022	109	18	12	2 170		
		%	0.4%	93.2%	5%	0.8%	0.6%	100%		
	38–47	**N**	12	1 275	96	28	5	1 416		
		%	0.8%	90%	6.8%	2%	0.4%	100%		
	48–57	**N**	29	747	79	0	7	862		
		%	3.4%	86.7%	9.2%	0%	0.8%	100%		
	58–67	**N**	5	576	26	1	0	608		
		%	0.8%	94.7%	4.3%	0.2%	0%	100%		
	68–77	**N**	3	245	10	7	0	265		
		%	1.1%	92.5%	3.8%	2.6%	0%	100%		
	78–87	**N**	0	54	2	1	0	57		
		%	0%	94.7%	3.5%	1.8%	0%	100%		
	88+	**N**	2	6	0	0	0	8		
		%	25%	75%	0%	0%	0%	100%		
Universitas Academic hospital	**18–27**	**N**	0	1 329	92	25	1	1 447	0.000	0.149
		%	0%	91.8%	6.4%	1.7%	0.1%	100%		
	28–37	**N**	6	2 600	141	17	9	2 773		
		%	0.2%	93.8%	5.1%	0.6%	0.3%	100%		
	38–47	**N**	0	2 979	69	19	1	3 068		
		%	0%	97.1%	2.2%	0.6%	0%	100%		
	48–57	**N**	0	1 434	35	3	11	1 483		
		%	0%	96.7%	2.4%	0.2%	0.7%	100%		
	58–67	**N**	0	623	19	2	0	644		
		%	0%	96.7%	3%	0.3%	0%	100%		
	68–77	**N**	0	537	6	22	0	565		
		%	0%	95%	1.1%	3.9%	0%	100%		
	78–87	**N**	0	59	0	0	0	59		
		%	0%	100%	0%	0%	0%	100%		
	88+	**N**	0	42	0	0	0	42		
		%	0%	100%	0%	0%	0%	100%		
	Missing	**N**	0	72	0	0	0	72		
		%	0%	100%	0%	0%	0%	100%		

Table 4.18 shows that the highest prevalence of TB-positive cases occurred among patients aged 28–37 years (11.6%), followed by those that are aged 38–47 years (8.6%). However, the majority of patients in all age groups tested TB-negative at intake.

At the Bongani Regional Hospital, the highest prevalence of TB-positive cases occurred among patients between the ages of 38 and 47 years (14%). The highest proportion of TB-negative cases was observed in patients aged 48–57 years (92.4%).

At the Mofumahadi Manapo Mopeli Regional Hospital, the highest prevalence of TB-positive cases occurred among patients aged 18–27 years (15.4%) and the highest proportion of TB-negative results was observed among patients aged between 78–87 years and 88+ years (100%). In addition, these groups comprised smaller proportions of the sample.

The last crosstabulation between patient age group and patient TB status, as determined by the GeneXpert Ultra assay TB test, was compared across the Universitas Academic hospital, where the highest proportion of positive cases amongst age groups occurred among the patients aged 18–27 years (6.4%), and the highest proportion of TB-negative results was observed among patients aged 78-87 years and 88+ years old (100%), following the trend of the Mofumahadi Manapo Mopeli Regional Hospital. Across all six mentioned hospitals in the sample, the crosstabulation between patient age group and TB status indicated that the highest prevalence of TB-positive results were more likely to occur in younger to middle-aged groups, with the peak that ranges from 6.4% (18–37 years) to 15.4% and 14% (38–47 years).

*Table 4.19: AGE-TESTED_YEARS * HIV-1/2 AB/AG (SCREEN)*

AGE_TESTED_YEARS * HIV-1/2 AB/AG (SCREEN)									
FACILITY NAME	**Age Group**		**None**	**NEGATIVE**	**POSITIVE**	**EQUIVOCAL**	**Total**	**z**	**phi**
Robert Mangaliso Sobukwe Provincial hospital	**18–27**	**N**	3 902	1 867	151	31	5 951	0.000	0.135
		%	65.6%	31.4%	2.5%	0.5%	100%		
	28–37	**N**	4 868	2 021	345	23	7257		
		%	67.1%	27.8%	4.8%	0.3%	100%		
	38–47	**N**	5 563	1 749	356	32	7 700		
		%	72.2%	22.7%	4.6%	0.4%	100%		
	48–57	**N**	2593	1 472	196	11	4 272		
		%	60.7%	34.5%	4.6%	0.3%	100%		
	58–67	**N**	1314	666	108	7	2 095		
		%	62.7%	31.8%	5.2%	0.3%	100%		
	68–77	**N**	396	432	22	4	854		
		%	46.4%	50.6%	2.6%	0.5%	100%		
	78–87	**N**	121	98	5	0	224		
		%	54%	43.8%	2.2%	0%	100%		
	88+	**N**	25	17	0	0	42		
		%	59.5%	40.5%	0%	0%	100%		
Bongani Regional Hospital	**18–27**	**N**	263	30	8	-	301	0.000	0.276
		%	87.4%	10%	2.7%	-	100%		
	28–37	**N**	386	19	7	-	412		
		%	93.7%	4.6%	1.7%	-	100%		
	38-47	**N**	172	11	10	-	193		
		%	89.1%	5.7%	5.2%	-	100%		
	48–57	**N**	175	25	10	-	210		
		%	83.3%	11.9%	4.8%	-	100%		
	58–67	**N**	215	9	19	-	243		
		%	88.5%	3.7%	7.8%	-	100%		
	68–77	**N**	41	6	0	-	47		
		%	87.2%	12.8%	0%	-	100%		
	78–87	**N**	14	14	0	-	28		
		%	50%	50%	0%	-	100%		
	88+	**N**	2	0	0	-	2		
		%	100%	0%	0%	-	100%		
	Missing	**N**	1	0	0	-	1		
		%	100%	0%	0%	-	100%		
National District Hospital	**18–27**	**N**	205	12	15	0	232	0.000	0.175
		%	88.4%	5.2%	6.5%	0%	100%		
	28–37	**N**	401	26	25	1	453		
		%	88.5%	5.7%	5.5%	0.2%	100%		
	38–47	**N**	375	10	12	3	400		
		%	93.8%	2.5%	3%	0.8%	100%		
	48–57	**N**	239	5	27	0	271		
		%	88.2%	1.8%	10%	0%	100%		
	58–67	**N**	189	18	8	0	215		
		%	87.9%	8.4%	3.7%	0%	100%		
	68–77	**N**	124	8	0	0	132		
		%	93.9%	6.1%	0%	0%	100%		
	78–87	**N**	34	1	0	0	35		
		%	97.1%	2.9%	0%	0%	100%		
	88+	**N**	8	0	0	0	8		
		%	100%	0%	0%	0%	100%		
Mofumahadi Manapo	**18–27**	**N**	60	5	0	0	65	0.000	0.570
		%	92.3%	7.7%	0%	0%	100%		

Mopeli Regional Hospital	**28–37**	**N**	58	58	9	0	125		
		%	46.4%	46.4%	7.2%	0%	100%		
	38–47	**N**	49	2	3	0	54		
		%	90.7%	3.7%	5.6%	0%	100%		
	48–57	**N**	32	8	0	0	40		
		%	80%	20%	0%	0%	100%		
	58–67	**N**	21	2	0	2	25		
		%	84%	8%	0%	8%	100%		
	68–77	**N**	9	0	0	0	9		
		%	100%	0%	0%	0%	100%		
	78–87	**N**	6	0	0	0	6		
		%	100%	0%	0%	0%	100%		
	88+	**N**	1	0	0	0	1		
		%	100%	0%	0%	0%	100%		
Pelonomi Regional Hospital	**18–27**	**N**	870	174	83	28	1155	0.000	0.131
		%	75.3%	15.1%	7.2%	2.4%	100%		
	28–37	**N**	1548	421	157	44	2170		
		%	71.3%	19.4%	7.2%	2%	100%		
	38-47	**N**	1028	288	94	6	1416		
		%	72.6%	20.3%	6.6%	0.4%	100%		
	48–57	**N**	603	173	80	6	862		
		%	70%	20.1%	9.3%	0.7%	100%		
	58–67	**N**	474	117	15	2	608		
		%	78%	19.2%	2.5%	0.3%	100%		
	68–77	**N**	223	39	3	0	265		
		%	84.2%	14.7%	1.1%	0%	100%		
	78–87	**N**	45	4	8	0	57		
		%	78.9%	7%	14%	0%	100%		
	88+	**N**	8	0	0	0	8		
		%	100%	0%	0%	0%	100%		
Universitas Academic hospital	**18–27**	**N**	871	434	57	85	1447	0.000	0.327
		%	60.2%	30%	3.9%	5.9%	100%		
	28–37	**N**	2253	476	44	0	2773		
		%	81.2%	17.2%	1.6%	0%	100%		
	38–47	**N**	2504	402	157	5	3068		
		%	81.6%	13.1%	5.1%	0.2%	100%		
	48–57	**N**	923	538	22	0	1483		
		%	62.2%	36.3%	1.5%	0%	100%		
	58–67	**N**	528	99	16	1	644		
		%	82%	15.4%	2.5%	0.2%	100%		
	68-77	**N**	463	96	6	0	565		
		%	81.9%	17%	1.1%	0%	100%		
	78-87	**N**	53	6	0	0	59		
		%	89.8%	10.2%	0%	0%	100%		
	88+	**N**	42	0	0	0	42		
		%	100%	0%	0%	0%	100%		
	Missing	**N**	49	11	12	0	72		
		%	68.1%	15.3%	16.7%	0%	100%		

Table 4.19 shows that at the Robert Mangaliso Sobukwe Provincial Hospital, the highest prevalence of HIV-positive cases occurred in patients aged between 58 and 67 years (5.2%). The highest HIV-negative results were obtained among patients aged 68–77 years (50.6%).

- At the Bongani Regional Hospital, the crosstabulation between patient age group and HIV status, as determined by the HIV-1/2 AB/AG Screen test, was conducted and the highest prevalence of HIV-positive cases occurred in patients between the ages of 78 and 87 years (50%).
- At the National District Hospital, the highest prevalence of HIV-positive cases occurred in patients aged 48–57 years (10%) and the highest prevalence of HIV-negative results was observed in patients aged 58–67 years (8.4%).
- At Mofumahadi Manapo Mopeli Regional Hospital, the highest prevalence of HIV-positive cases occurred among patients aged 28–37 years (7.2%), while the highest proportion of HIV-negative results was also observed in the same age group (46.4%).
- At Pelonomi Regional Hospital, the highest prevalence of HIV-positive results occurred among patients aged 78–87 years (14%) and the highest proportion of HIV-negative results was observed among patients aged 38–47 years (20.3%).
- Lastly, at the Universitas Academic Hospital, the highest prevalence of HIV-positive cases occurred among patients aged 38–47 years (5.1%), while the highest proportion of HIV-negative results was observed among patients' between 48–57years at (36.3%).

Table 4.20: The cross-tabulation between patient age group and HIV viral load

Age Group	**HIV-1/2 AB/AG (Screen)**		**HIV VIRAL LOAD**					**Total**
			none	*< 20–50*	*50 – 10,000*	*10,001 – 100,000*	*> 100,000*	
18-27	**none**	**N**	4 060	308	493	369	941	6171
		%	65.8%	5%	8%	6%	15.2%	100%
	HIV Negative	**N**	2 522	0	0	0	0	2 522
		%	100%	0%	0%	0%	0%	100%
	HIV Positive	**N**	314	0	0	0	0	314
		%	100%	0%	0%	0%	0%	100%
	Equivocal	**N**	144	0	0	0	0	144
		%	100%	0%	0%	0%	0%	100%
28-37	**none**	**N**	5 534	1 279	1 117	526	1 058	9 514
		%	58.2%	13.4%	11.7%	5.5%	11.1%	100%
	HIV Negative	**N**	3 021	0	0	0	0	3 021
		%	100%	0%	0%	0%	0%	100%
	HIV Positive	**N**	584	0	0	2	1	587
		%	99.5%	0%	0%	0.3%	0.2%	100%
	Equivocal	**N**	68	0	0	0	0	68
		%	100%	0%	0%	0%	0%	100%
38-47	**none**	**N**	5 733	1 344	1 249	572	793	9 691

		%	59.2%	13.9%	12.9%	5.9%	8.2%	100%
	HIV Negative	**N**	2 462	0	0	0	0	2 462
		%	100%	0%	0%	0%	0%	100%
	HIV Positive	**N**	630	0	0	0	2	632
		%	99.7%	0%	0%	0%	0.3%	100%
	Equivocal	**N**	46	0	0	0	0	46
		%	100%	0%	0%	0%	0%	100%
48-57	**none**	**N**	3 182	560	318	150	355	4 565
		%	69.7%	12.3%	7%	3.3%	7.8%	100%
	HIV Negative	**N**	2 221	0	0	0	0	2 221
		%	100%	0%	0%	0%	0%	100%
	HIV Positive	**N**	335	0	0	0	0	335
		%	100%	0%	0%	0%	0%	100%
	Equivocal	**N**	17	0	0	0	0	17
		%	100%	0%	0%	0%	0%	100%
58-67	**none**	**N**	2 117	278	153	57	136	2 741
		%	77.2%	10.1%	5.6%	2.1%	5%	100%
	HIV Negative	**N**	911	0	0	0	0	911
		%	100%	0%	0%	0%	0%	100%
	HIV Positive	**N**	164	2	0	0	0	166
		%	98.8%	1.2%	0%	0%	0%	100%
	Equivocal	**N**	12	0	0	0	0	12
		%	100%	0%	0%	0%	0%	100%
68-77	**none**	**N**	1 151	75	14	7	9	1 256
		%	91.6%	6%	1.1%	0.6%	0.7%	100%
	HIV Negative	**N**	581	0	0	0	0	581
		%	100%	0%	0%	0%	0%	100%
	HIV Positive	**N**	31	0	0	0	0	31
		%	100%	0%	0%	0%	0%	100%
	Equivocal	**N**	4	0	0	0	0	4
		%	100%	0%	0%	0%	0%	100%
78-87	**none**	**N**	270	1	-	-	2	273
		%	98.9%	0.4%	-	-	0.7%	100%
	HIV Negative	**N**	123	0	-	-	0	123
		%	100%	0%	-	-	0%	100%
	HIV Positive	**N**	13	0	-	-	0	13
		%	100%	0%	-	-	0%	100%
88+	**none**	**N**	82	-	2	-	2	86
		%	95.3%	-	2.3%	-	2.3%	100%
	HIV Negative	**N**	17	-	0	-	0	17
		%	100%	-	0%	-	0%	100%
Missing	**none**	**N**	34	15	1	-	-	50
		%	68%	30%	2%	-	-	100%
	HIV Negative	**N**	11	0	0	-	-	11
		%	100%	0%	0%	-	-	100%
	HIV Positive	**N**	12	0	0	-	-	12
		%	100%	0%	0%	-	-	100%

The crosstabulation on Table 4.20 between patient age group and HIV viral-load status reveals that most of the patients aged between 18 and 27 years have not tested for HIV viral load or are unaware of their viral load status (65.8% categorised as 'none'). With both HIV-negative and HIV-positive individuals in those age group, 100% had not been recorded for viral load.

Furthermore, the crosstabulation between patient age group and HIV viral-load status shows that 58.2% of patients aged 28 to 37 years have not tested for HIV viral load or do not know their status. However, within this age group, 11.7% of HIV-positive patients present a low viral load, while 0.2% have a high viral load. Among HIV-negative participants, 100% have no viral-load data recorded. The same is observed with 99.5% of HIV-positive participants with no viral load recorded.

Within the age group between 38–47 years, 59.2% have not tested for HIV viral load or do not know their status, while 13.9% of patients have not tested for HIV because they already know their HIV-positive status and are compliant with ART have an undetectable viral load recorded, while 0.3% of HIV-positive patients have a high viral load.

Among HIV-negative participants, 100% have no viral-load data recorded, and 99.7% of HIV-positive patients also have no viral-load data recorded. Within the age group between 48 and 57 years, 69.7% of patients do not know their HIV viral load or have not tested for it, while in this age group, 12.3% present with an undetectable viral load. No HIV-negative patients (100%) and HIV-positive patients (100%) have any viral-load data recorded.

The crosstabulation between patient age group and HIV viral-load status reveals that 77.2% of patients aged 58–67 years have not tested for HIV viral load or are unaware of their HIV status, while in this group, 5% of patients with unknown HIV status record a high viral load and 1.2% of HIV-positive patients present with an undetected viral load.

Among HIV-negative participants, 100% have no viral load data recorded, and 98.8% of HIV-positive participants similarly have no recorded viral load. 91.6% of patients aged between 68 and 77 years do not know their viral load or have not tested for it, while within this age group, 0.6% of those with unknown HIV status present with an undetectable viral load.

No HIV-negative participants (100%) and HIV-positive participants (100%) have any viral load data recorded. Lastly, within the age group of 78–87 years, 98.9% of patients do not know their HIV status and or have not tested for viral load In this group, 0.7%

of patients with unknown HIV-negative status (100%) and all HIV-positive status (100%) have no viral-load data recorded.

Table 4.21: Crosstabulation of HIV-1/2 AB/AG (SCREEN) against CD4 ARV

Crosstabulation of HIV-1/2 AB/AG (SCREEN) against CD4 ARV

AGE TESTED YEARS	**HIV-1/2 AB/AG (SCREEN)**		**CD4 ARV**				**Total**	**p-value**	**phi**
			none	*<350 cells/mm^3*	*350–499 cells/mm^3*	*≥500 cells/mm^3*			
18-27	**none**	**N**	3 368	2 232	234	336	6 170	0.000	0.462
		%	54.6%	36.2%	3.8%	5.4%	100%		
	HIV Negative	**N**	2 522	0	0	0	2 522		
		%	100%	0%	0%	0%	100%		
	HIV Positive	**N**	314	0	0	0	314		
		%	100%	0%	0%	0%	100%		
	Equivocal	**N**	144	0	0	0	144		
		%	100%	0%	0%	0%	100%		
28-37	**none**	**N**	5 003	3 423	577	511	9 514	0.000	0.445
		%	52.6%	36%	6.1%	5.4%	100%		
	HIV Negative	**N**	3 021	0	0	0	3 021		
		%	100%	0%	0%	0%	100%		
	HIV Positive	**N**	574	13	0	0	587		
		%	97.8%	2.2%	0%	0%	100%		
	Equivocal	**N**	68	0	0	0	68		
		%	100%	0%	0%	0%	100%		
38-47	**none**	**N**	4 844	3 636	661	550	9 691	0.000	0.439
		%	50%	37.5%	6.8%	5.7%	100%		
	HIV Negative	**N**	2 453	8	1	0	2 462		
		%	99.6%	0.3%	0%	0%	100%		
	HIV Positive	**N**	627	5	0	0	632		
		%	99.2%	0.8%	0%	0%	100%		
	Equivocal	**N**	46	0	0	0	46		
		%	100%	0%	0%	0%	100%		
48-57	**none**	**N**	2 689	1 265	198	413	4 565	0.000	0.444
		%	58.9%	27.7%	4.3%	9%	100%		
	HIV Negative	**N**	2 213	0	0	8	2 221		
		%	99.6%	0%	0%	0.4%	100%		
	HIV Positive	**N**	335	0	0	0	335		
		%	100%	0%	0%	0%	100%		
	Equivocal	**N**	17	0	0	0	17		
		%	100%	0%	0%	0%	100%		
58-67	**none**	**N**	1 816	656	84	185	2 741	0.000	0.354
		%	66.3%	23.9%	3.1%	6.7%	100%		
	HIV Negative	**N**	911	0	0	0	911		
		%	100%	0%	0%	0%	100%		
	HIV Positive	**N**	164	2	0	0	166		
		%	98.8%	1.2%	0%	0%	100%		
	Equivocal	**N**	12	0	0	0	12		
		%	100%	0%	0%	0%	100%		
68-77	**none**	**N**	1 129	85	11	31	1 256	0.000	0.188
		%	89.9%	6.8%	0.9%	2.5%	100%		
	HIV Negative	**N**	581	0	0	0	581		
		%	100%	0%	0%	0%	100%		
	HIV Positive	**N**	30	0	0	1	31		
		%	96.8%	0%	0%	3.2%	100%		

	Equivocal	**N**	4	0	0	0	4		
		%	100%	0%	0%	0%	100%		
78-87	**none**	**N**	270	2	-	1	273	0.842	0,059
		%	98.9%	0.7%	-	0.4%	100%		
	HIV Negative	**N**	122	0	-	1	123		
		%	99.2%	0%	-	0.8%	100%		
	HIV Positive	**N**	13	0	-	0	13		
		%	100%	0%	-	0%	100%	0.262	0.111
88+	**none**	**N**	80	6	-	-	86		
		%	93%	7%	-	-	100%		
	HIV Negative	**N**	17	0	-	-	17		
		%	100%	0%	-	-	100%		
Missing	**none**	**N**	34	13	-	3	50	0.051	0.359
		%	68%	26%	-	6%	100%		
	HIV Negative	**N**	11	0	-	0	11		
		%	100%	0%	-	0%	100%		
	HIV Positive	**N**	12	0	-	0	12		
		%	100%	0%	-	0%	100%		

Table 4.21 above demonstrates that participants between the ages of 18 and 27 years reported not knowing their HIV status (54.6%) and did not test for their CD4 count. Therefore, they do not know their level of immunosuppression. Among the participants with unknown HIV status, 3.8% show mild immunosuppression. No HIV-negative participants (100%) have tested for their CD4 count and therefore do not know their immunosuppression status, which is similar to all HIV-positive individuals (100%) who have not tested for their CD4 count.

In the age group between 28 and 37 years, 52.6% of those with unknown HIV status have not tested their CD4 count, while 6.1% show a mild immunosuppression.

With participants aged 38–47 years, 50% of those with unknown HIV status have not tested for their CD4 count, while 5.7% demonstrate no significant immunosuppression. Among HIV-negative participants, 99.6% have not tested for their CD4 count.

With participants aged between 48 and 57 years, 65.6% of those with unknown HIV status have not tested for their CD4 count, while 1.1% demonstrate no significant immunosuppression. Among HIV-negative participants, 96.3% have not tested for their CD4 count, while 3.7% demonstrate no significant immunosuppression. For the sample of participants aged between 58 and 67 years, 66% of those with unknown HIV status have not tested for their CD4 count, while 7% show no significant immunosuppression.

4.3.3 Summary crosstabulation of the resistance/sensitivity profile

The following section shows a summary crosstabulation of the resistance/sensitivity profile. The table shows the antibiotic against the microorganisms with the highest levels of resistance and the highest levels of sensitivity. The strength of the relationship is interpreted according to phi coefficient, and can be interpreted as follows: negligible/weak (<0.1), weak (0.1–0.2), moderate (0.2–0.4), strong (0.4–0.6), and very strong (>0.8).

Table 4.22: Crosstabulation of microorganisms resistance/sensitivity profile

Amikacin		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Acinetobacter Baumannii	N	1 867	350	2 832	1.183	0
	%	65.9%	12.4%	100%		
Klebsiella Pneumoniae Subsp Pneumoniae	N	90	3834	4 533		
	%	2%	84.6%	100%		
Amoxicillin Clavulanic Acid		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Klebsiella Pneumoniae Subsp Pneumoniae	N	1 564	2 213	4 533	1.070	0
	%	34.5%	48.8%	100%		
Proteus Mirabilis	N	76	1 566	1 794		
	%	4.2%	87.3%	100%		
Amphotericin B		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Candida Albicans	N	1	92	107	1.189	0
	%	0.9%	86%	100%		
***Candida* Species**	N	15	12	28		
	%	53.6%	42.9%	100%		
Ampicillin Amoxicillin		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Escherichia Coli	N	5 843	1 432	7 521	1.102	0
	%	77.7%	19%	100%		
Cefazolin		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Escherichia Coli	N	108	315	7 521	0.438	0
	%	1.4%	4.2%	100%		
Cefepime		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Acinetobacter Baumannii	N	1 243	0	2 832	1.128	0
	%	43.9%	0%	100%		
Escherichia Coli	N	5 843	1 432	7 521		
	%	77.7%	10%	100%		
Cefotaxime Ceftriaxone		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Escherichia Coli	N	1 404	5 920	7 521	1.119	0
	%	18.7%	78.7%	100%		
***Klebsiella Pneumoniae* Subsp Pneumoniae**	N	2 236	2 263	4 533		
	%	49.3%	49.9%	100%		
Cefoxitin		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-value**

***Enterobacter Cloacae* Subsp Cloacae**	N	1 262	0	1 270	1.159	0
	%	99.4%	0%	100%		
Escherichia Coli	N	263	6 702	7 521		
	%	3.5%	89.1%	100%		
Ceftazidime		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Acinetobacter Baumannii	N	2 595	117	2 832	1.119	0
	%	91.6%	4.1%	100%		
Escherichia Coli	N	1 195	6 009	7 521		
	%	15.9%	79.9%	100%		
Ceftriaxone CNS Infection		**Intermediate**	**Sensitive**	**Total**	**Phi**	**P-Value**
Streptococcus Pneumoniae	N	9	681	1 342	0.706	0
	%	0.7%	50.7%	100%		
Ceftriaxone Non-CNS Infection			**Sensitive**	**Total**	**Phi**	**P-Value**
Streptococcus Pneumoniae	N		892	1 342	0.809	0
	%		66.5%	100%		
Cefuroxime Oral		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Escherichia Coli	N	1 628	4 864	7 521	1.046	0
	%	21.6%	64.7%	100%		
***Klebsiella Pneumoniae* Subsp Pneumoniae**	N	2 282	2 160	4 533		
	%	50.3%	47.7%	100%		
Cefuroxime Parenteral		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Escherichia Coli	N	1 570	5 380	7 521	1.076	0
	%	20.9%	71.5%	100%		
***Klebsiella Pneumoniae* Subsp Pneumoniae**	N	2 270	2 160	4 533		
	%	50.1%	47.7%	100%		
Cephalexin		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Escherichia Coli	N	5	23	7 521	0.057	1
	%	0.1%	0.3%	100%		
Chloramphenicol		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Escherichia Coli	N	17	55	7 521	0.576	0
	%	0.2%	0.7%	100%		
Streptococcus Pneumoniae	N	5	225	1 342		
	%	0.4%	16.8%	100%		
Ciprofloxacin		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Acinetobacter Baumannii	N	2 536	226	2 832	0.854	0
	%	89.5%	8%	100%		
Escherichia Coli	N	1 711	5 461	7 521		
	%	22.7%	72.6%	100%		
Clindamycin		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Coagulase Negative *Staphylococcus*	N	3 110	2 383	5 655	1.036	0
	%	55%	42.1%	100%		
	N	919	4 798	6 022		

Staphylococcus Aureus	%	15.3%	79.7%	100%		
Cloxacillin		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Coagulase Negative *Staphylococcus*	N	4 103	1 318	5 655	1.131	0
	%	72.6%	23.3%	100%		
Staphylococcus Aureus	N	866	4 885	6 022		
	%	14.4%	81.1%	100%		
Colistin		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
***Klebsiella Pneumoniae* Subsp Pneumoniae**	N	14	3 825	4 533	1.113	0
	%	0.3%	84.4%	100%		
Proteus Mirabilis	N	1 203	1	1 794		
	%	67.1%	0.1%	100%		
Ertapenem		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Escherichia Coli	N	6	7 271	7 521	1.003	0
	%	0.1%	96.7%	100%		
***Klebsiella Pneumoniae* Subsp Pneumoniae**	N	472	3 708	4 533		
	%	10.4%	81.8%	100%		
Erythromycin Azithromycin		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Coagulase Negative *Staphylococcus*	N	4 346	1 114	5 655	1.184	0
	%	76.9%	19.7%	100%		
Staphylococcus Aureus	N	956	4 909	6 022		
	%	15.9%	81.5%	100%		
Fluconazole		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Candida Albicans	N	0	92	107	1.089	0
	%	0%	86%	100%		
Candida Parapsilosis	N	10	22	32		
	%	31.3%	68.8%	100%		
Fusidic Acid		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Coagulase Negative *Staphylococcus*	N	1 356	3 337	5 655	0.992	0
	%	24%	59%	100%		
Staphylococcus Aureus	N	456	4 888	6 022		
	%	7.6%	81.2%	100%		
Gentamicin		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Acinetobacter Baumannii	N	2 527	202	2 832	0.988	0
	%	89.2%	7.1%	100%		
Escherichia Coli	N	1 042	6 331	7 521		
	%	13.9%	84.2%	100%		
Gentamicin High Level Resistance		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Enterococcus Faecalis	N	401	709	1 262	0.958	0
	%	31.8%	56.2%	100%		
Enterococcus Faecium	N	436	154	625		
	%	69.8%	24.6%	100%		
Imipenem		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
		2 630	129	2 832	1.216	0

Acinetobacter Baumannii	%	92.9%	4.6%	100%		
Escherichia Coli	N	3	7 321	7 521		
	%	0%	97.3%	100%		
Levofloxacin		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Coagulase Negative *Staphylococcus*	N	64	22	5 655	0.492	0
	%	1.1%	0.4%	100%		
Streptococcus Pneumoniae	N	0	242	1 342		
	%	0%	18%	100%		
Linezolid		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Coagulase Negative Staphylococcus	N	4	4 657	5 655	0.894	0
	%	0.1%	82.4%	100%		
Enterococcus Faecalis	N	6	1 108	1 262		
	%	0.5%	87.8%	100%		
Meropenem		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Acinetobacter Baumannii	N	2 620	133	2 832	1.242	0
	%	92.5%	4.7%	100%		
Escherichia Coli	N	13	6 977	7 521		
	%	0.2%	92.8%	100%		
Mupirocin		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Staphylococcus Aureus	N		16	6 022	0.047	1
	%		0.3%	100%		
Moxifloxacin		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Coagulase Negative *Staphylococcus*	N	869	1 404	5 655	0.856	0
	%	15.4%	24.8%	100%		
Staphylococcus Aureus	N	510	4 396	6 022		
	%	8.5%	73%	100%		
Nitrofurantoin		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Escherichia Coli	N	271	5 930	7 521	1.025	0
	%	3.6%	78.8%	100%		
Proteus Mirabilis	N	1 593	2	1 794		
	%	88.8%	0.1%	100%		
Penicillin CNS Infection		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Streptococcus Alpha-Haemolytic	N	1	0	137	0.734	0
	%	0.7%	0%	100%		
Streptococcus Pneumoniae	N	110	623	1 342		
	%	8.2%	46.4%	100%		
Penicillin Non-CNS Infection		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Streptococcus Pneumoniae	N	5	908	1 342	0.821	0
	%	0.4%	67.7%	100%		
Rifampicin		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Coagulase Negative *Staphylococcus*	N	2 063	2 452	5 655	0.954	0
	%	36.5%	43.4%	100%		
Staphylococcus Aureus	N	311	4 238	6 022		
	%	5.2%	70.4%	100%		

Streptomycin High Level Resistance		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Enterococcus Faecalis	N	778	8	1 262	1.022	0
	%	61.6%	0.6%	100%		
Teicoplanin		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Coagulase Negative *Staphylococcus*	N	179	2 521	5 655	0.793	0
	%	3.2%	44.6%	100%		
Staphylococcus Aureus	N	17	4 881	6 022		
	%	0.3%	81.1%	100%		
Tetracycline		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Coagulase Negative *Staphylococcus*	N	1 866	949	5 655	0.922	0
	%	33%	16.8%	100%		
Staphylococcus Aureus	N	980	3 935	6 022		
	%	16.3%	65.3%	100%		
Tigecycline		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Escherichia Coli	N	14	5 899	7 521	0.994	0
	%	0.2%	78.4%	100%		
Proteus Mirabilis	N	1 546	10	1 794		
	%	86.2%	0.6%	100%		
Tobramycin		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Acinetobacter Baumannii	N	1 848	220	2 832	0.738	0
	%	65.3%	7.8%	100%		
Escherichia Coli	N	231	1 107	7 521		
	%	3.1%	14.7%	100%		
Tigecycline		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Escherichia Coli	N	14	5 899	7 521	1.052	0
	%	0.2%	78.4%	100%		
Proteus Mirabilis	N	1 546	10	1 794		
	%	86.2%	0.6%	100%		
Trimethoprim Sulfamethoxazole		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Escherichia Coli	N	5 138	2 121	7 521	0.92	0
	%	68.3%	28.2%	100%		
Staphylococcus Aureus	N	2 543	3 279	6 022		
	%	42.2%	54.5%	100%		
Vancomycin		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Staphylococcus Aureus	N	60	5 293	6 022	0.903	0
	%	1%	87.9%	100%		
Voriconazole		**Resistant**	**Sensitive**	**Total**	**Phi**	**P-Value**
Candida Albicans	N	2	88	107	0.969	0
	%	1.9%	82.2%	100%		
Candida Parapsilosis	N	4	20	32		
	%	12.5%	62.5%	100%		

Table 4.22 shows a summary of the results of the crosstabulations. As shown in the above table,

- *Acinetobacter baumannii* is resistant to Amikacin (65.9%), with only a 12.4% sensitivity.

- However, *Klebsiella pneumoniae* demonstrates a very low resistance (2%) and high sensitivity (84.6%). The Phi coefficient of 1.183 shows a very strong association between organisms, and the p-value of 0.000 affirms that this difference is statistically significant.

- *Klebsiella pneumoniae* also demonstrates a 34.5% prevalence of resistance and 48.8% of sensitivity to Amoxicillin Clavulanic Acid, while *Proteus mirabilis* has very low resistance (4.2%) and a very high sensitivity (87.3%). The Phi coefficient of 1.07 indicates a very strong relationship between the organism and drug response, with the p-value of 0.000 confirming statistical significance.

- With antibiotic Amphotericin B, *Candida albicans* demonstrates a sensitivity in 86% of cases. However, it has a number of cases of resistance (0.9%), while other *Candida* species show a higher resistance (53.6%) to Amphotericin B, in contrast to the lower sensitivity (42.9%).

- Furthermore, the Phi coefficient of 1.189 shows a very strong positive alliance between organism and susceptibility to Amphotericin B, with the p-value of 0.000 confirming significance.

- Ampicillin/Amoxicillin and Cefazolin both demonstrate high levels of resistance and sensitivity to *Escherichia coli.* Ampicillin/Amoxicillin shows a resistance rate of 77.7% and Cefazolin shows a resistance of rate of 1.2%. This is in contrast to Ampicillin/Amoxicillin at a sensitivity rate of 19%, and Cefazolin at a rate of 4.2%, which in this case is higher. Ampicillin/Amoxicillin shows a Phi coefficient of 1.102, which indicates a very strong association between organism and resistance, and the p-value of 0.000 confirms this is statistically significant.

- In comparison to this, Cefazolin has a Phi coefficient of 0.438, which displays a weak relationship between organism and antibiotic response, and the p-value of 0.000 shows that the association is still statistically significant.

- *Acinetobacter baumannii* displays a high level of resistance to Cefepime at the rate of 43.9% and no sensitive isolates were reported, while *Escherichia coli* displays a very high resistance (77.7%), with only a 10% sensitivity rate. The Phi coefficient of 1.128 indicates a very strong relationship between organism and Cefepime susceptibility, with the p-value of 0.000 affirming that this is statistically significant.

- *Escherichia coli* isolates are highly sensitive to Cefotaxime/Ceftriaxone at a rate of 78.7%, with 18.7% resistant.

- *Klebsiella pneumoniae* demonstrates an almost equal split of resistant 49.3% and sensitivity rate of 49.9% isolates. Therefore, the Phi coefficient of 1.119 shows a very strong relationship between organism and response to this antibiotic, with a p-value of 0.000 confirming statistically significance. This indicates that Cefotaxime/Ceftriaxone effectiveness differs greatly between organisms.

- *Enterobacter cloacae* subsp. cloacae isolates show an almost complete resistance to Cefoxitin at a rate of 99.4% with no sensitive isolates, while *Escherichia coli* shows a much lower resistance of 3.5% and high sensitivity rate of 89.1%. The Phi coefficient of 1.159 indicates a very strong association between organism and Cefoxitin susceptibility, with a p-value of 0.000 confirming statistical significance.

- *Acinetobacter baumannii* shows a very high resistance rate to Ceftazidime (91.6%) and only a 4.1% sensitivity rate, while *Escherichia coli* shows a low resistance rate of 15.9% and high sensitivity rate of 79.9% . The Phi coefficient of 1.224 demonstrates a very strong relationship between organism and antibiotic response, and the p-value of 0.000 confirms statistical significance.

- *Streptococcus pneumoniae* in CNS infections’ intermediate susceptibility is rare (0.7%), while sensitivity is 50.7% of isolates. The Phi coefficient of 0.706 indicates a moderate relationship between the organism and CNS Ceftriaxone response, with a p-value of 0.000 confirming statistically significance.

- However, *Streptococcus pneumoniae* in non-CNS infections shows that 66.5% of isolates are sensitive to Ceftriaxone and no resistant isolates are recorded in this category. Therefore, the Phi coefficient of 0.809 shows a very strong association between organism and non-CNS Ceftriaxone response, with the p-value of 0.000 confirming this relationship is statistically significant.

- In the case where Cefuroxime was administered orally, *Escherichia coli* displays 21.6% resistance and 64.7% sensitivity, while *Klebsiella pneumoniae* subsp. pneumoniae has a 50.3% resistance and a 47.7% sensitivity rate. The Phi coefficient of 1.093 indicates a very strong association between organism and Cefuroxime response, with the p-value of 0.000 confirming statistically significance.

- *Escherichia coli* displays 20.9% resistance and 71.5% sensitivity to parenteral Cefuroxime, while *Klebsiella pneumoniae* subsp. pneumoniae displayed 50.1% resistance and 47.7% sensitivity rate. Therefore, the Phi coefficient of 1.076 demonstrates a very strong association between organism and parenteral Cefuroxime susceptibility, with a p-value of 0.000 affirming statistical significance.

- *Escherichia coli* displays a very low resistance (0.1%) and low sensitivity (0.3%) rate to Cephalexin and the Phi coefficient of 0.057 indicates a negligible association between organism and Cephalexin susceptibility, with a p-value of 1 indicating no statistical significance.

- *Escherichia coli* displays a very low resistance (0.2%) and 0.7% sensitivity rate to Chloramphenicol, while *Streptococcus pneumoniae* displays 0.4% resistance and 16.8% sensitivity rate. Therefore, the Phi coefficient of 0.576 indicates a moderate association between organism and Chloramphenicol susceptibility, with a p-value of 0.000 confirming statistically significance.

- Ciprofloxacin shows high levels of resistance when administered in cases of *Acinetobacter baumannii* with a rate of 89.5% and only 8% sensitive cases were reported.

- In contrast, *Escherichia coli* displays a lower resistance rate of 22.7% and a higher sensitivity rate of 72.6% to Ciprofloxacin. Therefore, the Phi coefficient of 0.854 shows a very strong association between organism and Ciprofloxacin susceptibility, and the p-value of 0.000 affirms that this association is statistically significant.

- Coagulase-negative *Staphylococcus* has a 55% rate of resistant isolates, whereas for *Staphylococcus aureus*, 79.7% of isolates are sensitive. The Phi coefficient of 1.036 demonstrates a very strong association between organism and Clindamycin sensitivity, and the p-value of 0.000 confirms statistical significance.

- Coagulase-negative *Staphylococcus* demonstrates a high resistance to Cloxacillin (72.6%) compared to a 23.3% sensitivity rate, while *Staphylococcus aureus* displays a much lower resistance 14.4% and higher sensitivity (81.1%) rate. Therefore, the Phi coefficient of 1.131 indicates a very strong relationship between organism and Cloxacillin susceptibility, with a p-value of 0.000 affirming that this relationship is statistically significant.

- *Klebsiella pneumoniae* subsp. pneumoniae displays a very low resistance to Colistin (0.3%) with a high sensitivity of 84.4%, while *Proteus mirabilis* displays a high resistance of 67.1% and a sensitivity rate of 0.1%. Therefore, the Phi coefficient of 1.136 reflects a very strong association between organism and Colistin susceptibility, with a p-value of 0.000 affirming statistical significance.

- *Escherichia coli* shows a very low resistance to Ertapenem (0.1%) with a very high sensitivity (96.7%), while *Klebsiella pneumoniae* subsp. pneumoniae shows higher resistance (10.4%) with a still high sensitivity rate (81.8%). Furthermore, the Phi coefficient of 1.020 displays a very strong relationship between organism and Ertapenem susceptibility, and the p-value of 0.000 confirms statistical significance.

- *Staphylococcus aureus* displays a high sensitivity rate to Erythromycin/Azithromycin (78.2%) with 19.6% resistance, while Coagulase-negative *Staphylococcus* displayed high resistance (51.2%) and less sensitivity rate (47.8%). The Phi coefficient of 0.987 demonstrates a very strong relationship between organism and antibiotic susceptibility, and the p-value of 0.000 confirms that this relationship is statistically significant.

- Regarding *Candida albicans*, 0% of the isolates is resistant while 86% are sensitive to fluconazole, while in *Candida parapsilosis*, 31.3% of isolates are resistant and 68.8% are sensitive. Therefore, the phi coefficient of 1.089 shows a very strong relationship between *Candida* species and their fluconazole susceptibility, and the p-value of 0.000 affirms that this association is statistically significant.

- In Coagulase-negative *Staphylococcus*, 24% of the isolates are resistant and 59% display a sensitivity to Fusidic acid, while with *Staphylococcus aureus*, 7.6% isolates are resistant and 81.2% are sensitive. The phi coefficient of 1.002 displays a very strong positive relationship between the species type and susceptibility to Fusidic acid, and the p-value of 0.000 affirms statistical significance.

- *Acinetobacter baumannii* presents a high resistance to Gentamicin (77.1%) with only a 17.4% sensitivity observed, while *Escherichia coli* has lower resistance (13.8%) and a high sensitivity of 84.8%. Therefore, the Phi coefficient of 0.989 indicates a very strong relationship between organism and Gentamicin susceptibility, with a p-value of 0.000 confirming statistically significance. Amid *Enterococcus faecalis* isolates, 31.8% show resistance to Gentamicin high-level resistance testing, while 56.2% display sensitivity.

- However, *Enterococcus faecium* presents a much higher resistance rate at 69.8% and only 24.6% display sensitivity. The phi coefficient is 0.958, which indicates a very strong positive association between the species type and Gentamicin high-level resistance, and the p-value of 0.000 verifies that this relationship is statistically significant.

- *Escherichia coli* almost has a universal sensitivity to Imipenem at the rate of 98.7% and negligible resistance (0.1%), while *Klebsiella pneumoniae* subsp. pneumoniae has a higher resistance (8.7%) but still high sensitivity (83.4%). Therefore, the Phi coefficient of 1.022 reflects a very strong association between organism and Imipenem response, with a p-value of 0.000 confirming this is statistically significant.

- *Acinetobacter baumannii* shows very high resistance to Levofloxacin (91.3%) with only 5.6% sensitivity, while *Escherichia coli* has a much lower resistance (21.6%) and 73.3% sensitivity. The Phi coefficient of 0.981 reflects a strong association between organism and Levofloxacin susceptibility, and the p-value of 0.000 confirms statistical significance.

- *Staphylococcus aureus* and Coagulase-negative *Staphylococcus* show near-universal sensitivity to Linezolid with a rate of >98%, with negligible resistance. However, the Phi coefficient of 0.432 reflects only a weak association between organism and Linezolid sensitivity, even though the p-value of 0.000 shows the difference is still statistically significant.

- *Escherichia coli* displays extremely high sensitivity to Meropenem (99%) with almost no resistance cases, while *Klebsiella pneumoniae* subsp. pneumoniae is notably highly sensitive (88.2%) but also displays a resistance of 9.5%. Therefore, the Phi coefficient of 1.034 indicates a very strong association between organism and Meropenem susceptibility, and the p-value of 0.000 confirms statistically significance.

- With *Staphylococcus aureus*, no resistant isolates are recorded, while only 0.3% isolates are sensitive to mupirocin. Therefore, the phi coefficient of 0.055 indicates no association between organism type and susceptibility to Mupirocin. Furthermore, the p-value of 1.000 shows that this relationship is not statistically significant.

- *Escherichia coli* displays a very high sensitivity to Nitrofurantoin (95.7%) with low resistance (2.3%) recorded, while *Klebsiella pneumoniae* subsp. pneumoniae has a much lower sensitivity (35.1%) and high resistance (62.4%). The Phi coefficient of 1.071 indicates a strong relationship between organism and Nitrofurantoin sensitivity, and the p-value of 0.000 confirms statistical significance.

- Among S*treptococcus* alpha-haemolytic isolates, only 0.7% are recorded to be resistant to penicillin, with no sensitive isolates recorded, while among *Streptococcus pneumoniae* isolates, 8.2% are recorded to be resistant and 46.4% are sensitive. While the phi coefficient of 0.735 shows a strong positive relationship between organism type and penicillin resistance in CNS infections, the p-value of 0.000 indicates that this association is statistically significant.

- With *Streptococcus pneumoniae* in non-CNS infections, only 0.4% are recorded to be resistant and 67.7% are sensitive to penicillin. Therefore, the phi coefficient of 0.821 indicates a very strong positive relationship between the infection type and penicillin sensitivity, and the p-value of 0.000 shows this association is statistically significant.

- For coagulase-negative *Staphylococci*, 36.5% are recorded to be resistant to rifampicin and 43.4% are sensitive, while for *Staphylococcus aureus*, 5.2% are resistant compared with 70.4% sensitive isolates and the phi coefficient of 1.039 indicates a very strong positive association between organism type and rifampicin sensitivity, and the p-value of 0.000 confirms the relationship is statistically significant.

- *Enterococcus faecalis* displays that 61.6% of the isolates are resistant to high-level streptomycin, while only 0.6% are sensitive; therefore, the phi coefficient of 1.025 indicates a very strong positive relationship between *E. faecalis* and resistance to high-level streptomycin, the p-value of 0.000 shows that this relationship is statistically significant.

- For *Staphylococcus aureus*, only 0.3% of the isolates are reported to be resistant to Teicoplanin, while 81.1% are sensitive and the phi coefficient of 0.793 suggests a strong positive association between *E. faecalis* and resistance to high-level streptomycin, and the p-value of 0.000 shows that this association is statistically significant. For *Staphylococcus aureus*, 87.9% of isolates are recorded to be sensitive to vancomycin, while only 1% are seen to be resistant. The Phi coefficient of 0.92 shows a very strong positive association between S*. aureus* and vancomycin sensitivity, and the p-value of 0.000 indicates that this relationship is statistically significant.

- For *Candida albicans*, 82.2% of isolates are recorded to be sensitive to voriconazole, while only 1.9% show resistance. Therefore, the Phi coefficient of 0.969 displays a very strong positive relationship between *Candida albicans* and voriconazole sensitivity, and the p-value of 0.000 shows that this relationship is statistically significant.

Table 4.23: Frequency of the top six wards

Frequency of the top six wards		
Ward name	**Frequency**	**Percentage%**
A6 INTENSIVE CARE UNIT	1 587	10.1
EMERGENCY UNIT	3 593	22.9
M1 MEDICAL WARD	2 479	15.8
MEDICAL RECOVERY	3 246	20.7
MEDICAL WARD U5A	2 678	17
MULTIDISCIPLINARY UNIT	2 135	13.6
Total	15 718	100

Table 4.23 is a summary displaying the top six wards, which accounted for 15 718 of responses and shows the distribution of patients across different hospital wards within a subset of the total population. It also shows an overview of how patients were allocated in different ward units, highlighting the relative size and contribution of each ward to the overall patient population. Lastly, an understanding to this distribution is important for interpreting the patterns of antimicrobial sensitivity or resistance and other clinical characteristics in subsequent analyses. The table shows that the top six wards in this study consist of the following frequency rate: Emergency unit (22.9%), M1 Medical Ward (15.9%), Medical recovery unit (20.7%), Medical Ward U5A (17%), and the Multidisciplinary Unit 13.6%, as well as the A6 Intensive-Care Unit (ICU) with 10.1%.

Table 4.24: Crosstabulation of Ward Name Against Gender

Crosstabulation of Ward Name Against Gender								
			GENDER			**Total**	**Phi**	**P-value**
			Male	*Female*	*Unknown*			
WARD NAME	A6 INTENSIVE CARE UNIT	N	843	722	22	1 587	**0.126**	**0**
		%	53.1%	45.5%	1.4%	100%		
	EMERGENCY UNIT	N	1 745	1 839	9	3 593		
		%	48.6%	51.2%	0.3%	100%		
	M1 MEDICAL WARD	N	1 041	1 431	7	2 479		
		%	42%	57.7%	0.3%	100%		
	MEDICAL RECOVERY	N	1 734	1 485	27	3 246		
		%	53.4%	45.7%	0.8%	100%		

	MEDICAL WARD U5A	N	1 133	1 545	0	2 678		
		%	42.3%	57.7%	0%	100%		
	MULTIDISCIPLINARY UNIT	N	1 181	954	0	2 135		
		%	55.3%	44.7%	0%	100%		

- Table 4.24 shows that in the A6 Intensive-Care Unit, most of the patients are male, accounting for 53.1%, in contrast to the 45.5% of females and only 1.4% of the patients whose gender are unknown.
- In the Emergency Unit, most patients are females with 51.2% of the population, while males account for 48.6% of admissions into the Emergency unit, and 0.3% of population are classified under unknown.
- In the Medical Recovery ward, most of the patients are male (53.4%) and 45.7% are female.
- Medical ward U5A is recorded to have more females as part of the sampled patients (57.7%), in comparison to males (42.3%).
- The Multidisciplinary unit displays to have more males in the sample population, accounting for 55.3%, with 44.7% of women in the very same department; therefore, the phi coefficient of 0.126 shows a weak, but positive correlation between gender and ward name. However, the p-value of 0.000 shows a statistically significant association; therefore, it can be concluded that gender does influence the ward name in this study.

Table 4.25: Crosstabulation of Ward Name Against Age Category

Crosstabulation of Ward Name Against Age Category													
			AGE TESTED YEARS								**Total**	**Phi**	**P-value**
			18-27	*28-37*	*38-47*	*48-57*	*58-67*	*68-77*	*78-87*	*88 +*			
WARD NAME	**A6 INTENSIVE CARE UNIT**	**N**	224	344	423	321	187	66	12	10	1587	**0.259**	**0**
		%	14.1%	21.7%	26.7%	20.2%	11.8%	4.2%	0.8%	0.6%	100%		
	EMERGENCY UNIT	**N**	853	834	891	471	355	135	46	8	3 593		
		%	23.7%	23.2%	24.8%	13.1%	9.9%	3.8%	1.3%	0.2%	100%		
	M1 MEDICAL WARD	**N**	418	976	688	255	92	45	1	4	2 479		
		%	16.9%	39.4%	27.8%	10.3%	3.7%	1.8%	0%	0.2%	100%		
	MEDICAL RECOVERY	**N**	657	713	1043	523	184	84	36	6	3 246		
		%	20.2%	22%	32.1%	16.1%	5.7%	2.6%	1.1%	0.2%	100%		
	MEDICAL WARD U5A	**N**	335	796	1032	357	115	38	5	0	2 678		
		%	12.5%	29.7%	38.5%	13.3%	4.3%	1.4%	0.2%	0%	100%		

	MULTIDISCIPLINARY UNIT	**N**	402	627	380	311	283	116	14	2	2 135		
		%	18.8%	29.4%	17.8%	14.6%	13.3%	5.4%	0.7%	0.1%	100%		

Table 4.25 above is a crosstabulation of ward name against age category.

- In the A6 Intensive-Care Unit the most prevalent age group identified is 38–47 at a rate of 26.7%, compared to the 0.6% of the sample in the 88+ age group.
- In the Emergency Unit a similar trend is observed, with 24.8%, but compared to the A6 Intensive Care Unit, compared to the 0.2% of the patients in the 88+ age group.
- In the M1 Medical Ward, the largest group is observed between the ages of 28–37 years (39.4%), followed by 38–47 years (27.8%), with no patient aged 78–87 years and only 0.2% aged 88+ years.
- In the Medical Recovery ward, most patients are aged 38–47 years (32.1%) and 28–37 years (22%), with 1.1% patients aged 78–87 years and 0.2% aged 88+ years.
- In Medical Ward U5A, the highest population observed is 38–47 years (38.5%) followed by 28–37 years (29.7%), with 0.2% aged 78–87 years and no sampled patients above the age of 88 years.
- In the Multidisciplinary Unit, most patients are aged 28–37 years (29.4%), followed by 18–27 years (18.8%) and 38–47 years (17.8%), with only 0.7% aged 78–87 years and 0.1% aged 88+ years. The Phi coefficient displays that there is a weak, but statistically significant association between wards and age group (Phi = 0.259). In addition, the p-value of 0.000 is < 0.001, indicating that the association is statistically significant. Therefore, it can be safely concluded that age does influence the ward name.

4.3.4 Crosstabulation of ward name with the top antimicrobials that showed the highest sensitivity or resistance pattern.

Table 4.26: Crosstabulation of Ward name against Amikacin

Crosstabulation of Ward Name against Amikacin										
			AMIKACIN					**Total**	**Phi**	**P-value**
			None	*Resistant*	*Inter-mediate*	*Sensitive*	*Dose-Dependent Sensitive*			
WARD NAME	**A6 INTENSIVE CARE UNIT**	**N**	729	656	0	26	176	1 587	**0.289**	**0**
		%	45.9%	41.3%	0%	1.6%	11.1%	100%		
	EMERGENCY UNIT	**N**	1788	1 532	0	133	140	3 593		
		%	49.8%	42.6%	0%	3.7%	3.9%	100%		
	M1 MEDICAL WARD	**N**	1469	839	0	48	123	2 479		
		%	59.3%	33.8%	0%	1.9%	5%	100%		
	MEDICAL RECOVERY	**N**	1570	1 389	0	89	198	3 246		
		%	48.4%	42.8%	0%	2.7%	6.1%	100%		
	MEDICAL WARD U5A	**N**	2077	467	1	53	80	2 678		
		%	77.6%	17.4%	0%	2%	3%	100%		
	MULTI-DISCIPLINARY UNIT	**N**	842	934	0	13	346	2 135		
		%	39.4%	43.7%	0%	0.6%	16.2%	100%		

Table 4.26 above displays the Crosstabulation of Ward Name against antibiotic Amikacin. The ward A6 Intensive-Care Unit (45.9%), Emergency Unit (49.8%), M1 Medical Ward (59.3%), Medical Recovery (48.4%), and Medical Ward U5A (77.6%) demonstrate to have their highest percentage values coming from the “none” category. This indicates that these sampled participants were not treated with this antibiotic, as there were no antibiotic susceptibility records of the samples from laboratory results.

The Emergency Unit displays the highest frequency of cases of resistance with 1 532 cases, followed by Medical Recovery accounting for 1 389 cases. However, the Emergency Unit reports to have 133 cases of sensitivity against Amikacin. The Phi coefficient shows that there is a weak, but statistically significant relationship between ward and the antibiotic Amikacin, Phi = 0.289. In addition, the p-value of 0.000 is <0.001, indicates that the association is statistically significant. Therefore, it can safely be concluded that Amikacin does influence the ward name.

Table 4.27: Crosstabulation of Ward Name against Amoxicillin Clavulanic Acid

Crosstabulation of Ward Name against Amoxicillin Clavulanic Acid									
			AMOXICILLIN CLAVULANIC ACID				**Total**	**Phi**	**P-value**
			None	*Resistant*	*Sensitive*	*Dose Dependent Sensitive*			
WARD NAME	**A6 INTENSIVE CARE UNIT**	**N**	1 020	267	39	261	1 587	**0.255**	**0**
		%	64.3%	16.8%	2.5%	16.4%	100%		
	EMERGENCY UNIT	**N**	1 882	908	284	519	3 593		
		%	52.4%	25.3%	7.9%	14.4%	100%		
	M1 MEDICAL WARD	**N**	1 572	545	29	333	2 479		
		%	63.4%	22%	1.2%	13.4%	100%		
	MEDICAL RECOVERY	**N**	1 702	846	170	528	3 246		
		%	52.4%	26.1%	5.2%	16.3%	100%		
	MEDICAL WARD U5A	**N**	2 221	251	31	175	2 678		
		%	82.9%	9.4%	1.2%	6.5%	100%		
	MULTIDISCIPLINARY UNIT	**N**	1 381	310	62	382	2 135		
		%	64.7%	14.5%	2.9%	17.9%	100%		

Table 4.27 above presents the Crosstabulation of Ward Name against Amoxicillin Clavulanic Acid. The wards A6 Intensive Care Unit (64.3%), M1 Medical Ward (63.4%), Medical Ward U5A (82.9%) and the Multidisciplinary Unit (64.7%) indicate to have their highest percentage values in the "none" category. This indicates that the majority of patients in these wards were not treated with Amoxicillin Clavulanic Acid antibiotic.

The Emergency Unit accounts for the highest percentage of resistance with 908 (25.3%) cases, followed by Medical Recovery with 846 (26.1%) cases. Conversely, the Emergency Unit also reports the highest percentage of Amoxicillin Clavulanic Acid antibiotic sensitivity with 284 (7.9%) cases, followed by Medical Recovery reporting 170 (5.2%) cases. The Phi coefficient of 0.255 shows a weak but statistically significant relationship between ward and Amoxicillin Clavulanic Acid use. Additionally, the p-value of 0.000 is <0.001 indicates that this relationship is statistically significant; therefore, a conclusion can be made that the ward is associated with differences in the administration and resistance patterns of antibiotic Amoxicillin Clavulanic Acid.

Table 4.28: Crosstabulation Of Ward Name Against Cefuroxime Oral

Crosstabulation Of Ward Name Against Cefuroxime Oral										
			CEFUROXIME ORAL					**Total**	**Phi**	**P-value**
			None	*Resis-tant*	*Inter-mediate*	*Sensi-tive*	*Dose Dependent Sensitive*			
WARD NAME	**A6 INTENSIVE CARE UNIT**	**N**	986	281	1	23	296	1 587	0.199	0
		%	62.1%	17.7%	0.1%	1.4%	18.7%	100%		
	EMERGENCY UNIT	**N**	1 940	948	0	57	648	3 593		
		%	54%	26.4%	0%	1.6%	18%	100%		
	M1 MEDICAL WARD	**N**	1 611	499	0	4	365	2 479		
		%	65%	20.1%	0%	0.2%	14.7%	100%		
	MEDICAL RECOVERY	**N**	1 831	775	0	25	615	3 246		
		%	56.4%	23.9%	0%	0.8%	18.9%	100%		
	MEDICAL WARD U5A	**N**	2 127	233	0	26	292	2 678		
		%	79.4%	8.7%	0%	1%	10.9%	100%		
	MULTIDISCIPLINARY UNIT	**N**	1 304	351	0	28	452	2 135		
		%	61.1%	16.4%	0%	1.3%	21.2%	100%		

Table 4.28 above shows the Crosstabulation of Ward Name against oral Cefuroxime antibiotic.

- In the A6 Intensive Care Unit, 62.1% of cases are “none”, indicating that no antibiotic susceptibility results were received from the laboratory. Therefore, these patients were not treated with this antibiotic. 17.7% cases are resistant, 0.1% intermediate, 1.4% are sensitive, and 18.7% dose-dependent sensitive.

- In the Emergency Unit, 54% cases are “none”, 26.4% resistant, 0% intermediate, 1.6% patients samples show sensitivity to this antibiotic, and 18% are dose-dependent sensitive.

- In Medical Ward U5A, 79.4% patients are recorded under “none”, 8.7% patients samples show resistance to this antibiotic, 0% intermediate, 1% patients are sensitive to this antibiotic, and 10.9% dose-dependent sensitive.

- In the Multidisciplinary Unit, 61.1% are “none”, 16.4% patients are resistant, 0% intermediate, 1.3% patients are sensitive, and 21.2% dose-dependent sensitive.

The Phi coefficient of 0.199 demonstrates a weak, but statistically significant relationship between ward and oral Cefuroxime results, with a p-value of 0.000 (<0.001) confirming statistical significance.

Table 4.29: Crosstabulation of Ward Name against Ciprofloxacin

Crosstabulation Of Ward Name Against Ciprofloxacin									
			CIPROFLOXACIN				**Total**	**Phi**	**P-value**
			None	*Resistant*	*Sensitive*	*Dose-Dependent Sensitive*			
WARD NAME	**A6 INTENSIVE CARE UNIT**	**N**	186	640	32	729	1 587	0.408	0
		%	11.7%	40.3%	2%	45.9%	100%		
	EMERGENCY UNIT	**N**	480	2 255	75	783	3 593		
		%	13.4%	62.8%	2.1%	21.8%	100%		
	M1 MEDICAL WARD	**N**	176	1 147	55	1 101	2 479		
		%	7.1%	46.3%	2.2%	44.4%	100%		
	MEDICAL RECOVERY	**N**	446	1 983	38	779	3 246		
		%	13.7%	61.1%	1.2%	24%	100%		
	MEDICAL WARD U5A	**N**	1 322	867	30	459	2 678		
		%	49.4%	32.4%	1.1%	17.1%	100%		
	MULTI-DISCIPLINARY UNIT	**N**	464	1 021	19	631	2 135		
		%	21.7%	47.8%	0.9%	29.6%	100%		

Table 4.29, indicates the Crosstabulation of Ward Name against Ciprofloxacin antibiotic.

- In the A6 Intensive Care Unit, 11.7% of cases are recorded as “none”, with 40.3% patients resistant to this antibiotic, 2% patients show sensitivity to this antibiotic, and 45.9% are dose-dependent sensitive.
- In the Emergency Unit, 13.4% are “none”, 62.8% patients are resistant, 2.1% patients show sensitivity to this antibiotic, and 21.8% are dose-dependent sensitive.
- In the M1 Medical Ward, 7.1% are “none”, 46.3% patients show resistance, 2.2% patients are sensitive, and 44.4% are dose-dependent sensitive.
- In Medical Recovery, 13.7% are “none”, 61.1% show resistance, 1.2% display to be sensitive, and 24% are dose-dependent sensitive.

- In Medical Ward U5A, 49.4% no patients' antibiotic results are "none", 32.4% patients are resistant, 1.1% are sensitive, and 17.1% are dose-dependent sensitive.
- In the Multidisciplinary Unit, 21.7% are "none", 47.8% patients show resistance, 0.9% are sensitive, and 29.6% are dose-dependent sensitive.

Therefore, the Phi coefficient of 0.408 indicates a moderate and statistically significant association between ward and Ciprofloxacin outcomes, with a p-value of 0.000 (<0.001) confirming statistical significance.

Table 4.30: Crosstabulation of Ward Name against Imipenem

Crosstabulation Of Ward Name Against Imipenem

			IMIPENEM					**Total**	**Phi**	**P-value**
			None	*Re-sistant*	*Inter-mediate*	*Sen-sitive*	*Dose-Dependent Sensitive*			
WARD_NAME	**A6 INTENSIVE CARE UNIT**	**N**	641	420	0	54	472	1 587	0.367	0
		%	40.4%	26.5%	0%	3.4%	29.7%	100%		
	EMERGENCY UNIT	**N**	1 720	1 573	0	130	170	3 593		
		%	47.9%	43.8%	0%	3.6%	4.7%	100%		
	M1 MEDICAL WARD	**N**	1 424	825	0	20	210	2 479		
		%	57.4%	33.3%	0%	0.8%	8.5%	100%		
	MEDICAL RECOVERY	**N**	1 518	1 422	0	107	199	3 246		
		%	46.8%	43.8%	0%	3.3%	6.1%	100%		
	MEDICAL WARD U5A	**N**	2 064	534	0	10	70	2 678		
		%	77.1%	19.9%	0%	0.4%	2.6%	100%		
	MULTIDISCIPLINARY UNIT	**N**	815	850	2	45	423	2 135		
		%	38.2%	39.8%	0.1%	2.1%	19.8%	100%		

Table 4.30, shows how Imipenem sensitivity varies by ward.

- In the A6 Intensive Care Unit, 40.4% of isolates are "none", 26.5% are recorded to be resistant, 0% intermediate, 3.4% are found to be sensitive to the drug, and 29.7% dose-dependent sensitive.
- In the Emergency Unit, 47.9% are categorised as "none", 43.8% patients show resistance, 0% intermediate, 3.6% are sensitive, and 4.7% dose-dependent sensitive.
- In the M1 Medical Ward, 57.4% are "none", 33.3% show resistance to the drug, 0% intermediate, 0.8% are sensitive, and 8.5% dose-dependent sensitive.

- In Medical Recovery, 46.8% are recorded as “none”, 43.8% are resistant, 0% intermediate, 3.3% patients are sensitive to the drug, and 6.1% dose-dependent sensitive.
- In Medical Ward U5A, 77.1% are “none”, 19.9% show resistance, 0% intermediate, 0.4% are sensitive, and 2.6% dose-dependent sensitive.
- In the Multidisciplinary Unit, 38.2% are “none” 39.8% patients show resistance, 0.1% intermediate, 2.1% are sensitive to the drug, and 19.8% dose-dependent sensitive.

Therefore, the Phi coefficient of 0.367 indicates a moderate association between ward and Imipenem susceptibility, and the p-value of 0.000 (<0.001) shows this association is statistically significant.

Table 4.31: Crosstabulation of Ward Name against Moxifloxacin

Crosstabulation Of Ward Name Against Moxifloxacin

			MOXIFLOXACIN				**Total**	**Phi**	**P-value**
			None	*Resistant*	*Sensitive*	*Dose-Dependent Sensitive*			
WARD_NAME	**A6 INTENSIVE CARE UNIT**	**N**	1 191	164	69	163	1 587	0.329	0
		%	75%	10.3%	4.3%	10.3%	100%		
	EMERGENCY UNIT	**N**	2 416	922	34	221	3 593		
		%	67.2%	25.7%	0.9%	6.2%	100%		
	M1 MEDICAL WARD	**N**	1 445	338	345	351	2 479		
		%	58.3%	13.6%	13.9%	14.2%	100%		
	MEDICAL RECOVERY	**N**	2 200	778	54	214	3 246		
		%	67.8%	24%	1.7%	6.6%	100%		
	MEDICAL WARD U5A	**N**	1 966	537	94	81	2 678		
		%	73.4%	20.1%	3.5%	3%	100%		
	MULTIDISCIPLINARY UNIT	**N**	1 910	119	31	75	2 135		
		%	89.5%	5.6%	1.5%	3.5%	100%		

Table 4.31 presents the distribution of Moxifloxacin antibiotic susceptibility across wards.

- In the A6 Intensive Care Unit, 75% of isolates have results for this antibiotic “none”, 10.3% are resistant, 4.3% isolates are sensitive to this drug, and 10.3% dose-dependent sensitive.
- In the Emergency Unit, 67.2% are recorded as “none”, 25.7% are resistant, 0.9% are sensitive to this drug, and 6.2% dose-dependent sensitive.

- In the M1 Medical Ward, 58.3% are “none”, 13.6% patients show resistance to the antibiotic, 13.9% are sensitive, and 14.2% dose-dependent sensitive.
- In Medical Recovery, 67.8% are “none”, 24% are resistant, 1.7% are sensitive, and 6.6% dose-dependent sensitive.
- In Medical Ward U5A, 73.4% are “none”, 20.1% show resistance to the drug, 3.5% isolates are sensitive, and 3% dose-dependent sensitive.
- In the Multidisciplinary Unit, 89.5% are “none”, 5.6% are resistant, 1.5% are sensitive, and 3.5% dose-dependent sensitive.

Therefore, the Phi coefficient of 0.329 shows a moderate association between ward and Moxifloxacin antibiotic susceptibility, and the p-value of 0.000 (<0.001) confirms this relationship is statistically significant.

Table 4.32: Crosstabulation of Ward Name against Rifampicin

Crosstabulation of Ward Name Against Rifampicin									
			RIFAMPICIN						
			None	*Resistant*	*Sen-sitive*	*Dos-e Depen-dent Sensitive*	**Total**	**Phi**	**P-value**
WARD NAME	**A6 INTENSIVE CARE UNIT**	**N**	1 179	176	29	203	1 587	0.345	0
		%	74.3%	11.1%	1.8%	12.8%	100%		
	EMERGENCY UNIT	**N**	2 371	727	247	248	3 593		
		%	66%	20.2%	6.9%	6.9%	100%		
	M1 MEDICAL WARD	**N**	1 391	360	125	603	2 479		
		%	56.1%	14.5%	5%	24.3%	100%		
	MEDICAL RECOVERY	**N**	2 205	756	103	182	3 246		
		%	67.9%	23.3%	3.2%	5.6%	100%		
	MEDICAL WARD U5A	**N**	1 223	969	6	480	2 678		
		%	45.7%	36.2%	0.2%	17.9%	100%		
	MULTI-DISCIPLINARY UNIT	**N**	1 789	190	1	155	2 135		
		%	83.8%	8.9%	0%	7.3%	100%		

Table 4.32 shows the distribution of Rifampicin antibiotic susceptibility across hospital wards.

- In the A6 Intensive Care Unit, 74.3% of isolates’ antibiotic results show “none”, 11.1% are resistant, 1.8% isolates are sensitive, and 12.8% dose-dependent sensitive.

- The Emergency Unit has 66% patients isolates with no results “none,” 20.2% are resistant, 6.9% are sensitive to this drug, and 6.9% dose-dependent sensitive.
- M1 Medical Ward shows 56.1% under “none”, 14.5% are resistant, 5% isolates are sensitive, and 24.3% dose-dependent sensitive.
- Medical Recovery reports 67.9% “none,” 23.3% isolates show resistance, 3.2% are sensitive, and 5.6% dose-dependent sensitive.
- Medical Ward U5A has 45.7% under “none”, 36.2% display resistance, 0.2% are sensitive, and 17.9% dose-dependent sensitive.
- The Multidisciplinary Unit displays 83.8% under “none”, 8.9% show resistance to the drug, No sensitivity (0%) is recorded for this drug, and 7.3% are dose-dependent sensitive.

The Phi coefficient of 0.345 suggests a moderate relationship between wards and Rifampicin antimicrobial susceptibility, and the p-value of 0.000 indicates that this association is statistically significant.

Table 4.33: Crosstabulation of Ward Name against Teicoplanin

Crosstabulation Of Ward Name Against Teicoplanin									
			TEICOPLANIN				**Total**	**Phi**	**P-value**
			None	*Resistant*	*Sensitive*	*Dose-Dependent Sensitive*			
WARD NAME	**A6 INTENSIVE CARE UNIT**	**N**	1 138	391	24	34	1 587	0.204	0
		%	71.7%	24.6%	1.5%	2.1%	100%		
	EMERGENCY UNIT	**N**	2 389	1 143	51	10	3 593		
		%	66.5%	31.8%	1.4%	0.3%	100%		
	M1 MEDICAL WARD	**N**	1 340	1 069	53	17	2 479		
		%	54.1%	43.1%	2.1%	0.7%	100%		
	MEDICAL RECOVERY	**N**	2 247	940	31	28	3 246		
		%	69.2%	29%	1%	0.9%	100%		
	MEDICAL WARD U5A	**N**	1 973	612	75	18	2 678		

		%	73.7%	22.9%	2.8%	0.7%	100%		
	MULTI-DISCIPLINARY UNIT	**N**	1 794	330	4	7	2 135		
		%	84%	15.5%	0.2%	0.3%	100%		

Table 4.33 presents teicoplanin antimicrobial susceptibility across hospital wards.

- In the A6 Intensive Care Unit, 71.7% of the isolates do not have laboratory results of this antibiotic, 24.6% isolates are resistant, 1.5% are sensitive, and 2.1% dose-dependent sensitive.
- The Emergency Unit has 66.5% isolates with no results for this antibiotic “none”, 31.8% are resistant, 1.4% show sensitivity, and 0.3% dose-dependent sensitive.
- M1 Medical Ward 54.1% does not have results “none”, 43.1% are resistant, 2.1% are sensitive, and 0.7% dose-dependent sensitive.
- Medical Recovery has 69.2% under “none”, 29% isolates are resistant, 1% are sensitive, and 0.9% dose-dependent sensitive.
- Medical Ward U5A reports 73.7% under “none”, 22.9% isolates are resistant, 2.8% are sensitive, and 0.7% dose-dependent sensitive.
- The Multidisciplinary Unit has 84% “none”, 15.5% show resistance, 0.2% are sensitive, and 0.3% dose-dependent sensitive.

Therefore, the Phi coefficient of 0.204 indicates a weak to moderate relationship between ward and Teicoplanin antibiotic susceptibility, However, the p-value of 0.000 shows that this association is statistically significant.

Table 4.34: Crosstabulation of Ward Name against Tigecycline

Crosstabulation Of Ward Name Against Tigecycline									
			TIGECYCLINE				**Total**	**Phi**	**P-value**
			None	*Resistant*	*Sensitive*	*Dose-Dependent Sensitive*			
WA	**A6 INTENSIVE CARE UNIT**	**N**	310	1 002	54	221	1 587	0.341	0
		%	19.5%	63.1%	3.4%	13.9%	100%		
	EMERGENCY UNIT	**N**	870	2 389	20	314	3 593		
		%	24.2%	66.5%	0.6%	8.7%	100%		

RD NAME	**M1 MEDICAL WARD**	**N**	455	1 871	34	119	2 479		
		%	18.4%	75.5%	1.4%	4.8%	100%		
	MEDICAL RECOVERY	**N**	809	2 156	21	260	3 246		
		%	24.9%	66.4%	0.6%	8%	100%		
	MEDICAL WARD U5A	**N**	1 599	965	18	96	2 678		
		%	59.7%	36%	0.7%	3.6%	100%		
	MULTI-DISCIPLINARY UNIT	**N**	912	1 026	55	142	2 135		
		%	42.7%	48.1%	2.6%	6.7%	100%		

Table 4.34 presents Tigecycline susceptibility across hospital wards.

- In the A6 Intensive Care Unit, 19.5% of isolates do not have results for this antibiotic, 63.1% isolates are resistant, 3.4% are sensitive, and 13.9% dose-dependent sensitive.
- The Emergency Unit shows 24.2% patients do have results for this antibiotic, 66.5% are resistant, 0.6% patients show sensitivity, and 8.7% dose-dependent sensitive.
- M1 Medical Ward has 18.4% isolates with no results, 75.5% are resistant, 1.4% are sensitive, and 4.8% dose-dependent sensitive.
- Medical Recovery reports that 24.9% patients do not have results for this antibiotic, 66.4% are resistant, 0.6% are sensitive, and 8% dose-dependent sensitive.
- In Medical Ward U5A, 59.7% are recorded as “none”, 36% isolates are resistant, 0.7% are sensitive, and 3.6% dose-dependent sensitive.
- The Multidisciplinary Unit has 42.7% who do not have results for this antibiotic, 48.1% are resistant, 2.6% are sensitive, and 6.7% dose-dependent sensitive.

The Phi coefficient of 0.341 demonstrates a moderate association between ward and Tigecycline antibiotic susceptibility, and the p-value of 0.000 confirms this association is statistically significant.

Table 4.35: Crosstabulation of Ward Name against Nitrofurantoin

Crosstabulation of Ward Name Against Nitrofurantoin									
			NITROFURANTOIN				Total	Phi	P-value
			None	*Resistant*	*Sensitive*	*Dose-Dependent Sensitive*			
WARD NAME	A6 INTENSIVE CARE UNIT	N	1033	178	135	241	1 587	0.203	0
		%	65.1%	11.2%	8.5%	15.2%	100%		
	EMERGENCY UNIT	N	2083	825	309	376	3 593		
		%	58%	23%	8.6%	10.5%	100%		
	M1 MEDICAL WARD	N	1651	243	369	216	2 479		
		%	66.6%	9.8%	14.9%	8.7%	100%		
	MEDICAL RECOVERY	N	1 987	643	268	348	3 246		
		%	61.2%	19.8%	8.3%	10.7%	100%		
	MEDICAL WARD U5A	N	2 054	229	136	259	2 678		
		%	76.7%	8.6%	5.1%	9.7%	100%		
	MULTI-DISCIPLINARY UNIT	N	1 430	262	155	288	2 135		
		%	67%	12.3%	7.3%	13.5%	100%		

Table 4.35 presents the distribution of Nitrofurantoin antimicrobial susceptibility across different wards.

- In the A6 Intensive Care Unit, the most of the isolates (65.1%) fall into the “none” category due to not having a laboratory report for this antibiotic, while 11.2% are resistant, 8.5% are sensitive, and 15.2% dose-dependent sensitive.
- The Emergency Unit shows 58% under “none”, 23% are resistant, 8.6% are reported to be sensitive, and 10.5% dose-dependent sensitive.
- M1 Medical Ward has 66.6% under “none”, 9.8% are resistant, 14.9% isolates are reported to be sensitive, and 8.7% dose-dependent sensitive.
- In Medical Recovery, 61.2% are recorded under “none”, 19.8% a resistant, 8.3% are found to be sensitive, and 10.7% dose-dependent sensitive.
- Medical Ward U5A shows the highest proportion in the “none” category at 76.7%, with 8.6% isolates reported to be resistant, 5.1% isolates are sensitive, and 9.7% dose-dependent sensitive.
- The Multidisciplinary Unit has 67% isolates not having laboratory results “none”, 12.3% are reported as resistant, 7.3% are sensitive, and 13.5% dose-dependent sensitive.

The Phi coefficient of 0.203 demonstrates a weak association between ward and Nitrofurantoin antibiotic susceptibility, and the p-value of 0.000 (<0.001) demonstrates that this relationship is statistically significant.

CHAPTER 5: DISCUSSION AND CONCLUSION

5.1 DESCRIPTIVE STATISTICS

Descriptive statistics of the study was done based on district name, facility name, gender of the patients and age group of the patients. This retrospective, cross-sectional study consisted of 48 597 participants and most of the participants in the study were from the Frances Baard District Municipality in Kimberley in the Northern Cape Province (58.4%), followed by the Mangaung Metropolitan Municipality in the Free State Province (37.9%). The majority of the patients in the study (58.4%) were treated at the Robert Mangaliso Sobukwe Provincial Hospital (Northern Cape Province), followed by 20.9% patients treated at the Universitas Academic hospital (Free State Province). The Mofumahadi Manapo Mopeli Regional Hospital had the least patients (0.7%). The highest age group percentage in the study was 27.1%, which fell between 28 and 37 years, followed by 26.4% between the ages of 38 and 47 years, with the lowest population (0.8%) was found between 78 and 87 years. The study showed that fewer patients were admitted to hospital from the age of 58 years and above. This could mean that most of the patients in these age groups are aware of their medical conditions and they comply with their treatment, which results in them having fewer hospital admissions. Another contributing factor can be the participants' lifestyle. Most participants in the study were recorded to be female 49.9%). There was a slight difference among male (49.4%). The study also recorded that 0.7% of the patients' gender was unknown.

5.2 ADDITIONAL DESCRIPTIVES

In the study, data of patients who tested for Tuberculosis using the GeneXpert ultra assay were analysed. 6 541 participants in the study had TB results across all six different hospitals. The study showed that 89.4% of patients tested negatively for TB across all six hospitals. 6.8% patients tested positively for TB, while 1.6% and 1.8% patients' TB results were unknown or not tested, respectively. The National District Hospital recorded the highest number of patients who tested positively for TB at a rate of n=169 (9.7%), followed by Bongani Regional Hospital at a rate of n=119 (8.3%). Robert Mangaliso Sobukwe Provincial Hospital had n=2 226 (7.8%) TB-positive cases, Mofumahafi Manapo Mopeli Regional Hospital recorded n=23 (7.1%) TB-positive cases, Pelonomi Regional Hospital had n=409 (6.3%) positive cases and Universitas Academic hospital recorded n=362 (3.6%) TB-positive cases, which is the lowest. 54 597 patients' HIV results were received for this study. The majority of the participants in the patients in the study were not tested for HIV using the HIV-1/2 rapid screen test and of those who were tested, only 1.2% were reported to be HIV positive and 4.2% were negative. 70.9% of the patients did not have HIV-1/2 AB/AG screen results, while 24.4% tested negative and 4.3% tested positive.

The data show that only 0.6% of the patients had equivocal HIV results, which means that the HIV sample had to be repeated using a different machine for confirmation. The study showed that 7.9% (n=3 862/48 597) patients' HIV viral load were undetectable, which means that the patients were compliant with Antiretroviral Therapy (ART) treatment. However, this rate is very low when compared to the rate of patients on effective ART (65.3%) in the study that was conducted by Franceschini et al. (2020). The undetectable HIV viral load was <20-50 copies/mL, 6.9% patients had a low HIV viral load of 50-10 000 copies/mL and a population of n=3 299 (6.8%) was found to have a high HIV viral load >100 000 copies/mL. The study showed that 74.9% patients were not tested for HIV viral load. 68.9% of patients in this study did not have CD4 ARV results, so their immune systems were not monitored. 23.4% of the patients displayed a low immune system (<350 cells/mm$^{3)}$, which means that they were not complying with ART treatment. 3.6% of the patients had mild immunosuppression (350–499 cells/mm$^{3)}$ and 4.2% of the patients had a strong immune system, which means that they are complying with to ART treatment. These findings support the claims by Lubega et al. (2023) that low CD4 counts and detectable viral loads are risk factors for patients in microbial infections.

The study also evaluated the prevalence testing method for all the specimens submitted to the laboratory for microbes and antimicrobial testing. Automated culture was the method mostly used in the laboratory and it was reported to be at the rate of 42.8%, followed by culture urine (25.4%), culture pus (23.3%). Culture catheter tip was the least frequently used test method, displaying a rate of 8.5%. 48 597 specimens were reported to have been tested in the laboratory. In the study, the type of specimen collected from patients and sent to the laboratory for testing was also analysed. 48 597 specimens were collected. Blood culture (38.4%) was the most frequently collected specimen as the patients might have been suspected of having a bloodstream infection. This supports the claims from (Dewi et al., 2023) that critically ill patients in ICU have high chances of getting bacterial infections in the bloodstream. Urine was the second-most frequently collected specimen (16.5%), as the patients might have been suspected for having UTI. Swab (superficial) was reported in 15.6% cases, abscess (superficial swab) reported in 3.9% cases, Arterial Catheter Tip was reported in 3.1% cases, wound swab reported in 3.3% cases, catheter urine reported in 2.9% cases, and fluid/aspirate reported in 2.7% cases. The top 10 prevalent microorganisms from the sample isolates were *Escherichia Coli* (16.9%), *staphylococcus aureus* (14.5%), Coagulase Negative *staphylococcus* (11.9%), *Klebsiella Pneumoniae* subsp Pneumonia (9.4%), *Staphylococcus Epidermidis* (5.2%), *Streptococcus Pneumoniae* (4%), *Proteus Mirabilis* (4%), *Acinetobacter Baumannii* (3.7%), *Pseudomonas Aeruginosa* (3.2%), *Enterobacter Cloacae* subsp. Cloacae (2.9%).

The findings in this study correspond with the study of Kamara (et al.,2024), as they also report that *Staphylococcus aureus* was 35.7%, *Pseudomonas Aeruginosa* 19.6%, *Streptococcus Pneumoniae* 17.9% and *Enterobacter* species at 8.9%. Similar findings were observed from the study of Dewi et al. (2023), as they also report an increase in the prevalence of *Pseudomonas Aeruginosa* and *Acinetobacter Baumannii* microorganisms.

The study observed a prevalence of microorganisms in hospitals that are located in urban facilities, compared to facilities located in rural areas. This could be caused by patients being transferred from rural/district hospitals to urban/regional/ provincial/academic hospitals so that they can have access to advanced treatment. In contrast, with the study conducted by Tilahun et al. (2023), who report that more microorganisms are observed in rural facilities (64%) compared to urban facilities (40.8%).

5.3 GENDER GROUP COMPARISONS

At all six hospitals, the majority of the patients, both male and female, tested negatively for TB at intake.

- At the Robert Mangaliso Sobukwe Provincial Hospital, 8.2% female patients tested positively for TB and 7.7% male patients tested positively for TB.

- At the Bongani Regional Hospital, 12.9% female patients were found to have tested positively for TB and 3.8% male patients were TB positive.
- At the National District Hospital, 10.9% female and 8.4% male patients were found to have tested TB positively.
- The Mofumahadi Manapo Mopeli Regional hospital reported that 7.4% male and 6.6% female patients tested positively for TB.
- Pelonomi Regional Hospital reported that 6.4% male and 6.1% female tested positively for TB.
- Universitas Academic hospital recorded the lowest cases of patients that were TB positive: 4.5% female and 2.5% male patients were reported to have tested positively for TB.
- At both the Mofumahadi Manapo Mopeli Regional Hospital and the Pelonomi Regional Hospital TB prevalences in terms of gender were different from the other hospitals. The study showed that these two hospitals' statistics indicated that male patients are more prevalent regarding TB-positive results.

Most patients in this study had no records of their HIV status.

- Robert Mangaliso Sobukwe Provincial Hospital's HIV-positive results were higher in females (4.4%) than in males (4%).
- Bongani Regional Hospital's HIV-positive results were higher in males (6.5%) than in females (1.3%).
- The National District Hospital showed that HIV-positive results were higher in males (5.5%) compared to females (4.5%).
- Pelonomi Regional Hospital's HIV-positive results were more prevalent in males (7%) than in females (6.4%).
- Lastly, the Universitas Academic Hospital displayed that HIV-positive results were more prevalent in males (3.7%) compared to females (2.5%).

The study demonstrated that at all six hospitals, the number of male patients who tested positively for HIV was higher than in female patients. This is different from TB cases, as at four hospitals, the number of TB-positive cases was more prevalent in female than in male patients. Only at two hospitals it was found that the number of TB-positive cases were more prevalent in male patients than in female patients. The study showed that 10.2% of male patients had an HIV viral load of <50 copies/mL. This indicates viral suppression, which results from being compliant ART, while 7.5% of male patients in the study had a viral load >100 000 copies/mL, indicating that this patients are not complying to ART. Among females that were HIV positive, only 0.2% had records of an HIV viral load between 100 001–100 000 copies/mL, which indicate that the patients were not complying to ART. The study showed that 33.9% of male patients had a CD4 count of <350 cells/mm^3. These were already known HIV-positive patients. However, they did not comply with ART. 0.1% HIV-positive female patients have an ARV CD4 count of >500 cells/mm^3, which indicates complying with ARV treatment. However, 0.2% of female patients were reported to be positive for HIV, but the CD4 count was reported to be <350 cells/mm^3. This indicates possible non-compliance with ARV treatment. The study showed that the majority of male patients were non-compliant with ARV treatment as they were found to have the highest HIV viral load. The majority also had low CD4 counts.

5.4 AGE GROUP COMPARISON

The study showed that the highest prevalence of TB-positive patients were between 28–37 years at a rate of 11.6%, followed by 38–47 years with 8.6%. The study also showed that the majority of patients in all the different age groups were reported to be TB negative at intake.

- At Bongani Regional hospital, the most prevalent TB-positive cases were reported in patients between 38–47 years (14%) and the highest TB negative group was observed in patients between 48–57 years with 92.4%.
- Mofumahadi Manapo Mopeli Regional hospital showed that TB positive prevalence occurred in patients between 18–27 years with 15.4%.
- At Universitas Academic hospital, the study showed that the highest proportion of TB-positive patients was between 18–27 years at 6.4%.

The study showed that at six hospitals, TB-positive cases were more likely to occur in younger to middle-aged groups, with the peak ranges from 6.4% (18-37 years) to

15.4% and 14% (38-47%). Both Mofumahadi Manapo Mopeli Regional hospital and Universitas academic hospital showed the highest TB-positive prevalence between 18-27 years.

- The highest prevalence of HIV-positive cases observed at the Robert Mangaliso Sobukwe Provincial Hospital were in patients between 58 and 67 years (5.2%) and HIV-negative cases were observed in patients between 68 and 77 years.
- At the Bongani Regional Hospital, the highest HIV-positive cases were observed in patients between 78 and 87 years at a 50% rate.
- The National District Hospital reported the highest HIV-positive cases in patients between 48 and 57 years at the rate of 10% and HIV negative cases in the 58–67-year age group at 8.4%.
- At the Mofumahadi Manapo Mopeli Regional Hospital, the highest HIV-positive cases were observed in patients between 28 and 37 years at 7.2%, while in HIV-negative patients, the highest proportion was observed in the same age group at 46.6%.
- At Pelonomi Regional Hospital, the highest HIV-positive cases were observed between 78 and 87 years at 14% and the highest HIV-negative cases were observed in patients aged 38–47 years at 20.3%.
- Lastly, at the Universitas Academic Hospital the highest HIV-positive cases were observed in patients between 38 and 47 years at 5.1%, while the highest HIV-negative cases were observed between 48 and 57 years at 36.3%.

The study also showed similarities and differences within the same age group across the hospitals.

- The Robert Mangaliso Sobukwe Provincial Hospital reported the highest HIV-positive results in patients aged 58–67 years.
- In contrast, the same age group at the National District Hospital had the highest prevalence of HIV-negative cases.
- Bongani Regional Hospital reported the highest HIV-positive prevalence in patients aged 78 to 87 years.

- This is similar to the Pelonomi Regional Hospital, as HIV-positive patients were high at 78 to 87 years.
- At the National District Hospital, HIV-positive patients were high between the ages of 48 and 57 years.e
- Universitas Academic Hospital reported that the same age group had the highest HIV-negative results.
- Lastly, the Pelonomi Regional Hospital showed that the age group of 38 to 47 years had the highest prevalence in HIV-negative results.
- In contrast, Universitas Academic Hospital reported that the same age group had the highest HIV-positive cases.

The study discovered that the majority of patients that were HIV-positive admitted to hospital were 38 years and above. This support the claims made by Alem (2021) that age is a contributing risk factor in microbial infections.

5.5 MICROBIAL PROFILE AND ANTIMICROBIALS SHOWING THE HIGHEST SENSITIVITY OR RESISTANCE PATTERNS

- The study showed that the microorganism *Acinetobacter Baumannii* displayed the highest level of antimicrobial resistance in Amikacin n=1867 (65.9%), Ceftazidime n=2 595 (91.6%), Ciprofloxacin n=2 536 (89.5%), Gentamicin n=2 527 (89.2%), Imipenem n=2 630 (92.9%), Tobramycin n=1 848 (65.3%) and Meropenem n=2 620 (92.5%). The study showed that most antibiotics show high resistance to *Acinetobacter Baumannii.*
- *Klebsiella Pneumoniae* Subsp Pneumoniae microorganism displayed the highest level of resistance in Cefuroxime oral n=2282 (50.3%) and Cefuroxime parenteral n=2270 (50.1%), the same microorganism showed high sensitivity to Amikacin n=3834 (84.6%), Ertapenem n=3708 (81.8%) and Colistin n=3825 (84.4%). Amikacin was notably sensitive to *Klebsiella Pneumoniae* Subsp Pneumoniae.
- In contrast, Amikacin showed the highest level of resistance to *Acinetobacter Baumannii* and the Phi coefficient of 1.183 shows a very strong association

between organism, and the p-value of 0.000 affirms that this difference is statistically significant.

- The organism *Proteus Mirabilis* displayed a high level of resistance to Colistin n=1203 (67.1%), Nitrofurantoin n=1593 (88.8%) and Tigecycline n=1546 (86.2%). *Proteus Mirabilis* only showed the highest level of sensitivity to Amoxicillin Clavulanic Acid n=1566 (87.3%). Most antibiotics showed a high level of sensitivity to *Proteus Mirabilis.*
- *Klebsiella pneumoniae* also demonstrated a 34.5% prevalence of resistance and 48.8% of sensitivity to Amoxicillin Clavulanic Acid, while *Proteus mirabilis* had very low resistance (4.2%) and very high sensitivity (87.3%). The Phi coefficient of 1.07 indicates a very strong relationship between the organism and drug response, with the p-value of 0.000 confirming statistical significance.
- *Candida albicans* displayed high level of sensitivity to most antibiotics, Amphotericin B n=92 (86%), Fluconazole n=92 (86%) and Voriconazole n=88 (82.2%). The *Candida* species displayed resistance to Amphotericin B by n=15 (53.6%) and sensitivity to the same drug was n=12 (42.9%). With antibiotic Amphotericin B, *Candida albicans* demonstrated a sensitivity in 86% of cases, and resistance was found in 0.9% cases, while other *Candida* species showed a higher resistance (53.6%) to Amphotericin B, in contrast to the lower sensitivity (42.9%). The Phi coefficient of 1.189 showed a very strong positive alliance between organism and susceptibility to Amphotericin B, with the p-value of 0.000 confirming significance.
- The *Escherichia coli* microorganism showed a high level of resistance to Trimethoprim Sulfamethoxazole n=5 138 (68.3%), Ampicillin Amoxicillin n=5843 (77.7%) and Cefepime n=5843 (77.7). The highest level of *E.coli* sensitivity was found in Tigecycline n=5899 (78.4%), Cefotaxime Ceftriaxone n=5 920 (78.7%), Cefoxitine n=6 702 (89.1%), Ceftazidime n=6 009 (79.9%), Cefuroxime oral n=4 864 (64.7%), Cefuroxime parenteral n=5 380 (71.5%), Ciprofloxacin n=5 461 (72.6%), Ertapenem n=7 271 (96.7%), Gentamicin n=6 331 (84.2%), Imipenem n=7 321 (97.3%), Meropenem n=6 977 (92.8%) and Nitrofurantoin n=5 930 (78.8%). The study showed that *E.coli* was sensitive to most drugs of choice.

- *Enterobacter Cloacae* Subsp *Cloacae* displayed complete resistance to the antibiotic Cefoxitine n=1 262 (99.4%), while no sensitivity was recorded for this organism.
- The organism *streptococcus Pneumoniae* showed a high level of sensitivity to Ceftriaxone CNS Infection n=681 (50.7%), Ceftriaxone non-CNS Infection n=892 (66.5%),and Penicillin non-CNS Infection n=908 (67.7%). The organism was sensitive to most antibiotics and displayed a resistance to the very same antibiotics, less than <9%.
- Coagulas-negative *Staphylococcus* showed a high resistance to Clindamycin n=3 110 (55%), Cloxacillin n=4 103 (72.6%) and Erythromycin azithromycin n=4 346 (76.9%) and high sensitivity rates were reported in Fusidic Acid n=3 337 (59%) and Linezolid n=4 657 (82.4%).
- The *Streptococcus aureus* organism was sensitive to most antibiotics: Clindamycin n=4 798 (79.7%), Cloxacillin n=1 318 (81.1%), Fusidic Acid n=4 888 (81.2%), Moxifloxacin n=4 396 (73%), Rifampicin n=4 238 (70.4%), Teicoplanin n=4 881 (81.1%), Tetracycline n=3 935 (65.3%), Trimethoprim Sulfamethoxazole n=3 279 (54.5%) and Vancomycin n=5 293 (87.9%). The organism also showed the highest resistant cases in Trimethoprim Sulfamethoxazole n=2 543 (42.2%).
- The study showed that the *Candida Parapsilosis* organism showed high cases of antibiotic sensitivity in Fluconazole n=32 (68.8%) and Voriconazole n=20 (62.5%).
- *Enterococcus Faecalis* displayed low cases of resistance to the Linezolid antibiotic n=6 (0.5%). In contrast, the same antibiotic showed high sensitivity at the rate of n=1 108 (87.8%).
- *Streptomycin* a high-level resistance antibiotic, showed a n=778 (61.8%) level of resistance to the organism. Lastly, Gentamicin, a high-level resistance, showed a high level of sensitivity at n=709 (56.2%).
- The *Enterococcus Faecium* organism had a resistance of n=436 (69.8%).

- Lastly, the study showed that the *Streptococcus Alpha-Haemolytic* organism was found to be resistant and sensitive to Penicillin CNS Infection at 0.7% and 0%, respectively.

The study showed that Trimethoprim-sulfamethoxazole antibiotic showed high resistance ton both gram-negative and gram-positive bacteria, 68.3% and 42.2%, respectively. In contrast, Trimethoprim-sulfamethoxazole antibiotic was reported to be resistant to only gram-positive bacteria by (Okon et al., 2023). In the study, Gentamicin showed high antibiotic resistance in gram-positive bacteria (*Enterococcus faecalis* at 31.8% and *Enterococcus Faecium* at 69.8%). This is similar to the findings of Okon et al. (2023), as the antibiotic also showed high resistance in gram-positive bacteria at 44.4%. The study showed that *Streptococcus Pneumoniae* had high sensitivity (50.7%) to Ceftriaxone antibiotic. This is similar to the study of Lubega et al. (2023) as they reported a 100% sensitivity to this antibiotic.

5.6 PREVALENCE OF THE TOP 10 ANTIMICROBIAL SENSITIVITY OR RESISTANCE IN DIFFERENT WARD

In the A6 Intensive Care Unit, the antibiotic cefuroxime oral was reported to be resistant in n=281 (17,1%) cases, while n=23 (1.4%) cases displayed to be sensitive to this antibiotic. Ciprofloxacin was found to be resistant in n=640 (40.3%) cases, in contrast to n=32 (2%) sensitive cases. Imipenem antibiotic displayed n=420 (26.5%) level of resistance, while n=54 (3.4%) isolates were sensitive to the antibiotic. Moxifloxacin displayed a n=164 (10.3%) resistance rate and n=69 (4.3%) were reported to have been sensitive to this antibiotic. Rifampicin showed resistance of n=176 (11.1%) cases and sensitivity was reported in n=29 (1.8%) cases. Teicoplanin was found to display resistance in n=391 (24.6%) cases and sensitivity was found in n=24 (1.5%) isolates. Tigecycline antibiotic was reported to be resistant in n=1 002 (63.1%) cases and sensitive in n=54 (3.4%) cases, lastly in this ward, Nitrofurantoin was resistant in n=178 (11.2%) cases and sensitive in n=135 (8.5%) cases.

In the Emergency Unit, the antibiotic Amikacin displayed resistance in n=1 532 (42.6%) cases while sensitivity cases were found in n=133 (3.7%) isolates. Amoxicillin Clavulanic Acid showed a resistance rate in n=908 (25.3%) cases and sensitivity was noted in n=284 (7.9%) cases. The resistance rate in Cefuroxime oral antibiotic was n=948 (26.4%), while sensitivity was observed in n=57 (1.6%) cases. Ciprofloxacin antibiotic in this ward displayed resistance in n=2 255 (62.8%) cases, while sensitivity was observed in n=75 (2.1%). Imipenem was reported to be resistant in n=1573 (43.8%) cases, while sensitivity was observed in n=130 (3.6%) cases. Rifampicin was observed to be resistant in n=727 (20.2%) isolates and sensitivity was observed in n=247 (6.9%) isolates. Teicoplanin antibiotic in this ward showed resistance in n=1 143 (31.8%) and sensitivity was observed in n=51 (1.4%) isolates. Lastly, Nitrofurantoin antibiotic in this ward showed resistant in n=825 (23%) cases and sensitivity was reported in n=309 (8.6%) cases.

In M1 Medical ward, the antibiotic Ciprofloxacin showed resistance in n=1 147 (46.3%) cases and sensitivity was observed in n=55 (2.2%) cases. Moxifloxacin antibiotic displayed almost the same percentage when it comes to resistance and sensitivity (13.6% and 13.9%), respectively. Rifampicin antibiotic in this ward showed resistance in n=360 (14.5%) isolates and sensitivity was reported in n=125 (5%) isolates. Teicoplanin showed resistance in n=1069 (43.1%) cases and was sensitive in n=53 (2.1%) cases. Tigecycline showed high resistance in n=1871 (75. 5%) isolates, compared to n=34 (1.4%) sensitive cases. Nitrofurantoin antibiotic showed resistance in n=243 (9.8%) cases and sensitivity was observed in n=369 (14.9%) cases.

In the Medical Recovery ward, Amikacin was reported to be resistant in n=1389 (42.8%) isolates. Amoxicillin Clavulanic Acid was resistant in n=846 (26.1%) cases, while sensitive in n=170 (5.2%) cases. Ciprofloxacin was reported to be resistant in n=1 983 (61.1%) and sensitive in n=38 (1.2%) cases. Imipenem antibiotic was resistant in n=1 422 (43.8%) isolates and sensitive to n=107 (3.3%) isolates. Moxifloxacin was resistant in 778 (24%) isolates from this ward and sensitive in n=54 (1.7%) isolates. Rifampicin antibiotic was resistant in n=756 (23.3%) and sensitive in n=103 (3.2%) isolates. Teicoplanin in this ward was found to be resistant in n=940 (29%) cases and sensitive in n=31 (2.1%) cases. Nitrofurantoin in this ward was resistant in n=643 (19.8%) cases and sensitive in n=268 (8.3%) cases.

In Medical ward U5A, the antibiotic Cefuroxime oral was observed to be resistant in n=233 (8.7%) cases and sensitive in n=26 (1%) cases. Ciprofloxacin was reported resistant in n=867 (32.4%) isolates, while sensitive in n=30 (1.1%) isolates. Moxifloxacin antibiotic in this ward was resistant in n=537 (20.1%) cases and sensitive in n=94 (3.5%) cases. Teicoplanin antibiotic was reported resistant in n=612 (22.9%) cases and sensitive in n=75 (2.8%) cases. Lastly, it was reported Nitrofurantoin antibiotic showed resistance in n=229 (8.6%) cases and sensitive in n=136 (5.1%) cases.

In the Multidisciplinary Unit, the antibiotic Cefuroxime oral was reported to be resistant in n=351 (16.4%) cases and observed to be sensitive in n=28 (1.3%) cases. Imipenem was found to be resistant in n=850 (39.8%) isolates and sensitive in n=45 (2.1%) isolates. Moxifloxacin was resistant in n=119 (5.6%) cases and sensitive in n=31 (1.5%) cases. Tigecycline antibiotic showed resistance in n=1 026 (48.1%) cases and sensitive in n=55 (2.6%) cases. Lastly, Nitrofurantoin antibiotic in this ward showed resistance in n=262 (12.3%) isolates and sensitive in n=155 (7.3%) isolates.

The study proved that the ward type where patients were admitted to plays a huge risk factor in antibiotic treatment. Most patients who were admitted to Medical wards showed a very high prevalence of antimicrobial resistance. Resistance was observed in all the antibiotics. The same trend was observed in both ICUs, in the A6 Intensive Care Unit and Multidisciplinary unit. Most patients showed a high prevalence of resistance to most antibiotics. These findings support the claims made by (Temesgen et al., 2023) that bacterial contamination of indoor hospitals, particularly in Intensive Care Units is a serious health hazard in the world with high morbidity rates. The findings in the study support the claims made by Temesgen et al. (2023), as they mention that treatment of patients with empirical antibiotics often leads to antimicrobial resistance. Bhat et al. (2021), claim that immunocompromised patients often suffer from antibiotics resistance. The same was observed in the study with HIV- and TB-positive patients. The study also showed that the Nitrofurantoin antibiotic displayed high sensitivity in most wards. The study showed that antibiotic Imipenem was sensitive to microorganisms in most wards. This is similar to the findings of Okon et al. (2023), as they report a high sensitivity rate for this antibiotics in most microorganisms.

A systematic review of previous studies found that opportunistic microorganisms cause a high mortality rate in immunocompromised patients.

5.7 CONCLUSION

The study showed that the majority of patients had a high HIV viral load and low CD4 count, which show non-compliance with ART. The majority of male patients had a detectable viral load and a low CD4 count, which is a risk factor for acquiring microbial infections. There was a high prevalence of antimicrobial resistance from different wards in the study.

5.8 RECOMMENDATIONS

It is not recommended for clinicians to use an antibiotic that shows intermediate sensitivity, as that drug is not guaranteed to work in the patient. This increases the statistics of MDR in patients. The use of empirical antibiotics in patients should be discontinued, as it also contributes to the increase of MDR. The government must initiate programmes to encourage male patients regarding compliance with ART. The government must conduct regular studies to check the microbial profile prevalences in different hospitals, as this will aid in implementing new systems.

5.9 STUDY LIMITATION

The limitation in this study is that from the laboratory results provided, the researchers did not know which antibiotic was actually administered to the patients by clinicians and how the patients responded to that particular antibiotic, as the researchers did not have access to the patients' medical file in the wards.

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APPENDICES

APPENDIX A: ARTICLES FRONT PAGE SCREENSHOT

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Global Patterns Of Microbial Prevalence And Antibiotic Resistance: A Literature Review Highlighting Research Gaps In The Free State And Northern Cape Provinces Of South Africa

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Abstract
Hospital-acquired infections (HAIs) are a growing public health challenge in Sub-Saharan Africa, particularly among hospitalized patients where bacteria account for the majority of microbial infections. Gram-negative bacteria (GNB), especially Enterobacteriaceae, are the most commonly observed drug-resistant pathogens in healthcare settings. Multi-drug resistant Enterobacteriaceae (MRDE) infections are associated with poor clinical outcomes and high mortality, especially in low- and middle-income countries. Studies show significant variability in resistance patterns across hospitals, with some reporting up to 57.3% MDR and 3.5% XDR strains of Enterobacteriaceae. Extended-spectrum β-lactamase-producing Enterobacteriaceae (ESBL-E) also present an increasing threat, with prevalence rates ranging from 0.7% in Malawi to 75.8% in Egypt. Notably, mortality was higher in ESBL-positive patients (47.3%) compared to ESBL-negative patients (22.4%). Additionally, infections with Carbapenem-resistant Enterobacteriaceae (CRE) have demonstrated the highest 30-day mortality rate (63.8%) among resistant organisms. In South Africa, the emergence of multidrug-resistant organisms such as MRSA, CRAB, and CRE further exacerbates the burden of HAIs. Despite these alarming trends, there is a lack of comprehensive data on microbial prevalence and antibiotic susceptibility patterns in regional hospitals of the Free State and Northern Cape provinces. This literature review highlights these critical gaps and underscores the urgent need for localized studies to inform effective infection control and antibiotic stewardship strategies

Keywords: *Hospital-acquired infections, Multidrug-resistant organisms, Antibiotic resistance, Enterobacteriaceae, Carbapenem-resistant Enterobacteriaceae*

INTRODUCTION

Hospital-acquired infections (HAIs) remain a major public health concern globally, with the burden particularly severe in low- and middle-income countries, including those in Sub-Saharan Africa. These infections, commonly caused by bacteria such as *Staphylococcus aureus*, *Enterobacteriaceae*, *Acinetobacter baumannii*, *Klebsiella pneumoniae*, *Enterococci*, and *Pseudomonas spp.*, are associated with increased morbidity, prolonged hospital stays, and high mortality rates. Drug-resistant Gram-negative bacteria (GNB), particularly multidrug-resistant *Enterobacteriaceae* (MDRE), pose a significant challenge to patient safety and effective treatment. The emergence of extended-spectrum β-lactamase-producing *Enterobacteriaceae* (ESBL-E) and carbapenem-resistant strains (CRE) has further complicated infection control and antibiotic therapy in hospital settings.

Although multiple studies have documented rising antimicrobial resistance globally, there is limited data on microbial prevalence and antibiotic susceptibility specific to hospitalized patients in regional and provincial hospitals of South Africa, especially in the Free State and Northern Cape provinces. Additionally, inconsistencies in infection prevention strategies and antibiotic stewardship policies contribute to the proliferation of multidrug-resistant organisms in healthcare facilities. Understanding the regional burden of resistant infections, particularly among vulnerable and immunocompromised patients, is crucial for informing local policies and public health interventions. This literature review aims to identify existing research gaps and highlight the need for targeted epidemiological studies in these underrepresented provinces.

APPENDIX B: ETHICAL LETTERS

UNIVERSITY OF THE
FREE STATE
UNIVERSITEIT VAN DIE
VRYSTAAT
YUNIVESITHI YA
FREISTATA

UFS
HEALTH SCIENCES

Health Sciences Research Ethics Committee

09-Dec-2024

Dear **Ms Thabiso Mkhatshwa**

Ethics Clearance: **Microbial profile and antimicrobial sensitivity patterns in patients hospitalised in the six regional/provincial hospitals in the Free State and Northern Cape from 2018 to 2022.**
Principal Investigator: **Ms Thabiso Mkhatshwa**
Department: **CUT - Central University of Technology**
Submission Page

APPLICATION APPROVED

Please ensure that you read the whole document

With reference to your application for ethical clearance with the Faculty of Health Sciences, I am pleased to inform you on behalf of the Health Sciences Research Ethics Committee that you have been granted ethical clearance for your project.

Your ethical clearance number, to be used in all correspondence is:**UFS-HSD2024/1404/2801**

The ethical clearance number is valid for research conducted for one year from issuance. Should you require more time to complete this research, please apply for an extension.

We request that any changes that may take place during the course of your research project be submitted to the HSREC for approval to ensure we are kept up to date with your progress and any ethical implications that may arise. This includes any serious adverse events and/or termination of the study.

A progress report should be submitted within one year of approval, and annually for long term studies. A final report should be submitted at the completion of the study.

Research conducted in any Department of Health facility: Researchers are required to sign and return the HSREC approval letters to the provincial Department of Health where they applied. It is also a requirement for researchers to submit electronic copies of their final research findings, and/or make a presentation of their findings and recommendations at departmental research days when and where indicated.

The HSREC functions in compliance with, but not limited to, the following documents and guidelines: The SA National Health Act. No. 61 of 2003; Ethics in Health Research: Principles, Structures and Processes (2015); SA GCP(2020); Declaration of Helsinki; The Belmont Report; The US Office of Human Research Protections 45 CFR 461 (for non-exempt research with human participants conducted or supported by the US Department of Health and Human Services- (HHS), 21 CFR 50, 21 CFR 56; CIOMS; ICH-GCP-E6 Sections 1-4; International Council for Harmonisation (ICH) Harmonised Guideline, Integrated Addendum to ICH E6(R1), Guideline for Good Clinical Practice (GCP) E6(R2), 2016, SAHPRA Guidelines as well as Laws and Regulations with regard to the Control of Medicines, Constitution of the HSREC of the Faculty of Health Sciences.

The Principal Investigator (PI) bears final responsibility for the RIMS application. In the event of any misconduct or improper activities perpetuated by a third party, the PI will be held vicariously liable. The HSREC will bear no responsibility or liability for any actions of a PI and/or third party or breach of confidentiality caused by the PI and/or third party.

For any questions or concerns, please feel free to contact HSREC Administration: 051-4012650/9860 or email EthicsFHS@ufs.ac.za.

Thank you for submitting this proposal for ethical clearance and we wish you every success with your research.

Yours Sincerely

Dr. C. Armour (Barrett)
Chairperson: Health Sciences Research Ethics Committee

Health Sciences Research Ethics Committee
T: +27 (0)51 401 2650/9860 | E: ethicsfhs@ufs.ac.za
IRB 00011992; REC 230408-011; IORG 0010096; FWA 00027947

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11 November 2024

Applicant: Thabiso Khulile Mkhatshwa
Institution: Cape University of Technology
E-mail Address: mkhatshwakhulile@gmail.com
Cell: 079 868 0040

Project Title: Microbial profile and antimicrobial sensitivity patterns in patients hospitalised in the six regional/provincial hospitals in the Free State and Northern Cape from 2018 to 2022.

Reference Number: PR2455098

Research Application Type(s):
1. Request for Data

RE: APPROVAL LETTER: REQUEST TO ACCESS NHLS RESOURCES FOR RESEARCH PURPOSES

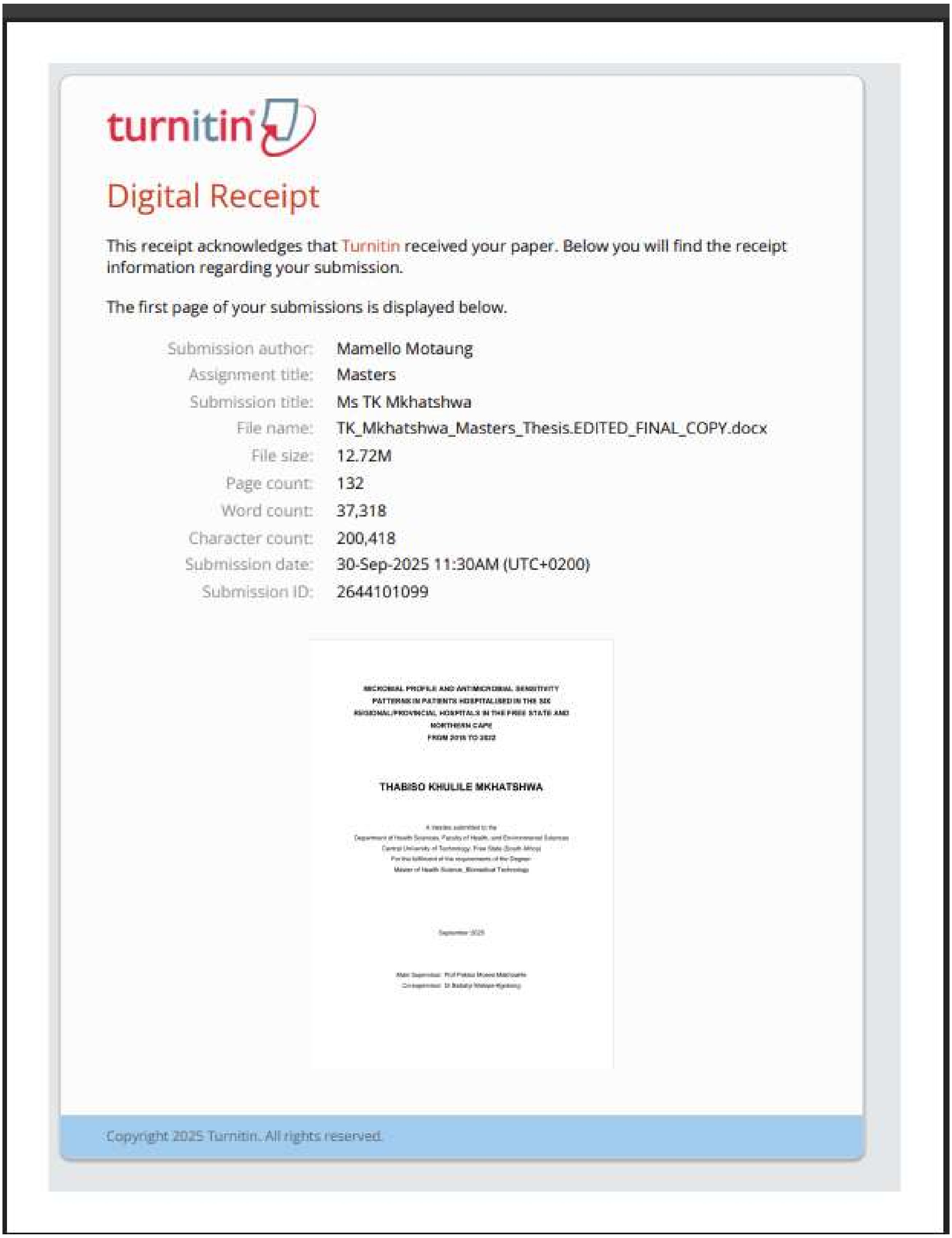
This letter serves to advise that the application requesting permission to conduct the above-mentioned research using the listed NHLS resources has been reviewed and **"Approved"**. Please note that the approval is granted **without undergoing the full internal peer review process** on the condition of the **urgency of the request and its time-sensitive nature**, **therefore further clarity may be required by the processing unit.** You are required to comply with the NHLS Research Material and Data Access Policy and requirements stated below.

1. All material and data requested shall be used as per the research protocol submitted to the NHLS and as approved by the relevant Health Research Ethics Committee (HREC) in South Africa.
2. Access to the NHLS material and/or data shall be limited to the minimum required for successful completion of the approved study and shall be made available ***without patient names and other patient identifiers (including, but not limited to, national identity numbers, hospital/clinic file numbers, addresses and telephone numbers)***.
3. Confidentiality shall be maintained at the participant and institutional level and there shall be no disclosure of personal information or confidential information.
4. Data and/or material shall not be shared with other parties unless approved by the NHLS
5. The material and/or data obtained from the NHLS shall be anonymised and not, for any reason, be used to track or recruit patients as no pre-approval/consent is obtained from patients.
6. Processes shall be discussed with the relevant NHLS departments (i.e. Corporate Data Warehouse (CDW), NHLS Laboratory Management, Operations Office, etc.) and agreed upon.
7. Any amendments to the study requirements, including the use of the material and/or data for purposes not initially disclosed to the NHLS) shall be cleared by an approved HREC and submitted to the NHLS for approval via the AARMS system – https://aarms.nhls.ac.za.
8. The NHLS shall be acknowledged as a source of material and/or data in any output, such as abstracts and journal articles, emanating from the project.
9. A final report of the research study and any published output resulting from this study shall be submitted to the NHLS via AARMS

Please note that this letter constitutes approval by the NHLS Academic Affairs and Research Office. The NHLS entities tasked with providing the material and/data may have additional requirements for access. Data related queries may be directed to NHLS CDW, email: zarina.sabat@nhls.ac.za; contact number: 011 386 6074 and sample related queries (if applicable) shall be directed to the relevant business manager.

Dr Babatyi Malope-Kgokong
National Manager: Academic Affairs and Research

APPENDIX C: TURNITIN REPORT



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Character count:	200,418
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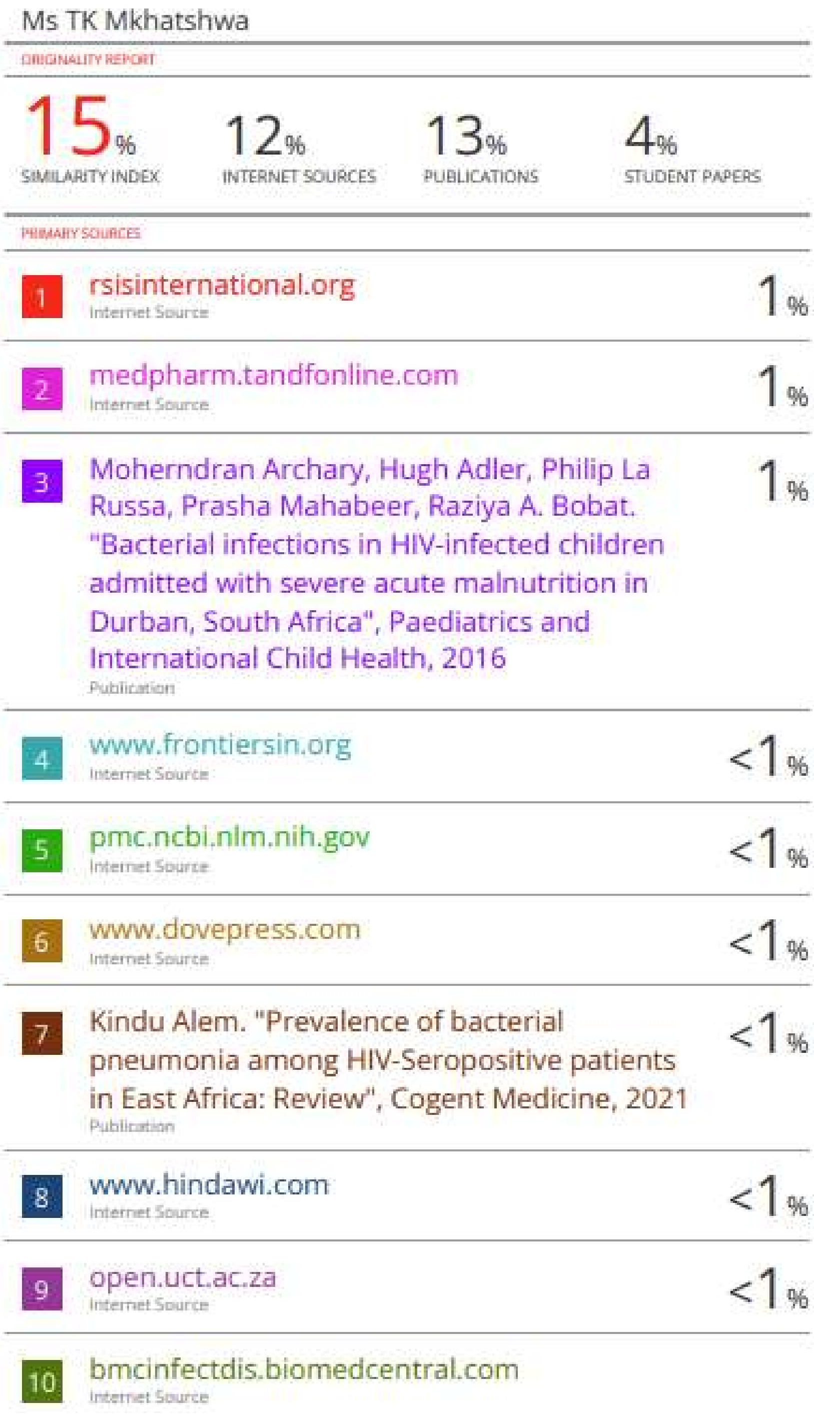
THABISO KHULILE MKHATSHWA



Ms TK Mkhatshwa

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