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ISOLATION OF MICROORGANISMS FROM THE HUMAN NOSE AMONG STUDENTS OF SOKOTO STATE POLYTECHNIC

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Article Info

Abstract

The human nasal cavity serves as a critical ecological niche for a diverse array of microorganisms, including both commensal and pathogenic bacteria and fungi. This study aimed to isolate, identify, and characterize the microbial flora present in the nasal passages of students at Sokoto State Polytechnic, Nigeria, while also assessing antibiotic resistance patterns and associated risk factors. A total of 100 nasal swab samples were collected from randomly selected healthy students, cultured on selective and differential media, and subjected to standard microbiological and biochemical identification techniques. The study revealed a high prevalence of Staphylococcus aureus (45%), followed by Staphylococcus epidermidis (30%), Streptococcus pneumoniae (15%), and Pseudomonas aeruginosa (10%). Fungal isolates included Candida albicans (8%) and Aspergillus species (5%). Antibiotic susceptibility testing demonstrated concerning resistance patterns, with S. aureus exhibiting 85% resistance to penicillin but 90% sensitivity to gentamicin. Risk factor analysis indicated that poor hand hygiene (OR = 3.2, p = 0.01) and recent antibiotic use (OR = 2.5, p = 0.03) were significantly associated with nasal colonization by pathogenic bacteria. These findings underscore the importance of nasal microbiota in public health, particularly in densely populated academic environments where microbial transmission risks are heightened. The study recommends enhanced hygiene education, routine antimicrobial susceptibility testing, and further surveillance for methicillin-resistant *Staphylococcus aureus* (MRSA) in the student population.

Keywords:
Microorganisms, Staphylococcus aureus, Sokoto, Polytechnic, Human Nose.

1. Introduction

1.1 Background of the Study

The human nasal cavity is a complex microbial ecosystem that harbors a diverse community of bacteria, fungi, and, in some cases, viruses. The anterior nares, in particular, serve as a primary reservoir for Staphylococcus aureus, a bacterium responsible for a wide range of infections, from minor skin abscesses to life-threatening conditions such as sepsis, pneumonia, and endocarditis (Wertheim et al., 2005). While some nasal microorganisms exist as harmless commensals, others can act as opportunistic pathogens, especially in immunocompromised individuals or under conditions of disrupted microbial balance (Krismer et al., 2017).

In institutional settings such as schools and hospitals, the risk of microbial transmission is heightened due to close interpersonal contact, shared facilities, and varying hygiene standards. Previous studies in Nigeria have reported high nasal carriage rates of S. aureus among university students, with prevalence ranging from 30% to 50% (Adebayo et al., 2019; Musa et al., 2020). However, limited data exists on the nasal microbial profile of polytechnic students, particularly in Sokoto State, where environmental and socio-economic factors may influence colonization patterns.

1.2 Statement of the Problem

Despite the recognized role of nasal microbiota in infection transmission, there is a paucity of research on the microbial composition of the nasal passages among students in Nigerian polytechnics. Sokoto State Polytechnic, with its high student population density and variable hygiene conditions, presents an ideal setting for investigating nasal microbial carriage. Understanding the prevalence of pathogenic bacteria and fungi, as well as their antibiotic resistance profiles, is crucial for developing effective infection control strategies.

1.3 Objectives of the Study

The primary objectives of this study were:

1. To isolate and identify bacterial and fungal species colonizing the nasal passages of students at Sokoto State Polytechnic.
2. To determine the antibiotic susceptibility patterns of isolated bacterial strains.
3. To assess potential risk factors associated with nasal colonization by pathogenic microorganisms.

1.4 Research Questions

1. What are the predominant bacterial and fungal species present in the nasal cavities of the students?
2. What is the antibiotic resistance profile of the isolated bacterial strains?
3. Are there significant associations between hygiene practices, antibiotic use, and nasal microbial carriage?

1.5 Significance of the Study

This study provides valuable data on nasal microbial colonization among students, which can inform public health interventions aimed at reducing infection transmission in academic environments. Additionally, the findings contribute to the growing body of knowledge on antimicrobial resistance in Nigeria, where antibiotic misuse remains a significant concern. 1.6 Scope and Limitations

The study was limited to students of Sokoto State Polytechnic, and findings may not be generalizable to other institutions. Additionally, molecular techniques for microbial identification (e.g., PCR) were not employed due to resource constraints.

2. Literature Review

2.1 The Human Nasal Microbiome

The nasal microbiome consists of a dynamic community of microorganisms influenced by host genetics, immune status, environmental exposures, and hygiene practices (Frank et al., 2010). The most commonly isolated bacteria include:

2.1.1 Gram-Positive Bacteria

-Staphylococcus Aureus: A major pathogen associated with skin infections, pneumonia, and toxic shock syndrome. Nasal carriage is a known risk factor for subsequent infections (Wertheim et al., 2005).

-Staphylococcus Epidermidis: A commensal that can cause infections in immunocompromised individuals (Otto, 2009).

-Streptococcus Pneumoniae: A leading cause of respiratory infections, particularly in children and the elderly (Bogaert et al., 2004).

2.1.2 Gram-Negative Bacteria

-Pseudomonas Aeruginosa: An opportunistic pathogen associated with hospital-acquired infections (Ramsey et al., 2016).

- Klebsiella Pneumoniae: Known for causing urinary tract and respiratory infections (Podschun & Ullmann, 1998).

2.1.3 Fungal Colonization

-Candida albicans: A commensal yeast that can cause thrush and systemic infections in immunocompromised hosts (Pfaller & Diekema, 2007).

- Aspergillus spp.: Environmental molds that can lead to allergic reactions or invasive aspergillosis in susceptible individuals (Latgé & Chamilos, 2019).

2.2 Factors Influencing Nasal Microbial Colonization

2.2.1 Hygiene Practices

Poor hand hygiene and lack of sanitation facilities increase the risk of S. aureus transmission (Boyce & Pittet, 2002).

2.2.2 Antibiotic Use

Overuse of antibiotics disrupts normal microbiota and promotes resistant strains (Lowy, 2003).

2.2.3 Immune Status

Immunocompromised individuals are more susceptible to colonization by opportunistic pathogens (Frank et al., 2010).Low

2.3 Previous Studies on Nasal Carriage in Nigeria

- A study in Lagos reported a 40% S. aureus nasal carriage rate among university students (Adebayo et al., 2019).

Research in Kano found a 22% prevalence of MRSA (Musa et al., 2020).

-Findings suggest regional variations in microbial carriage, necessitating localized studies.

3. Materials and Methods

3.1 Study Design and Population

A cross-sectional study involving 100 students (50 males, 50 females) aged 18–30 years was conducted.

3.2 Sample Collection and Processing

- Sterile cotton swabs moistened with normal saline were used to collect nasal specimens.

-Samples were transported in Stuart's transport medium and processed within 2 hours.

3.3 Microbial Culturing and Identification

Bacterial culture, Blood Agar, Mannitol Salt Agar, MacConkey Agar.

-Fungal culture: Sabouraud Dextrose Agar (SDA) with chloramphenicol.

-Biochemical tests: Catalase, coagulase, oxidase, and sugar fermentation tests.

3.4 Antibiotic Susceptibility Testing

Kirby-Bauer disc diffusion method (CLSI, 2021 guidelines) using:

- Penicillin (10 IU)

- Gentamicin (10 µg)

- Ciprofloxacin (5 µg)

- Erythromycin (15 µg)

3.5 Statistical Analysis

Data were analyzed using SPSS v26, with chi-square tests for associations ($p < 0.05$).

4. Results

4.1 Microbial Isolation Rates

Microorganisms	**Prevalence(%)**
Staphylococcus aureus	85%
Streptococcus pneumoniae	30%
Starphylococcus epidermidis	60%
Pseudomonas aeruginosa	10%
Aspergillus spp	5%
| Candida albicans	8%

4.2 Antibiotic Resistance Patterns

-S. aureus: 85% resistant to penicillin, 90% sensitive to rgentamicin.

-P. aeruginosa: 60% resistant to ciprofloxacin.

4.3 Risk Factors

- Poor hand hygiene (OR = 3.2, $p = 0.01$).

- Recent antibiotic use (OR = 2.5, $p = 0.03$).

5. Discussion

The high S. aureus carriage rate (45%) aligns with previous Nigerian studies but exceeds rates in developed nations, likely due to differences in hygiene and antibiotic regulation. The absence of MRSA contrasts with findings from Kano, Nigeria suggesting regional resistance variations.

6. Conclusion and Recommendations

This study confirms significant nasal colonization by pathogenic microbes among Sokoto State Polytechnic students. Recommendations include:

-Enhanced hygiene education programs in schools.

-Antimicrobial stewardship to curb resistance.

-Further MRSA surveillance in the region.

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