ISOLATION AND IDENTIFICATION OF AIRBORNE BACTERIA FROM HALL 2 READING ROOM IN UNIVERSITY OF BENIN

BY

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LSC2007270

(MICROBIOLOGY TECHNIQUES)

DEPARTMENT OF SCIENCE LABORATORY TECHNOLOGY

FACULTY OF LIFE SCIENCES

UNIVERSITY OF BENIN

BENIN CITY.

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A PROJECT SUBMITTED TO THE DEPARTMENT OF SCIENCE LABORATORY TECHNOLOGY, FACULTY OF LIFE SCIENCES, UNIVERSITY OF BENIN, BENIN CITY IN PARTIAL FULFILMENT OF THE REQUIREMENTS FOR THE AWARD OF THE DEGREE OF BACHELOR OF SCIENCES (B.Sc.) IN SCIENCE LABORATORY TECHNOLOGY (MICROBIOLOGY TECHNIQUES)

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CERTIFICATION

This is to certify that this undergraduate project work was carried out by Lydia AKPOVOGBETA (Miss) with Matriculation number LSC2007270, under the supervision of MR HARUNA O. of the Department of Science Laboratory technology, University of Benin, Benin City in partial fulfilment of the requirements for the award of Bachelor of Science Degree (BSc. Hons.) in Science Laboratory Technology.

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DEDICATION

I dedicate this project work foremost to Almighty God who helped, strengthened me during the course of this project work. His loving provisions were too constant. Worthy of mention are my parents and siblings for their never-ending prayers, support and encouragement.

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I want to extend special thanks to Almighty God, who has been my source of strength, understanding and wisdom throughout my project work. Indeed, He came through for me.

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ABSTRACT

This study aimed to isolate and identify airborne bacteria present in the Hall 2 reading room using the passive settle plate method. Ten nutrient agar plates were exposed at different locations within the room, while a control plate was kept sealed to ensure sterility. After 24–48 hours of incubation, all exposed plates showed visible bacterial growth. This growth indicates spatial variation in airborne microbial load likely influenced by airflow, human activity, and proximity to ventilation sources. A total of seven distinct bacterial isolates were obtained through subculturing and were characterized based on colony morphology, including size, color, shape, elevation, and texture. Cream to off-white colonies were the most common, while golden and yellow colonies suggested the presence of Staphylococcus aureus and Micrococcus luteus, respectively. Slimy or irregular colonies pointed to the presence of encapsulated or motile species such as Bacillus spp. Gram staining and microscopic examination revealed that 6 of the 7 isolates were Gram-positive, with both rod- and cocci-shaped bacteria present. Rods in singles, chains, or clusters were indicative of Bacillus species, while cocci in clusters suggested Staphylococcus spp. The only Gram-negative isolate, Sub 10, appeared as rod-shaped cells loosely clustered, consistent with environmental bacteria such as Escherichia coli or Enterobacter. The predominance of Gram-positive bacteria reflects their ability to survive desiccation and environmental stress, making them common in indoor air. The presence of a Gram-negative species, though limited, may indicate localized moisture or surface contamination. Overall, the study demonstrates that the Hall 2 reading room contains a diverse airborne bacterial population, primarily originating from human activity and environmental sources. These findings emphasize the need for routine microbial air quality assessments in public and academic spaces to maintain hygienic indoor environments.

CHAPTER ONE

INTRODUCTION

1.1. Background of the study

Microorganisms, also known as microbes, are microscopic living organisms that can exist as single cells or in a colony of cells. They are generally too small to be seen with the naked eye and require a microscope for observation (Madigan *et al*., 2017). Microorganisms include a diverse group of organisms such as bacteria, archaea, fungi, protozoa, algae, and viruses, although viruses are sometimes debated as being non-living due to their dependence on host cells for reproduction (Prescott *et al*., 2002). The study of microorganisms is known as microbiology. This scientific field began in the 17th century with the invention of the microscope by Antonie van Leeuwenhoek, who is often referred to as the "father of microbiology" (Gest, 2004). He was the first to observe and describe single-celled organisms, which he called "animalcules". Microorganisms are ubiquitous, meaning they are found almost everywhere on Earth, including extreme environments such as deep ocean vents, acidic springs, polar ice caps, and the upper atmosphere (Cavicchioli *et al*., 2019). Their adaptability and metabolic diversity allow them to thrive in conditions that are inhospitable to most life forms. These organisms play crucial roles in ecological and biological processes. For example, they are essential in nutrient cycling (e.g., nitrogen fixation, decomposition), the production of oxygen (by photosynthetic cyanobacteria and algae), and symbiotic relationships (such as those between humans and gut microbiota) (Falkowski *et al*., 2008; Sender *et al*., 2016). In industry, microorganisms are used in fermentation (e.g., yeast in bread and alcohol production), biotechnology (e.g., genetically engineered bacteria for insulin production), and waste treatment.In agriculture, nitrogen-fixing bacteria like Rhizobium enhance soil fertility by converting atmospheric nitrogen into forms usable by plants (Van Elsas *et al*., 2007). In the food industry, bacteria and yeasts are used in fermentation to

produce yogurt, cheese, bread, and alcoholic beverages (Prescott *et al*., 2002). In biotechnology, genetically engineered microbes produce insulin, vaccines, and enzymes (Timmis *et al*., 2019). In environmental science, microbes are used for bioremediation, where they degrade pollutants and clean oil spills (Gentry *et al*., 2004). Despite their beneficial roles, some microorganisms are pathogenic and can cause diseases in humans, animals, and plants. Bacteria such as Mycobacterium tuberculosis cause tuberculosis, while viruses like HIV and SARS-CoV-2 cause AIDS and COVID-19, respectively (Ryan and Ray, 2004; WHO, 2020). Pathogenic bacteria such as Mycobacterium tuberculosis cause tuberculosis. Protozoa like Plasmodium species cause malaria. Fungi such as Candida albicans cause infections in immunocompromised individuals. Viruses like HIV and SARS-CoV-2 cause AIDS and COVID-19 respectively (WHO, 2020; Ryan and Ray, 2004). With advancements in molecular biology, microbiologists can now sequence microbial genomes, identify novel species, and manipulate microbes for use in medicine, agriculture, and environmental science (Rinke *et al*., 2013). The development of metagenomics has further expanded our understanding of microbial diversity, especially of unculturable microbes from environmental samples. The human microbiome refers to the community of microorganisms that reside on and within the human body. These microbes are critical for digestion, immune function, and even mental health. Imbalances in the microbiome have been linked to diseases such as obesity, inflammatory bowel disease, and allergies (Sender *et al*., 2016; Turnbaugh *et al*., 2007). Modern techniques like genomic sequencing, metagenomics, and CRISPR-Cas systems have transformed microbiology. Researchers can now identify previously unknown microbial species, understand microbial communities in the environment, and genetically engineer microbes for medical and industrial purposes (Rinke *et al*., 2013; Doudna and Charpentier, 2014). Microbes are being explored as solutions to global challenges. For example, photosynthetic microbes like algae are being investigated for biofuel production,

and soil microbes are crucial for sustainable agriculture. Additionally, microbes can capture carbon dioxide and help mitigate climate change (Cavicchioli *et al*., 2019).

1.2 Statement of the Problem

Indoor air quality is a critical determinant of human health, particularly in enclosed environments where individuals spend extended periods. Microorganisms such as bacteria are ubiquitous in the atmosphere and can easily become airborne through human activities, ventilation systems, and environmental disturbances. In densely populated indoor spaces like reading rooms, these microorganisms may accumulate and pose potential health risks, including respiratory infections, allergic reactions, and other airborne diseases. Despite the growing concern about indoor microbial contamination, limited attention has been given to assessing the bacterial load and diversity in institutional reading environments within Nigeria. Hall 2 Reading Room, which accommodates a large number of students daily, presents a typical microenvironment conducive to the proliferation and transmission of airborne bacteria due to factors such as poor ventilation, crowding, and inadequate hygiene practices. However, there is a scarcity of empirical data on the nature, prevalence, and potential pathogenicity of airborne bacterial species in this facility. The absence of such data limits the ability of management and health authorities to implement evidence-based measures that ensure a safe and hygienic indoor environment for users. Therefore, a systematic isolation, identification, and characterization of airborne bacteria in Hall 2 Reading Room is essential to provide baseline information on microbial air quality and associated health implications.

1.3 Justification of the Study

The quality of indoor air has a profound impact on the well-being and productivity of individuals, especially in learning environments where students spend prolonged hours. This

study is justified by the increasing recognition of airborne bacteria as significant contributors to indoor air pollution and potential vectors of communicable diseases. Identifying and characterizing these microorganisms within Hall 2 Reading Room will not only provide insight into the microbial composition of the indoor environment but will also serve as a foundation for developing effective control and mitigation strategies. Additionally, this research will contribute to the existing body of knowledge on environmental microbiology by establishing a microbial profile specific to a university reading room setting. The findings will aid institutional authorities in designing proper ventilation systems, enforcing regular sanitation protocols, and promoting public health awareness among students. The study will also enhance preventive health practices and contribute to safer indoor environments.

1.4. Aim and Objectives of the Study

The aim of this study is to isolate and identify airborne bacteria present in the Hall 2 reading room.

The objectives of the study were to:

1. isolate airborne bacteria from hall 2 reading room in university of Benin.
2. identify the isolated bacteria using morphological characteristics.
3. determine the Gram reaction of the isolated bacteria using Gram staining methods.

CHAPTER TWO

LITERATURE REVIEW

2.1. Airborne Bacteria

Indoor air quality is an important factor affecting human health, especially in places like reading rooms where people spend long hours in enclosed spaces. Airborne bacteria are a key part of bioaerosols in indoor air and have been linked to respiratory diseases, allergies, and infections, making their study vital for public health (Nevalainen *et al*., 2015; Li *et al*., 2007). To isolate airborne bacteria from indoor environments such as reading rooms, researchers commonly use air sampling methods like impaction, filtration, or sedimentation. Impaction samplers collect airborne particles by impacting them onto nutrient agar plates, which allows bacterial colonies to grow (Rajasekar *et al*., 2012). Filtration methods involve drawing air through membrane filters that are then incubated to culture bacteria (Bharti and Kataria, 2011). Sedimentation is a passive method where exposed agar plates capture settling bacteria over time but is less quantitative compared to active sampling (Pasquarella *et al*., 2000). These culturing techniques provide bacterial isolates for further analysis. For bacterial identification, initial steps often include morphological examination and biochemical tests such as Gram staining, catalase, and oxidase tests. However, molecular techniques like 16S rRNA gene sequencing have become standard due to their accuracy and ability to identify bacteria at the species level (Ueda *et al*., 2019; Prussin and Marr, 2015). Other methods like PCR-based assays and MALDI-TOF mass spectrometry are also increasingly used to rapidly and accurately identify airborne bacteria (Fang *et al*., 2007). Characterization of airborne bacteria involves studying their properties related to survival and health risks. Antibiotic resistance profiling has revealed that many airborne bacteria carry resistance genes, which poses a significant public health concern (Fang *et al*., 2007). Characterizing virulence factors

helps assess the pathogenic potential of these bacteria, especially for vulnerable populations (Pasquarella *et al*., 2000). Environmental tolerance studies show that airborne bacteria in indoor air often survive harsh conditions such as desiccation and UV radiation, which help them persist in these environments (Tang, 2009). Research consistently shows that Gram-positive bacteria dominate airborne bacterial populations in indoor environments like reading rooms. Species from the genera Bacillus, Staphylococcus, and Micrococcus are commonly isolated (Nevalainen *et al*., 2015). This predominance is partly because Bacillus species can form resistant spores, and Staphylococcus and Micrococcus are commonly shed from human skin, contributing to indoor microbial loads (Pasquarella *et al*., 2000). The concentration and diversity of airborne bacteria are influenced by factors such as occupancy, ventilation, temperature, and humidity (Bharti and Kataria, 2011; Li *et al*., 2007; Tang, 2009). Prolonged exposure to airborne bacteria in enclosed spaces like reading rooms can increase the risk of respiratory infections and allergic reactions, particularly in children, the elderly, and immunocompromised individuals (Nevalainen *et al*., 2015). Therefore, identifying and characterizing airborne bacteria in such environments is essential for improving indoor air quality. This knowledge aids in designing effective air filtration systems, establishing cleaning protocols, and improving ventilation to reduce microbial exposure and protect occupant health (Li *et al*., 2007).

2.2. The Prevalence of Bacteria

Bacteria are among the most abundant and diverse forms of life on Earth. They exist in soil, water, air, and on or inside animals, plants, and humans. According to the National Institutes of Health (NIH), the human body alone contains trillions of bacterial cells, particularly in the gut, skin, mouth, and respiratory and urogenital tracts (NIH Human Microbiome Project, 2012). It is estimated that the human microbiome—especially in the gut—contains more than

1,000 different bacterial species at any given time. These bacteria play vital roles in digestion, immune function, and protection against harmful microbes (NIH, 2012). Bacterial infections are a major global health burden. In 2019, they were linked to approximately 7.7 million deaths globally, representing about one in every eight deaths worldwide. This burden is particularly high in low- and middle-income countries (Global Burden of Disease Study, 2022). Certain bacteria are responsible for most of the fatal infections. Five major bacterial species—Staphylococcus aureus, Escherichia coli, Streptococcus pneumoniae, Klebsiella pneumoniae, and Pseudomonas aeruginosa—account for over half of all bacterial infection-related deaths worldwide (The Lancet, 2022). In terms of disease type, lower respiratory tract infections such as pneumonia were the leading cause of death from bacterial infections, resulting in nearly 4 million deaths in 2019. Bloodstream infections followed closely, contributing around 2.9 million deaths globally in the same year (The Lancet, 2022). Bacterial skin diseases are also common and are increasing worldwide. In 2021, around 90 million new cases of bacterial skin disease were reported globally. This number is projected to rise to about 1.2 billion annual cases by 2045, largely due to factors such as population growth and urbanization (PubMed, 2024). Antibiotic resistance is significantly worsening the burden of bacterial infections. In 2019, approximately 4.95 million deaths were associated with antimicrobial resistance (AMR), and about 1.27 million of these were directly caused by drug-resistant bacteria. This means that resistance is making otherwise treatable infections potentially deadly (Lancet, 2022). Globally, the number of antibiotics in clinical and preclinical development has increased (from about 80 in 2021 to 97 in 2023), but many of the newer agents do not yet adequately cover the most threatening AMR pathogens, especially Gram-negative bacteria. The prevalence and impact of bacterial diseases vary significantly across regions. Sub-Saharan Africa has the highest bacterial infection-related death rates, while high-income regions such as Western Europe and North America report much lower

rates. These differences are often due to disparities in healthcare access, sanitation, vaccination, and antibiotic availability (Oxford University, 2022). Despite their association with disease, most bacteria are not harmful. In fact, many are essential to human health. Beneficial bacteria help digest food, produce vitamins, and protect against infections by outcompeting harmful microbes. Disrupting this balance—such as through excessive antibiotic use—can lead to illness and increased vulnerability to disease (NIH, 2012). Bacterial antimicrobial resistance (AMR) is increasing rapidly worldwide, with bacteria that were once easily treatable now becoming difficult or impossible to manage using existing antibiotics. The World Health Organization (WHO) updated its Bacterial Priority Pathogens List in 2024, identifying 15 families of resistant bacteria grouped into critical, high, and medium priority to help guide research and public health interventions. Critical pathogens include carbapenem-resistant Acinetobacter baumannii, third-generation cephalosporin-resistant and carbapenem-resistant Enterobacterales, and rifampicin-resistant Mycobacterium tuberculosis (WHO, 2024). Globally, the number of antibiotics in clinical and preclinical development has increased from about 80 in 2021 to 97 in 2023. However, many of these newer agents do not yet adequately cover the most threatening AMR pathogens, especially Gram-negative bacteria (WHO, 2024). A recent narrative review analyzing over 2,500 studies across 187 countries found that infections with multidrug-resistant (MDR) bacteria have increased by around 43% globally. Healthcare-associated infections rose by approximately 67%, and community-acquired infections increased by about 38% in areas with high antibiotic misuse. Key MDR pathogens identified include methicillin-resistant Staphylococcus aureus (MRSA), extended-spectrum β-lactamase (ESBL)-producing Enterobacteriaceae, and carbapenem-resistant Enterobacteriaceae (Baral *et al.*, 2023). The burden of bacterial AMR is large and growing. In 2019, antibiotic resistance was directly responsible for an estimated 1.27 million deaths globally and was associated with about 5

million deaths where resistance played a contributory role. Without intervention, projections estimate that by 2050 there could be about 1.91 million deaths per year directly attributable to AMR bacteria and 8.22 million deaths per year associated with them (Wellcome Trust, 2023). The age distribution of AMR-related mortality is shifting. Deaths among children under five have declined substantially over recent decades, partly due to improved vaccination, sanitation, and infection control. In contrast, deaths among adults aged 70 years or older have increased significantly. These trends are projected to continue, with deaths in the elderly due to AMR expected to roughly double by 2050 (Italian GBD Initiative, 2024). Regional disparities in AMR are pronounced. Low- and middle-income countries often have higher prevalence of resistance than high-income countries. For example, fluoroquinolone-resistant Escherichia coli shows resistance rates of 40–60% in some South Asian regions; carbapenem-resistant Klebsiella pneumoniae prevalence exceeds 50% in parts of Asia and Africa (Bioresscientia, 2023). In Europe, surveillance data for 2023 showed mixed trends. Methicillin-resistant Staphylococcus aureus (MRSA) bloodstream infections have declined compared to 2019; however, the incidence of bloodstream infections caused by carbapenem-resistant Klebsiella pneumoniae has increased by more than 50% since 2019. Third-generation cephalosporin-resistant E. coli bloodstream infections remain roughly stable or slightly decreased but are still above target thresholds (ECDC, 2023). Overall, the economic impact of AMR is large. One review estimates annual global healthcare costs associated with resistant infections exceed US$100 billion, excluding wider economic losses from longer hospital stays and lost productivity (Baral *et al*., 2023).

2.3. Bacteria Morphology

Bacterial morphology refers to the shape, size, and arrangement of bacterial cells. Bacteria exhibit a limited range of characteristic shapes, which are important for classification and

identification. The three main shapes of bacteria are cocci (spherical), bacilli (rod-shaped), and spirilla (spiral or helical-shaped). For example, Staphylococcus aureus is a coccus, Escherichia coli is a bacillus, and Spirillum volutans is a spirillum (Madigan *et al*., 2018). Depending on how they divide and remain attached, bacteria can form various arrangements. Cocci can appear in pairs (diplococci), chains (streptococci), clusters (staphylococci), or tetrads. Bacilli may also occur singly, in pairs (diplobacilli), or in chains (streptobacilli) (Tortora *et al*., 2021). Some bacteria exhibit less common shapes such as vibrios (comma-shaped), spirochetes (flexible spirals), and filamentous forms. These shapes may help bacteria adapt to specific environments or modes of movement (Prescott *et al*., 2017). Morphology can influence nutrient uptake, motility, surface attachment, and resistance to environmental stresses. For instance, the small size and high surface area-to-volume ratio of bacteria enhance nutrient absorption (Madigan *et al*., 2018).

2.4. Bacteria Diversity

Bacteria represent one of the most diverse groups of organisms on Earth, encompassing an incredible range of forms, metabolic capabilities, and ecological roles. This diversity is fundamental to many natural processes and has significant implications for health, industry, and the environment. Bacterial diversity can be examined through several dimensions: morphological, genetic, physiological, ecological, and evolutionary. Morphologically, bacteria vary in shape, size, and structural complexity. The most common bacterial shapes include cocci (spherical), bacilli (rod-shaped), spirilla (spiral-shaped), and filamentous forms. Some bacteria have specialized structures like flagella for motility, pili for attachment, or capsules for protection (Madigan *et al*., 2018). Genetically, bacteria exhibit vast diversity. Their genomes vary widely in size, gene content, and organization, reflecting adaptations to diverse environments. Horizontal gene transfer (HGT) through mechanisms such as

transformation, transduction, and conjugation contribute significantly to bacterial genetic diversity, enabling rapid adaptation and evolution (Ochman *et al*., 2000). This genetic plasticity complicates bacterial classification but also promotes resilience and innovation. Physiologically, bacteria display a wide array of metabolic strategies. Some are autotrophic, capable of photosynthesis or chemosynthesis, while others are heterotrophic, relying on organic compounds. Bacteria can be aerobic or anaerobic, with some capable of facultative anaerobic metabolism, allowing them to survive in oxygen-rich or oxygen-poor environments. This metabolic versatility allows bacteria to colonize nearly every habitat on Earth, from deep-sea vents and hot springs to human guts and arctic ice (Madigan *et al*., 2018). Ecologically, bacteria fulfill diverse roles. They are crucial decomposers, recycling nutrients such as carbon, nitrogen, and sulfur. Nitrogen-fixing bacteria, such as Rhizobium species, form symbiotic relationships with plants, converting atmospheric nitrogen into forms usable by plants, thereby supporting ecosystems and agriculture (Sylvia *et al*., 2005). Some bacteria are pathogens, causing diseases in humans, animals, and plants, while others form beneficial microbiomes essential for health. Bacterial diversity is also reflected in their evolutionary history. Bacteria are among the earliest forms of life, with fossil evidence suggesting their existence for over 3.5 billion years. Molecular phylogenetics, especially analysis of 16S rRNA genes, has revolutionized understanding of bacterial relationships, revealing deep branches and previously unknown groups (Woese and Fox, 1977). The advent of metagenomics has uncovered immense bacterial diversity, much of it from uncultured species, suggesting that the vast majority of bacterial life remains uncharacterized (Rinke *et al*., 2013). The classification of bacteria has evolved from phenotypic traits to molecular methods. Modern bacterial taxonomy relies heavily on sequencing technologies, leading to the identification of new phyla and restructuring of traditional groups. For instance, the discovery of the Candidate Phyla Radiation (CPR) highlighted a large, diverse, and mostly uncultivated

group of bacteria with unusual genomic features (Brown *et al*., 2015). In applied contexts, bacterial diversity is exploited for biotechnology, medicine, and environmental management. Industrial microbiology utilizes bacteria for fermentation, bioremediation, and production of antibiotics, enzymes, and biofuels. Understanding bacterial diversity helps combat antibiotic resistance and develop novel therapeutics (Demain and Sanchez, 2009).

2.5. Prokaryotes and Eukaryotes

Prokaryotes are unicellular organisms that lack a true nucleus and membrane-bound organelles. Their genetic material is found in a region called the nucleoid, which is not enclosed by a membrane. Eukaryotes can be unicellular or multicellular organisms. They possess a true nucleus that encloses their DNA and have numerous membrane-bound organelles such as mitochondria, endoplasmic reticulum, and Golgi apparatus. Prokaryotic cells are generally smaller, typically ranging from 0.1 to 5 micrometers in diameter. Eukaryotic cells are larger, usually between 10 to 100 micrometers. In prokaryotes, DNA is circular and free-floating within the cytoplasm in the nucleoid region. They may also contain small rings of DNA called plasmids. Eukaryotic DNA is linear and organized into chromosomes within the nucleus, associated with histone proteins. Prokaryotes divide by a simple process called binary fission, which does not involve mitosis or meiosis. Eukaryotes divide by mitosis (for growth and repair) and meiosis (for sexual reproduction), both of which involve complex chromosome segregation. Prokaryotes lack membrane-bound organelles but may have structures such as ribosomes (which are smaller than those in eukaryotes), cell walls, and sometimes flagella or pili. Eukaryotes have membrane-bound organelles including mitochondria (energy production), chloroplasts (in plants for photosynthesis), endoplasmic reticulum, Golgi apparatus, lysosomes, and peroxisomes. Most prokaryotes have a rigid cell wall. In bacteria, it is mainly composed of peptidoglycan.

Archaea have cell walls made of different substances like pseudopeptidoglycan. Eukaryotic cells may or may not have cell walls. Plant cells and fungi have cell walls made of cellulose and chitin, respectively, while animal cells lack cell walls.

Prokaryotes exhibit diverse metabolic pathways, including aerobic and anaerobic respiration, photosynthesis, nitrogen fixation, and more. Many can survive in extreme environments. Eukaryotes generally rely on aerobic respiration and have less metabolic diversity than prokaryotes. Examples of Prokaryotes include bacteria and archaea. Eukaryotes include animals, plants, fungi, and protists.

2.6. Human Bacterial Diseases

Human bacterial diseases are illnesses caused by pathogenic bacteria—single-celled microorganisms capable of infecting various parts of the body. While many bacteria live harmlessly in or on the human body as part of the normal microbiota, some can cause disease under certain conditions. These harmful bacteria may invade tissues, produce toxins, or trigger immune responses that result in illness. According to MSD Manuals, bacteria can be either harmless, helpful, or harmful depending on their type and location in the body (MSD Manuals, n.d.). To cause disease, bacteria must first enter the human body through different routes such as inhalation, ingestion, open wounds, sexual contact, or through insect vectors. Once inside, they attach to host cells using specific molecules that help them colonize the tissues. Some bacteria can evade the immune system by producing protective capsules, secreting enzymes, or even hiding inside host cells. After establishing themselves, they can damage tissues either by multiplying within them or by releasing toxins. Some bacterial infections stay localized, while others spread throughout the body, leading to systemic illnesses like sepsis (Cleveland Clinic, 2022; MSD Manuals, n.d.). The symptoms of bacterial infections vary depending on the part of the body affected and the specific bacteria involved.

Common general symptoms include fever, chills, fatigue, and inflammation. Localized infections may cause redness, swelling, pain, or pus. Lung infections can lead to coughing, chest pain, and difficulty breathing, while gastrointestinal infections may cause diarrhea, vomiting, and stomach cramps. In severe cases, bacterial infections can lead to organ failure, confusion, or death if not treated promptly (Cleveland Clinic, 2022; IMB, University of Queensland). Tuberculosis is caused by Mycobacterium tuberculosis and primarily affects the lungs, leading to symptoms such as a persistent cough, weight loss, and night sweats. Pneumonia, often caused by Streptococcus pneumoniae or Haemophilus influenzae, involves inflammation of the lungs and may cause fever, cough, and chest pain. Urinary tract infections, most commonly caused by Escherichia coli, result in painful urination and increased frequency. Other examples include meningitis (inflammation of the brain and spinal cord membranes), skin infections (like cellulitis or impetigo), foodborne illnesses (caused by Salmonella or Listeria), and sexually transmitted infections like gonorrhea and syphilis. These conditions can vary in severity and may become life-threatening without proper treatment (IMB, University of Queensland; Cleveland Clinic, 2022). Diagnosing bacterial diseases typically involves a combination of clinical evaluation and laboratory tests. Doctors assess symptoms and collect samples such as blood, urine, cerebrospinal fluid, or tissue swabs. These samples are then tested through culture techniques, Gram staining, or molecular methods like PCR. Antibiotic sensitivity testing helps determine which antibiotics will be most effective against the bacteria found (MSD Manuals, n.d.). The primary treatment for bacterial diseases is antibiotics. The choice of antibiotic depends on the type of bacteria, the site of infection, and the resistance patterns in the community or hospital. Supportive care, such as hydration, fever management, and wound care, may also be necessary. However, the rise of antibiotic resistance—where bacteria become less responsive to drugs—has become a major global concern. In some cases, surgical interventions may be required, especially for

infections like abscesses or necrotizing fasciitis (PubMed, 2007; Cleveland Clinic, 2022). Preventing bacterial diseases involves several strategies. Vaccination is available for many bacterial pathogens, including those that cause pneumonia, meningitis, and tuberculosis. Practicing good hygiene—such as handwashing, safe food handling, and safe sex—can reduce the risk of infection. In hospitals, strict infection control practices help prevent the spread of bacteria, especially those that are resistant to antibiotics. Public health measures like surveillance, education, and sanitation are also essential in reducing the spread of bacterial diseases (IMB, University of Queensland; ReAct Group). Bacterial diseases continue to be a major global health burden, especially in low- and middle-income countries. Diseases like pneumonia and tuberculosis are leading causes of death, particularly in children under five and people with weakened immune systems. One of the biggest challenges is the growing issue of antibiotic resistance, which renders standard treatments ineffective and increases the risk of severe disease and death. Access to timely diagnosis, proper antibiotics, and healthcare infrastructure remains uneven worldwide, compounding the issue (ReAct Group; PubMed, 2023).

2.7. Sexually Transmitted Diseases

Sexually transmitted diseases (STDs) caused by bacteria are among the most common and treatable infections worldwide. These bacterial STDs are primarily transmitted through unprotected vaginal, anal, or oral sex. The most prevalent bacterial STDs include chlamydia, gonorrhea, syphilis, and chancroid. Each of these is caused by a specific type of bacteria and can lead to serious health complications if left untreated. Chlamydia is caused by the bacterium Chlamydia trachomatis. It often presents no symptoms, especially in women, which allows it to spread unnoticed. When symptoms occur, they may include abnormal genital discharge and burning during urination. If untreated, chlamydia can lead to pelvic

inflammatory disease (PID), infertility, and complications during pregnancy (CDC, 2023). Gonorrhea, caused by Neisseria gonorrhoeae, is another common bacterial STD. Like chlamydia, it often presents without symptoms. When symptoms are present, they can include discharge from the genitals, painful urination, and, in more severe cases, joint pain or systemic infection. Gonorrhea has become increasingly resistant to antibiotics, making treatment more challenging in some cases (CDC, 2023). Syphilis is caused by the bacterium Treponema pallidum. It progresses in stages, starting with a painless sore at the site of infection (primary stage), followed by skin rashes and mucous membrane lesions (secondary stage), and eventually leading to serious complications such as organ damage or neurological issues if not treated (tertiary stage). Syphilis can also be transmitted from mother to child during pregnancy, resulting in congenital syphilis, which can cause stillbirth or severe health problems in the infant (World Health Organization [WHO], 2021). Chancroid, although less common globally, is caused by Haemophilus ducreyi. It is characterized by painful genital ulcers and swollen lymph nodes. It is more frequently seen in parts of Africa and the Caribbean, often associated with poor access to health care and higher rates of co-infection with HIV (WHO, 2021). Diagnosis of these bacterial STDs is typically done through laboratory testing of urine, genital swabs, or blood samples. Early diagnosis is crucial, as these infections are curable with antibiotics, and timely treatment prevents complications and transmission to others. However, increasing antibiotic resistance, particularly in gonorrhea, has raised public health concerns and highlights the need for careful antibiotic stewardship and development of new treatment options.

2.8. Importance of Bacteria

Bacteria are microscopic, single-celled organisms found almost everywhere on Earth — in soil, water, air, and inside other living organisms, including humans. Despite sometimes

being associated with disease, bacteria have crucial positive roles that sustain life and benefit society in many ways.

2.8.1. Role in Human Health

Bacteria are fundamental to human health through their symbiotic relationships within the body, especially in the digestive system. The human gut harbors trillions of bacteria, collectively known as the gut microbiota. These bacteria help digest complex carbohydrates and fibers that humans alone cannot break down, producing short-chain fatty acids that nourish intestinal cells and influence metabolism (Human Microbiome Project Consortium, 2012). Additionally, gut bacteria synthesize essential vitamins such as vitamin K, which is critical for blood clotting, and some B vitamins (B12, biotin, folate) (Madigan *et al*., 2018). They also play a key role in training and regulating the immune system, helping it distinguish between harmful pathogens and harmless substances, thus preventing autoimmune diseases and allergies. Furthermore, beneficial bacteria act as a defense mechanism by outcompeting harmful microbes for space and nutrients and producing antimicrobial substances that inhibit pathogens. For example, Lactobacillus species in the vaginal microbiota maintain an acidic environment that prevents infections (Macklaim *et al*., 2015).

2.8.2 Environmental Importance

Bacteria are essential drivers of nutrient cycling in ecosystems. Through processes such as nitrogen fixation, certain bacteria convert atmospheric nitrogen (N_2), which most organisms cannot use, into ammonia (NH_3), a form accessible to plants. This process is critical for soil fertility and plant growth (Madigan *et al*., 2018). Other bacteria participate in decomposition, breaking down dead organic matter and recycling nutrients back into the soil and water, which supports the entire food web. Bacteria also contribute to biogeochemical cycles, such as sulfur and carbon cycles, maintaining ecological balance. Some bacteria can degrade

pollutants, including oil spills, pesticides, and heavy metals, in a process called bioremediation. This ability helps in cleaning contaminated environments and reducing human impact on ecosystems (Tyagi *et al*., 2011).

2.8.3 Industrial and Biotechnological Applications

Bacteria have been harnessed by humans for thousands of years for food production. They are essential in fermentation processes that produce yogurt, cheese, sauerkraut, kimchi, and sourdough bread. These fermentations not only preserve food but also enhance nutritional value and flavor. In modern biotechnology, bacteria are indispensable tools. They serve as hosts for genetic engineering, producing important medicines such as insulin, growth hormones, and vaccines (Madigan *et al*., 2018). Bacteria also produce antibiotics — for example, Streptomyces species produce streptomycin, an antibiotic used to treat tuberculosis. In agriculture, bacterial biofertilizers enhance crop productivity by fixing nitrogen or promoting plant growth through other mechanisms. Moreover, bacteria are used in waste treatment plants to decompose organic waste and reduce pollution. Bacteria are much more than disease-causing agents; they are vital to life on Earth. They maintain human health by supporting digestion, immune function, and protecting against pathogens. Environmentally, they regulate nutrient cycles and help maintain ecological balance. Industrially, they are used in food production, medicine, agriculture, and environmental cleanup. The vast benefits bacteria provide underscore their indispensable role in natural and human systems.

2.9. Common Bacteria found in Public Residences

Public residences such as hostels are environments where many individuals live in close proximity, sharing facilities like bathrooms, kitchens, and common areas. These conditions promote the spread and colonization of various bacteria, some of which can cause infections or degrade hygiene standards (Ryan and Ray, 2010). One of the most common bacteria found in such settings is Staphylococcus aureus, including methicillin-resistant strains (MRSA). This bacterium typically colonizes the skin and nasal passages of healthy individuals but can cause infections if it enters through cuts or abrasions. Crowded living environments with shared personal items increase the risk of transmission (Todar, 2023; CDC, 2022). Escherichia coli (E. coli), normally part of the intestinal flora, is another frequent bacterium found on contaminated surfaces, water, or food in hostels. Certain pathogenic strains of E. coli cause gastrointestinal illness and urinary tract infections. Transmission often results from poor hand hygiene and inadequate sanitation of shared bathrooms and kitchens (Mahon *et al*., 2018). Foodborne pathogen Salmonella spp. is also a concern in hostel environments, particularly due to improper food handling and preparation. Salmonella causes symptoms such as diarrhea, fever, and abdominal cramps and can spread rapidly in communal living spaces (Ryan and Ray, 2010). Pseudomonas aeruginosa thrives in moist environments common in hostels, such as sinks and showers. It is an opportunistic pathogen causing infections especially in immunocompromised individuals or those with wounds (Todar, 2023). Enterococcus species, particularly Enterococcus faecalis and Enterococcus faecium, are gut flora bacteria that often exhibit antibiotic resistance. They can survive on surfaces for long periods and cause infections such as urinary tract infections and wound infections in compromised hosts (CDC, 2022; Mahon *et al*., 2018). While less frequently isolated, Clostridium difficile can be problematic in shared living spaces when disrupted gut flora and improper hygiene facilitate its spread, leading to severe diarrhea and colitis (Ryan and Ray,

2010). Environmental bacteria like Bacillus species and Micrococcus species are commonly found on surfaces and dust but are generally less pathogenic. Their presence, however, indicates levels of microbial contamination and hygiene in shared areas (Mahon *et al*., 2018). To minimize bacterial contamination and transmission in hostels, regular cleaning and disinfection of common areas, good hand hygiene, avoiding sharing personal items, and safe food handling practices are critical. Educating residents about hygiene helps further reduce bacterial spread (CDC, 2022).

2.10. Laboratory Analysis of Bacteria

Laboratory analysis of bacteria is a critical process in microbiology used for the detection, identification, classification, and characterization of bacterial species. This analysis is essential in clinical diagnostics, food safety, water testing, and pharmaceutical quality control. The process usually begins with sample collection, which must be performed using sterile techniques to avoid contamination. The type of sample collected depends on the suspected site of infection or the purpose of testing—examples include blood, urine, sputum, food samples, or swabs from surfaces or wounds (Mahon *et al.,* 2018). Following collection, sample processing typically involves culturing the bacteria. Samples are inoculated onto nutrient media, which support bacterial growth. Common types include nutrient agar, blood agar, MacConkey agar, and mannitol salt agar. These media may be selective, differential, or enriched, helping microbiologists isolate and identify specific bacterial species based on their growth characteristics and biochemical properties (Forbes *et al*., 2016). Once colonies have grown, colony morphology is assessed. Characteristics such as shape, color, size, edge, and elevation of the colonies can give preliminary clues about the bacterial species. For example, Staphylococcus aureus produces golden-yellow colonies on mannitol salt agar, while E. coli

shows pink colonies on MacConkey agar due to lactose fermentation (Ryan and Ray, 2010). Microscopic examination is another critical step. Bacteria are stained using the Gram stain, which differentiates organisms into Gram-positive and Gram-negative based on cell wall structure. Gram-positive bacteria retain the crystal violet stain and appear purple, while Gram-negative bacteria appear pink due to the counterstain (safranin). This distinction is fundamental for guiding further testing and treatment decisions (Benson, 2012). Biochemical testing helps identify bacteria based on their metabolic properties. Common tests include the catalase test, oxidase test, coagulase test, indole test, citrate utilization, urease test, and triple sugar iron (TSI) test. Each test provides data on how a bacterium metabolizes certain substances, allowing for more precise identification (Forbes *et al*., 2016). In modern laboratories, automated identification systems like VITEK, MALDI-TOF MS (Matrix-Assisted Laser Desorption/Ionization Time-of-Flight Mass Spectrometry), and BD Phoenix are frequently used. These systems rapidly identify bacteria by analyzing biochemical reactions or bacterial protein profiles with high accuracy and speed (Spanu *et al*., 2012). Molecular techniques are also increasingly used, especially in clinical or research settings. Polymerase Chain Reaction (PCR) is a powerful method for detecting bacterial DNA directly from samples, enabling rapid diagnosis of infections, even when culturing is difficult. Other molecular techniques include DNA sequencing, ribotyping, and nucleic acid hybridization (Wilson, 2012). Another crucial part of bacterial analysis is antimicrobial susceptibility testing (AST). This determines which antibiotics are effective against the isolated bacterium. The Kirby-Bauer disk diffusion method, E-test, and broth dilution methods are commonly used. These results guide clinicians in choosing the appropriate antibiotic therapy (CLSI, 2020). Finally, proper reporting and interpretation of laboratory results are essential. Microbiologists must correlate laboratory findings with clinical data, environmental conditions, or epidemiological context to draw meaningful conclusions.

2.11. Treatment of Bacteria Diseases

The treatment of bacterial diseases primarily relies on antibiotic therapy, which involves the use of medications designed to kill or inhibit the growth of bacteria. Antibiotics can be broad-spectrum, targeting a wide variety of bacteria, or narrow-spectrum, aimed at specific bacterial strains. Commonly used classes of antibiotics include penicillins (e.g., amoxicillin), macrolides (e.g., erythromycin), fluoroquinolones (e.g., ciprofloxacin), tetracyclines (e.g., doxycycline), and cephalosporins (CDC, 2021). Accurate diagnosis is crucial before starting treatment, as not all infections are caused by bacteria. Laboratory tests such as blood cultures, urine cultures, throat swabs, and wound cultures help identify the specific bacterial pathogen and determine its sensitivity to antibiotics. This ensures the right medication is prescribed and reduces the risk of antibiotic resistance (Mayo Clinic, 2023). Infections caused by antibiotic-resistant bacteria, such as MRSA (Methicillin-resistant Staphylococcus aureus) or ESBL-producing organisms, require more complex treatment approaches. These may include the use of newer or last-resort antibiotics like vancomycin or colistin, often in combination with other supportive measures. In some cases, infectious disease specialists are consulted to tailor individualized treatment plans (WHO, 2020). Supportive care plays a vital role in recovery. This includes ensuring adequate hydration, controlling fever with antipyretics, managing pain, and supporting the immune system. In more severe infections, such as sepsis, pneumonia, or bacterial meningitis, hospitalization and intravenous antibiotics may be required for more aggressive treatment (MedlinePlus, 2022). When infections lead to abscess formation or necrotic tissue, surgical intervention may be necessary to drain the infected material or remove damaged tissues. This is common in infections like diabetic foot ulcers or severe skin and soft tissue infections. Vaccination is another key component of bacterial disease prevention and treatment. Vaccines are available for several bacterial infections, including Streptococcus pneumoniae, Neisseria meningitidis, Haemophilus influenzae type b, and

Bordetella pertussis (CDC, 2021). Vaccination reduces the incidence of these infections and thus the need for antibiotics. Patient adherence to prescribed antibiotic regimens is essential. Failure to complete the full course of antibiotics, even if symptoms improve, can lead to relapse and the development of resistant bacteria. Education on responsible antibiotic use is a critical aspect of public health strategies (WHO, 2020). Finally, antibiotic stewardship programs in hospitals and communities are designed to monitor and guide the appropriate use of antibiotics. These programs aim to reduce unnecessary prescriptions, promote effective treatments, and help combat the global challenge of antimicrobial resistance (CDC, 2021).

CHAPTER THREE

3.0. MATERIALS AND METHODS

3.1. Sampled area

The study was conducted in the University of Benin (UNIBEN), located in Benin City, Edo state, Nigeria. Samples were collected from Hall 2 Hostel, one of the major student hostels on the Ugbowo Campus with a high population of female students. The reading room serves as a study area where students gather daily for academic activities, often resulting in limited ventilation and increased occupancy for hours. These conditions make it a suitable environment for the accumulation and transmission of airborne microoganisms. The selection of this area for sample collection was based on its high usage rate and limited airflow.

3.2. METHODS

3.2.1 Sample Preparation

Equipment: Autoclave

Apparatus: Petri dishes and masking tape

Nutrient agar was prepared according to manufacturer's instructions. The agar was sterilized by autoclaving at 121 °C for 15 minutes and allowed to cool to about 45 °C before being aseptically dispensed into sterile Petri dishes.

3.2.2 Exposure of Culture Plates

Equipment: Incubator

Ten (10) Petri dishes containing sterile nutrient agar were used. Nine plates were exposed in Hall 2 reading room for 30 minutes at different positions, while one plate was kept covered

and served as the control. After exposure, the plates were covered, sealed, and incubated at 37 °C for 24–48 hours.

3.2.3 Subculturing of Distinct Colonies

Apparatus: Inoculating loop

Nutrient agar was prepared for subculturing. Distinct colonies from the primary plates were carefully picked and streaked onto fresh sterile agar plates to obtain pure cultures. Subcultured colonies were incubated at 37 °C for 24 hours. Pure isolates were examined microscopically based on: Colony color, Size, Shape, Margin, Elevation and Texture.

3.2.6 Gram Staining and Microscopic Examination

Equipment: Microscope

Apparatus: Microscopic slides, Pasteur pipettes

Reagents: Staining reagents (Gram stain kit: Crystal violet, Gram's iodine, Ethanol, Safranin)

Gram staining was performed on the isolates. Smears were prepared on clean slides, heat-fixed, and sequentially stained with crystal violet, iodine, decolorized with ethanol, and counterstained with safranin. Slides were examined under the microscope using oil immersion (×100 objective). Bacteria were identified as Gram-positive or Gram-negative, and cell morphology was recorded as cocci or rods (arrangement: single, clusters, or chains).

CHAPTER FOUR

4.0 RESULTS

4.1. Morphological and Microscopic Characteristics of Isolate

The isolates were identified based on their color, shape and Gram reactionin. Probable bacterial species were suggested according to their observed features.

Table 1: Identification of airborne bacterial isolates

Representative Isolate	Colony Chart	Gram Reaction	Identified Isolate
Sub 1	Cream pigment, irregular shape and smooth	Gram positive rods; in singles	Possibly *Corynebacterium*
Sub 3a	White pigment, irregular shape and smooth	Gram positive rods; in chains	Possibly *Lactobacillus spp*
Sub 3b	White pigment, undulate and rough	Gram positive rods; in chains	Possibly *Bacillus cereus*
Sub 5	Cream pigment, undulate and slimy	Gram positive rods; in clusters	Possibly *Bacillus subtilis*
Sub 6	Golden pigment, entire and smooth	Gram positive cocci; in singles	Possibly *Staphylococcus aureus*
Sub 7	Yellow pigment, entire and smooth	Gram positive cocci; in clusters	Possibly *Micrococcus luteus*
Sub 10	Cream pigment, entire and smooth	Gram negative rods; Loosely in cluster	Possibly *Escherichia coli*

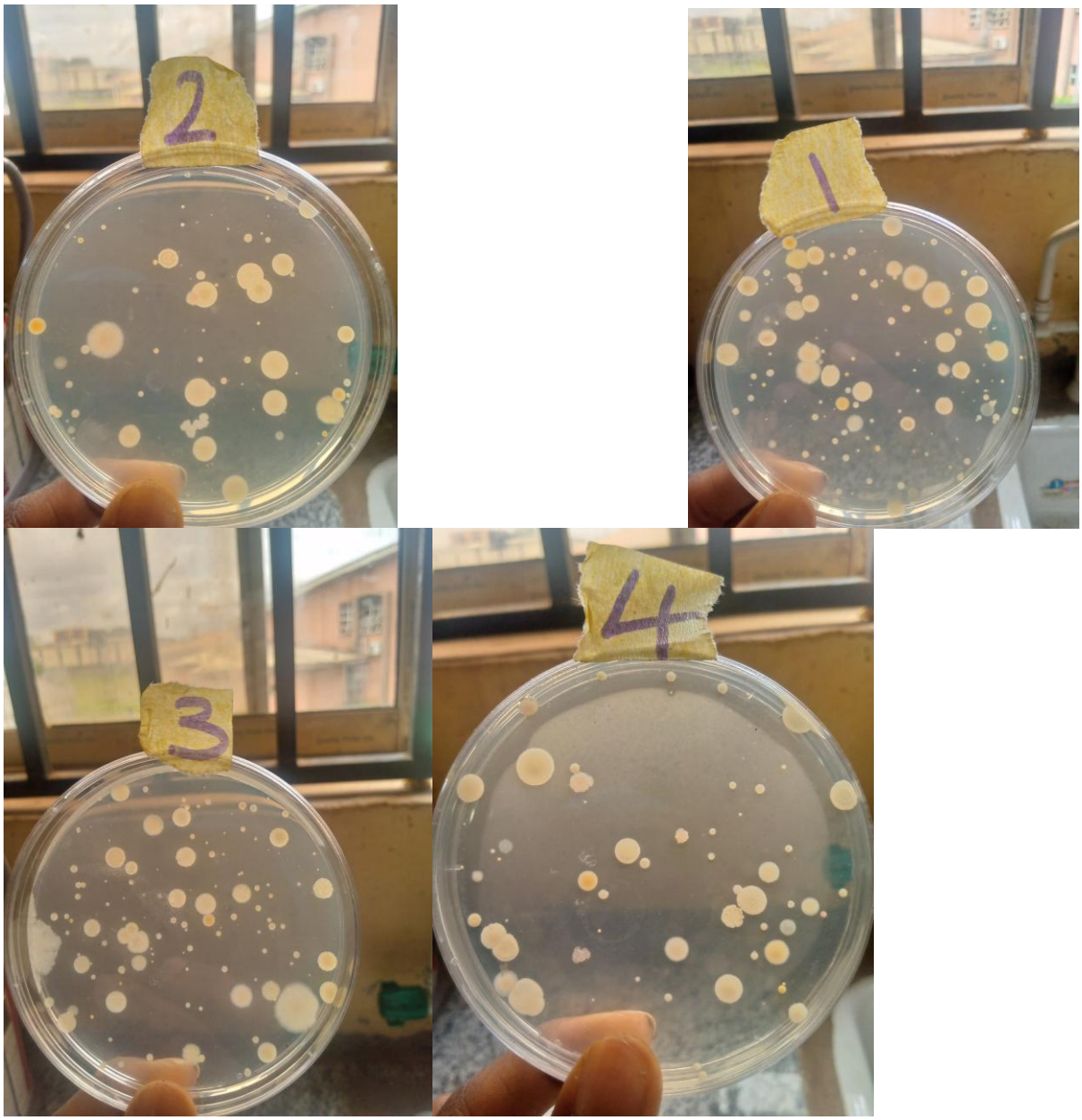


Plate 4.1: Isolated bacterial plates

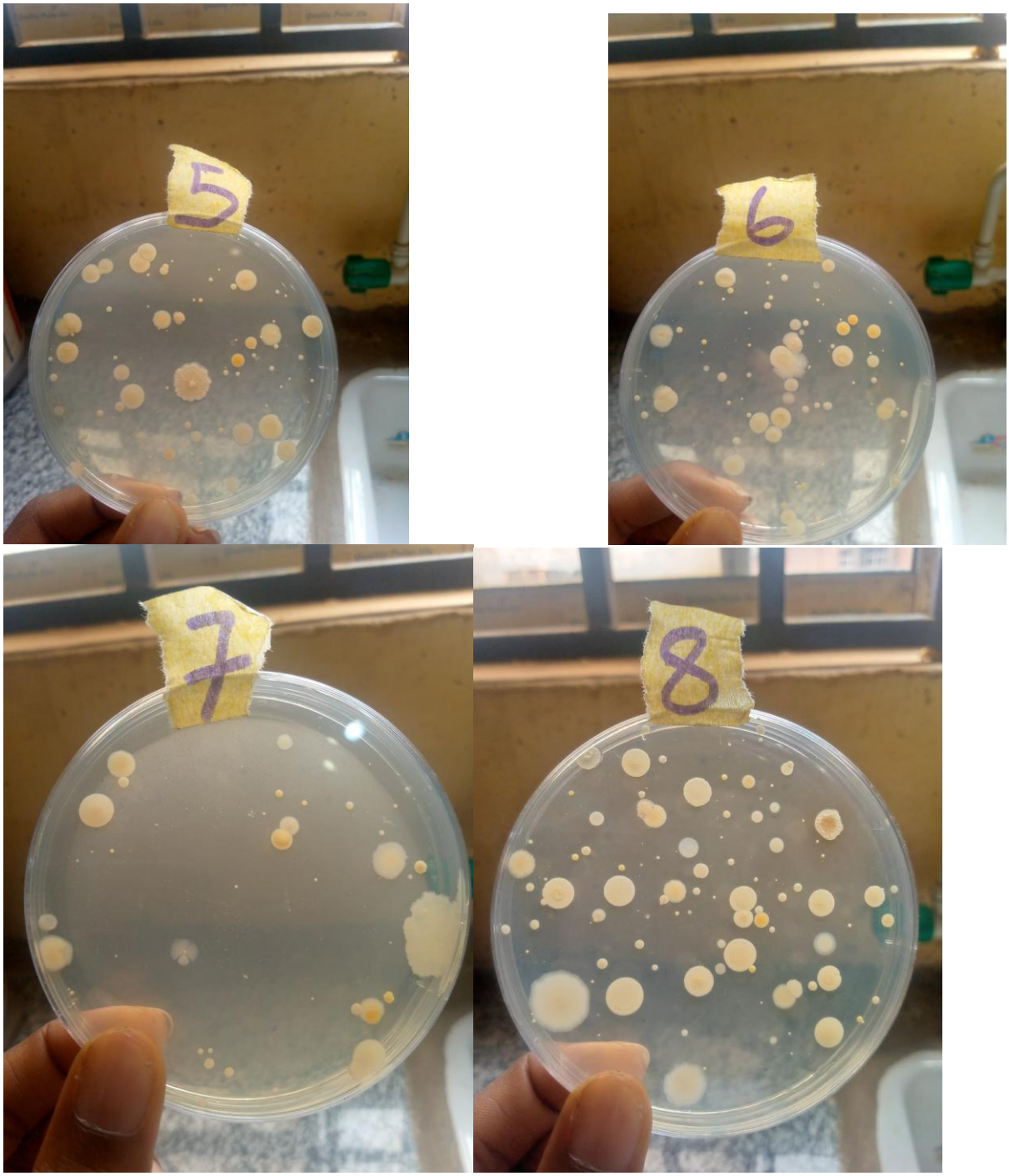
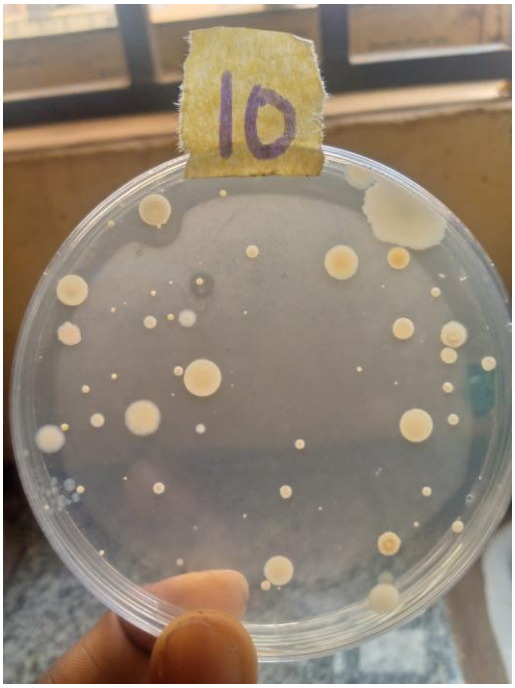


Plate 4.2: Isolated bacterial plates



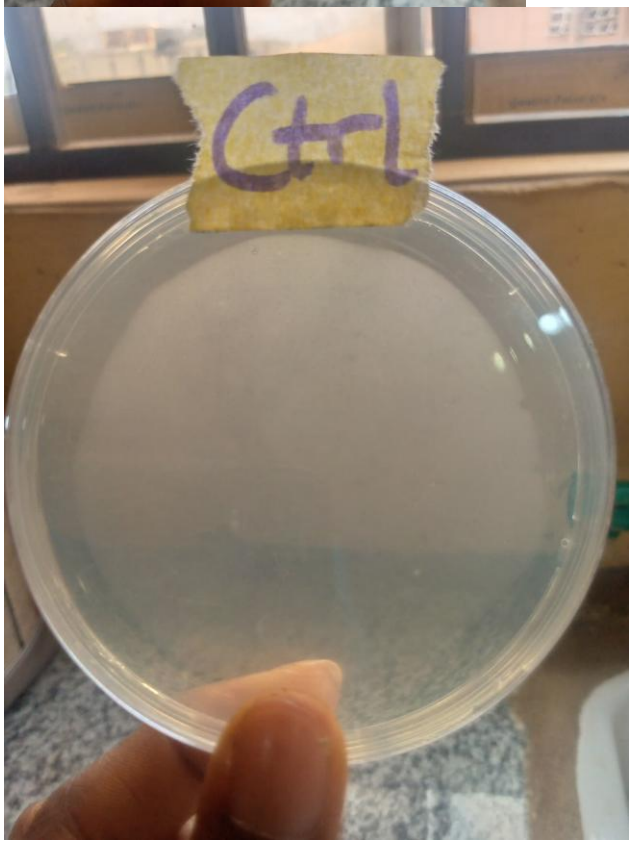
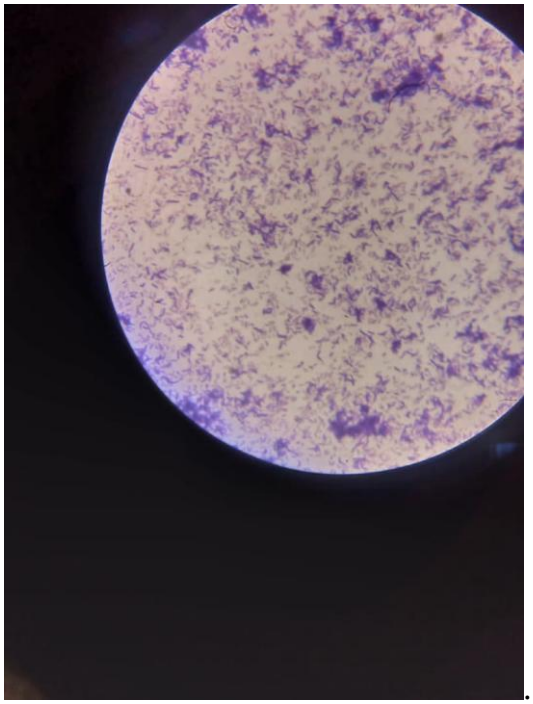
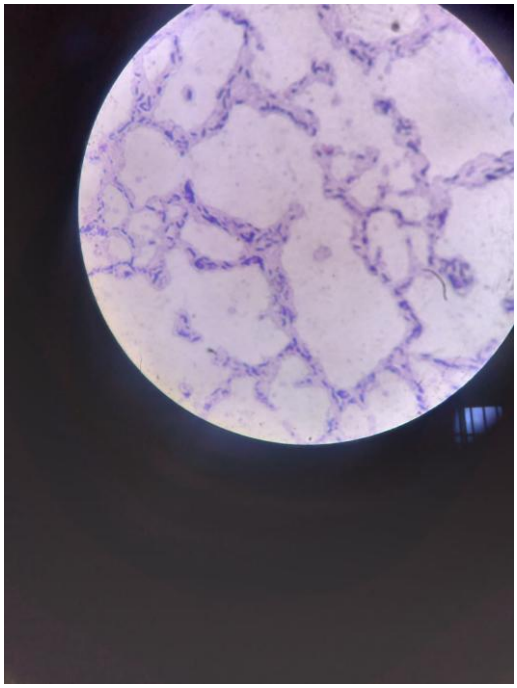


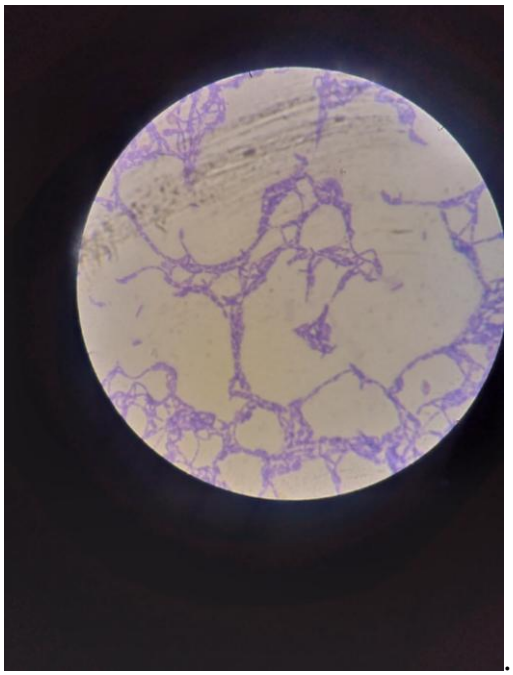
Plate 4.3: Isolated bacterial plates



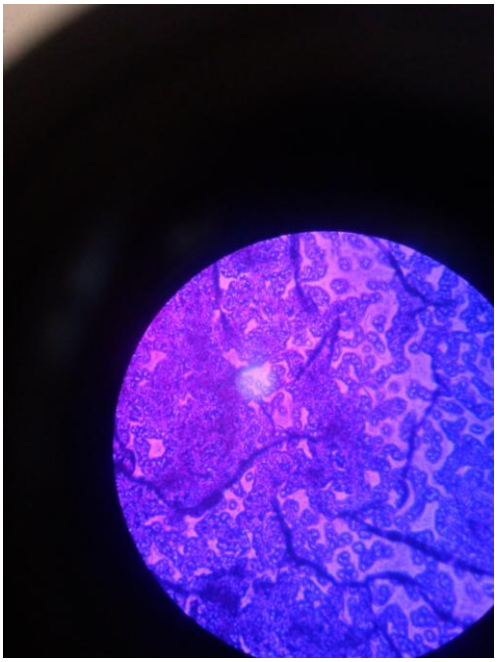
Sub 1



Sub 3a

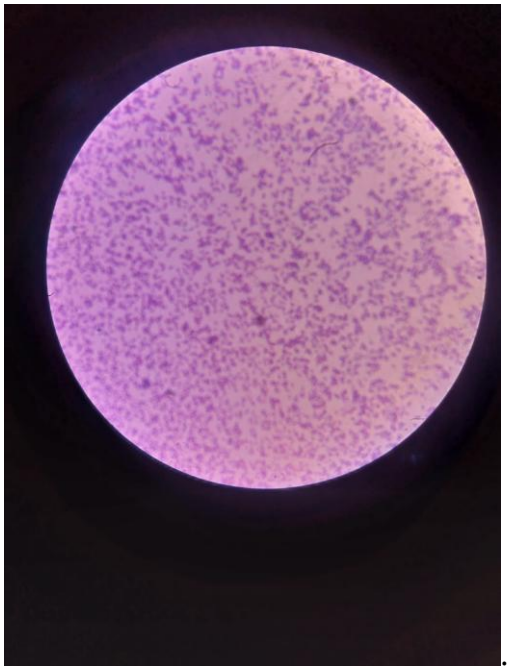


Sub 3b

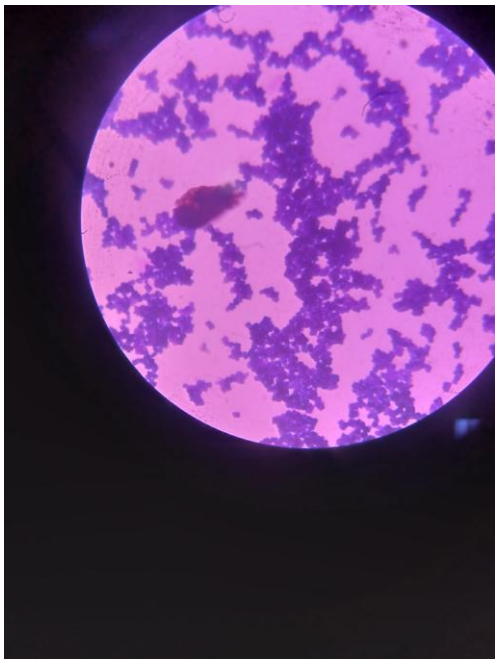


Sub 5

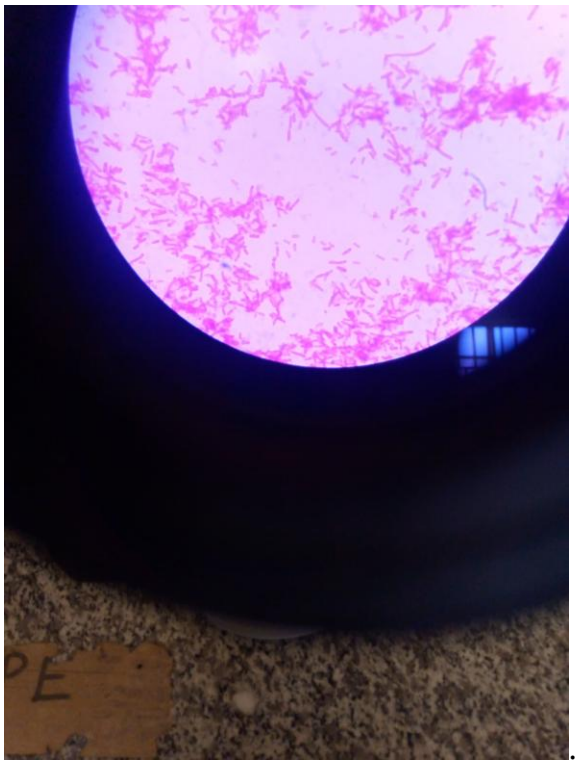
Plate 4.4: Gram reactions of the isolates



Sub 6



Sub 7.



Sub 10

Plate 4.5: Gram reactions of the isolates

CHAPTER FIVE

5.0. DISCUSSION AND CONCLUSION

In this study, all the exposed plates showed visible microbial growth after 24 to 48 hours of incubation, while the control plate showed no growth. The absence of growth on the control plate confirms that the experimental setup was not contaminated and that the colonies observed on the test plates originated solely from the sampled environment. These variations in colony counts likely reflect the uneven distribution of airborne microorganisms in the sampled environment. Factors such as air flow, human movement, proximity to open windows or doors, ventilation systems, and surface cleanliness can influence the microbial load in specific locations. The relatively high number of colonies on some plates may indicate that those locations had more exposure to microbial sources, such as dust, human skin, clothing, or moisture-rich areas. In contrast, lower colony counts suggest comparatively cleaner or less disturbed airspace. Since airborne bacteria often originate from skin, soil particles, respiratory droplets, and contaminated surfaces, these results suggest that the environment tested contains a diverse and active microbial population. This data is particularly useful in environmental monitoring, especially in hygiene-sensitive areas like hospitals, laboratories, food-processing facilities, and pharmaceutical environments.

Seven distinct bacterial isolates were successfully obtained through subculturing, and their morphological characteristics were studied based on colony appearance. These characteristics included texture, colour, size, shape, margin, and elevation, which are commonly used in preliminary bacterial identification. Several colonies were cream or off-white in colour, including isolates such as Sub 1, which are typical of common environment, possibly Corynebacterium. Sub 6 was golden in color, which is a key trait of Staphylococcus aureus, known for producing golden carotenoid pigments called staphyloxanthin. Sub 7 was

distinctly yellow and small in size, suggesting it may be Micrococcus luteus, a non-pathogenic bacterium commonly found in dust and on human skin. The isolates varied in size from small to large, and in shape from round to irregular. Isolates with irregular shapes and undulate or rough margins, such as Sub 5 and Sub 3b, could represent motile or spreading bacteria, which is characteristic of genera such as Bacillus. Sub 5 was also noted for its slimy texture, which may suggest the presence of a capsule or biofilm-producing bacterium. Such characteristics are often observed in environmental bacteria like Bacillus subtilis. The combination of morphological features suggests a heterogeneous population consisting of several bacterial genera, which is consistent with the complex and variable nature of microbial communities found in the air and on exposed surfaces.

The Gram staining technique was used to differentiate the bacterial isolates based on their cell wall composition. Out of the seven isolates, six were Gram-positive, while only one isolate (Sub 10) was Gram-negative. This dominance of Gram-positive bacteria is not surprising, as they are generally more resistant to desiccation and harsh environmental conditions compared to Gram-negative bacteria. Gram-positive bacteria have a thick peptidoglycan layer that helps them survive in dry and nutrient-poor environments, such as airborne dust particles or indoor surfaces. Among the Gram-positive isolates, several were rod-shaped, appearing either in singles, clusters, or chains. Isolates such as Sub 1 (rods in singles), Sub 3a, and Sub 3b (rods in chains) are likely to belong to the genus Bacillus, which are spore-forming, rod-shaped bacteria commonly found in soil and air. Sub 5 which showed rods in clusters, could also belong to the Bacillus group or other environmental genera. Some isolates, including Sub 7, was Gram-positive cocci arranged in clusters, a common feature of Micrococcus species. Sub 6, which showed cocci in singles, may be a less common arrangement but still fits within the Gram-positive cocci group. These types of bacteria are frequently found on human skin and can be easily dispersed into the air through skin

shedding or contact with surfaces. Sub 10 was the only Gram-negative isolate, appearing as rods loosely arranged in clusters. This morphological pattern is consistent with environmental Gram-negative bacteria such as Escherichia coli or Enterobacter. These organisms are less common in dry environments but may thrive in moist areas, such as sinks, washbasins, or poorly ventilated spaces. The presence of a Gram-negative organism, though rare in this case, may indicate localized moisture or surface contamination.

CONCLUSION

The results of this investigation confirm that the sampled environment contains a diverse population of bacteria, most of which are Gram-positive. This indicates a predominance of organisms that are well adapted to dry, indoor environment, where such bacteria are more likely to survive. Factors such as airflow, human activity, and level of environmental cleanliness may have influenced the distribution and variety of organisms observed. The morphological characteristics of the bacterial colonies provide preliminary clues to their identity, with several isolates resembling Staphylococcus, Bacillus, and Micrococcus species. Microscopic analysis through Gram staining supports these observations, revealing a mix of rods and cocci in different arrangements. The predominance of Gram-positive bacteria is typical of dry, indoor environments where such organisms are better adapted to survive. The detection of a single Gram-negative isolate further highlights the potential presence of opportunistic pathogens in specific areas of the environment. Overall, this study emphasizes the importance of routine environmental monitoring, particularly in hygiene-sensitive settings. Further biochemical tests (such as catalase, oxidase, and sugar fermentation) and molecular techniques (such as 16S rRNA gene sequencing) would be needed for identification to a specie level. Based on these findings, regular cleaning and proper ventilation should be maintained to reduce bacterial buildup, especially in areas of the hostel with limited airflow. Since Gram-positive bacteria like Staphylococcus and Bacillus can persist on surfaces for long periods, routine disinfection of frequently touched surfaces such as the tables and chairs is important. Overall, consistent hygiene practices and periodic microbial assessments will help sustain a healthier environment for students.

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