Elite Journal of Medicine. Volume 2 issue 6(2024), Pp. 10-21
https://epjournals.com/journals/EJM

Nasal Carrier of Methicillin-Resistance *Staphylococcus Aureus* in Apparently Healthy Individuals in Kwara State University, Malete, Nigeria

[1] Abdulrazaq Mustapha[*], [1] Tolulope Joseph Ogunniyi, [1]Tajudeen Sulaiman Olaide, [2]Catherine Olutoyin Adekunle and [3]Abdulrahman Abdulbasit Opeyemi and [4]Emmanuel Ifeanyi Obeagu

[1]Department of Medical Laboratory Sciences, Faculty of Basic Medical Sciences, Kwara State University, Malete. [2]Department of Medical Microbiology and Parasitology, Faculty of basic clinical science, Osun State University, Osogbo. [3]Department of Medical Laboratory Science, Achievers University Owo. Ondo State, Nigeria
[4]Department of Medical Laboratory Sciences, Kampala International University, Uganda.

Email: ayodeji.mustapha@kwasu.edu.ng

Abstract

Infections in hospitals and the general population are frequently caused by *Staphylococcus aureus*. Methicillin-resistant *Staphylococcus aureus* is still a significant nosocomial pathogen, and because of its resistance to several medications, infections are frequently hard to treat. As such the study aim to isolate *Staphylococcus aureus* in nasal carrier of an apparently healthy students in Kwara state university, using standard bacteriological method, and determine the prevalence of MRSA and MSSA from the isolate. The study is a cross-sectional study done to determine the distribution of MRSA among Kwara state university students using a Nasal swab. Microbial isolates were identified based on their colonial morphology and biochemical reaction and antimicrobial susceptibility testing was carried out using Mueller Hinton Agar following the disk diffusion method with cefoxitin disk while the zone of inhibition was recorded using the CLSI standard. A total number of 100 nasal swab samples were collected from 100 apparently healthy students of Kwara state university and were screened for Methiciillin Resistant *Staphylococcus aureus*. Out of 100 samples screened (50 from males and females participants each), 42 (42%) of the isolates were *Staphylococcus aureus* based on morphology and biochemical tests. Of the 42 *Staphylococcus aureus* isolated, 19 (45%) and 23 (55%) was from males and females participant respectively. The prevalence of MSSA and MRSA is 8 (16%) and 11 (22%) respectively among males participant, and 9 (18%) and 14 (28%) respectively among the females participant.
The study reported a significant rate of Methicillin-resistant *Staphylococcus aureus* (MRSA) among the study participants and emphasized the need for

Keywords: *Methicillin-resistant Staphylococcus aureus (MRSA), Nasal carrier, antimicrobial resistance.*

Citation: Mustapha A, Ogunniyi TJ, Olaide TS, Adekunle CO, Opeyemi AA, Obeagu EI. Nasal Carrier of Methicillin-Resistance *Staphylococcus Aureus* in Apparently Healthy Individuals in Kwara State University, Malete, Nigeria. Elite Journal of Medicine, 2024; 2(6): 10-21

Introduction

Antimicrobial is a term used to describe drugs that treat many types of infections by killing or slowing the growth of microbes (bacteria, viruses, fungi, and parasites) causing the infection (1). Antimicrobial resistance (AMR) is a term that describes when these microbes change over time and no longer respond to medicines, making infections harder to treat and increasing the risk of disease spread, severe illness, and death. The WHO defines antimicrobial resistance as a microorganism's resistance to an antimicrobial drug that was once able to treat an infection by that microorganism. As a result of drug resistance, antibiotics and other antimicrobial medicines become ineffective, and infections become increasingly difficult or impossible to treat. Antimicrobial resistance (AMR) occurs when microbes evolve mechanisms that protect them from the effects of antimicrobial agents (2). Methicillin-resistant *Staphylococcus aureus* (MRSA) is an important cause of healthcare-associated infections worldwide (3). In recent years, cases of MRSA infection have been reported more frequently in healthy community individuals with no traditional risk factors for MRSA infection (4).

These infections, apparently acquired in the community, are termed community-associated MRSA infections. Community-associated MRSA (CA-MRSA) strains differ from healthcare-associated MRSA strains in terms of epidemiology, microbiology, and clinical manifestations (5). CA-MRSA strains are generally susceptible to most antibiotics, contain staphylococcal chromosome cassette mecA type IV, produce the virulence factor Panton-Valentine leukocidin, and cause mainly skin and soft-tissue infections. It is well recognized that nasal carriage of MRSA represents a major risk factor for subsequent infection and transmission of this pathogen (6). First identified in purulent fluid from a leg abscess by Ogston in the 1880s and formally isolated by Rosenbach not long after, *Staphylococcus aureus* is well adapted to its human host and the healthcare environment. *S. aureus* is both a frequent commensal and a leading cause of endocarditis, bacteremia, osteomyelitis, and skin and soft tissue infections (7).

With the rise of hospital-based medicine, *S. aureus* quickly became a leading cause of healthcare-associated infections as well. Penicillin offered short-lived relief; resistance arose in the 1940s, mediated by the β-lactamase gene blaZ. The first semi-synthetic anti-staphylococcal penicillin was developed around 1960, and methicillin-resistant *S. aureus* (MRSA) was observed within 1 year of their first clinical use. In fact, genomic evidence suggests that methicillin resistance even preceded the first clinical use of anti-staphylococcal penicillin. Methicillin resistance is mediated by mecA and acquired by horizontal transfer of a mobile genetic element designated staphylococcal cassette chromosome mec (SCCmec). The gene mecA encodes penicillin-binding protein 2a (PBP2a), an enzyme responsible for cross-linking the peptidoglycans in the bacterial cell wall. PBP2a has a low affinity for β-lactams, resulting in resistance to this entire class of antibiotics (8).

MRSA was first observed among clinical isolates from patients hospitalized in the 1960s, but since the 1990s, it has spread rapidly in the community (9). Although MRSA infection occurs globally, there is no single pandemic strain. Instead, MRSA tends to occur in waves of infection, often

characterized by the serial emergence of predominant strains. Recent examples of emergent MRSA strains include the health-care-associated MRSA (HA-MRSA) clonal complex 30 (CC30) in North America and Europe, the community-associated MRSA (CA-MRSA) USA300 in North America, and the livestock-associated MRSA (including ST398) and ST93 in Australia. Rates of both CA-MRSA and HA-MRSA appear to be declining in several regions, a trend first noted with HA-MRSA in the United Kingdom (10). The reason for the serial rise and fall of specific strain types remains poorly understood. MRSA colonization increases the risk of infection, and infecting strains match colonizing strains in as many as 50–80% of cases. Nearly any item in contact with skin can serve as a fomite in MRSA transmission, from white coats and ties to pens and mobile telephones. Colonization can persist for long periods of time. MRSA may also persist in the home environment, complicating attempts at eradication. At the same time, colonization is not static, as strains have been found to evolve and even to be replaced within the same host (11).

Through the findings of MRSA prevalence among university students, the study aims to contribute to knowledge depth on the extent of MRSA colonization in this population.

Methodology

Sample Collection and Transport

Samples was collected with sterile cotton swab pre-wetted with sterile saline; the swab was inserted and gently rotated in the two anterior nares of subjects who met the inclusion criteria and transported to the laboratory for analysis.

Sample Processing

The swab samples were aseptically applied to a small area (the well) of Mannitol Salt Agar plates whose surfaces have been dried in the incubator shelf at 37 °C for 10 minutes prior to use. Each inoculum was aseptically streaked out from the well to obtain discrete colonies. The plates were then incubated aerobically at 37 °C for 24 hours. The characteristics golden yellow colonies were aseptically isolated subcultured onto nutrient agar slants and further identified using established microbiological methods that include colonial morphology, Gram stain characteristics and biochemical tests. Isolates that were Gram positive cocci in clusters, catalase positive and coagulase positive were considered as S. *aureus* in this study.

Antimicrobial Susceptibility Testing Using Disc Diffusion

MSSA and MRSA was demonstrated by sub-culturing the growth on Mueller Hinton Agar and treat with Cefoxitin. The plate was incubated overnight at 37^0C and followed by determination of Zone of Inhibition which is measure to the nearest millimeters (mm) using a millimeter ruler.

Data Analysis

The variables were expressed in means and standard deviation. Student t-test and Analysis of Variance (ANOVA) was statistical methods used. Levels of significance was considered at $P<0.05$. pie chart was also applied.

Result

A total number of 100 nasal swab samples were collected from 100 apparently healthy students of Kwara state university and were screened for Methiciillin Resistant *Staphylococcus aureus*. Out of 100 samples screened (50 from males and females participants each), 42 (42%) of the isolates were *Staphylococcus aureus* based on morphology and biochemical tests. Of the 42 *Staphylococcus aureus* isolated, 19 (45%) and 23 (55%) was from males and females participant respectively. The prevalence of MSSA and MRSA is 8 (16%) and 11 (22%) respectively among males participant, and 9 (18%) and 14 (28%) respectively among the females participant.

Socio-Demographic Factor of The Participants

Table 1: represent Socio-demographic factor of the participants. The most participant fall within the age group of 16-20 years (61%), and zero participant was recorded within the age group of 31-35 years. Both male and female has equal distribution.

Table 1 shows the Socio-demographic factor of the Participants

Variable	Frequency	Percentage
Age group		
16-20 years	61	61
21-25 years	36	36
26-30 years	2	2
31-35 years	0	0
36-40 years	1	1
Gender		
Male	50	50
female	50	50

Table 4.1: Socio-demographic factor of the Participants (n=100)

Prevalence of *Staphylococcus aureus*

Fig 1 represents prevalence of *Staphylococcus aureus.* Out of 100 samples screened, 42 (42%) of the isolates were *Staphylococcus aureus* based on morphology and biochemical tests.

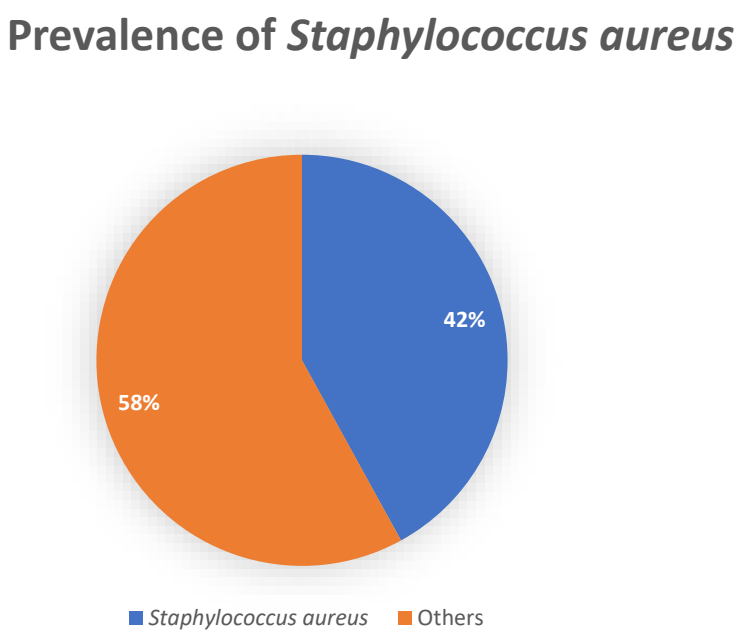

Figure 1: Prevalence of *S. aureus* in participant nasal swab (n=100)

Prevalence Rate of MSSA and MRSA Colonization

Fig 2 represents the prevalence rate of MSSA and MRSA colonization. A total of 42 *Staphylococcus aureus* were isolated from 100 nasal swab samples screened. 25 (59.5%) of the isolates were Methicillin Resistance *Staphylococcus aureus* (MRSA), while the remaining 17 isolates were Methicillin Susceptible *Staphylococcus aureus* (MSSA).

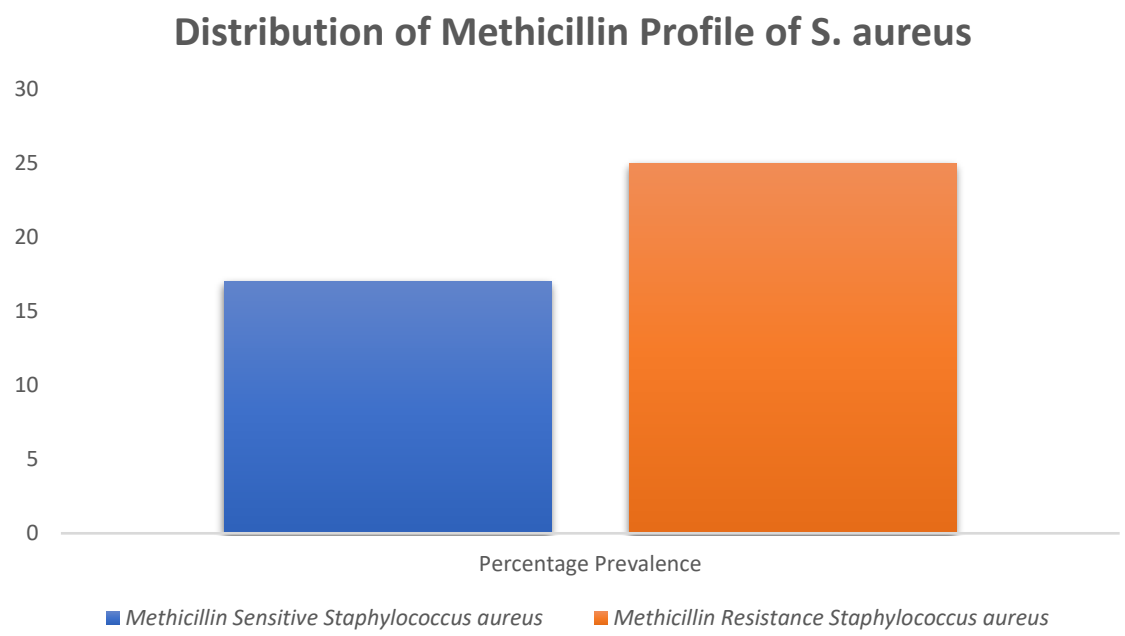

Figure 2: Distribution of Methicillin Resistance Profile *S. aureus*

Table 2: Association between Methicillin profile of *S. aureus* and Socio-demographic factor of the participants

Variable	Methicillin Sensitive *S. aureus* N(%)	Methicillin Resistance *S. aureus* N(%)	Others N(%)
Gender			
Male	8(16)	11(22)	31(62)
Female	9(18)	14(28)	27(54)
Pvalue	0.707		
Age Group			
16-20 years	11(18)	16(26.2)	34(55.7)
21-25 years	5(13.9)	9(25)	22(61.1)
26-30 years	0	0	2(100)
31-35 years	0	0	0
36-40 years	1(100)	0	0
Pvalue	0.347		

Table 2 represent the association between Methicillin profile of *Staphylococcus aureus* and socio-demographic factor of the participants. Based on gender distribution, the females participant has

the highest methicillin sensitive *Staphylococcus aureus* (18%), and also has the highest methicillin resistance *Staphylococcus aureus* (14%). Based on the age group, age group 16-20 years has the highest methicillin sensitive *Staphylococcus aureus*(18%), and also has the highest methicillin resistance *Staphylococcus aureus* (16%).

Table 3: Association between Risk factor and Methicillin profile of *S. aureus* among the participant

Variable	Methicillin Sensitive *S. aureus* N(%)	Methicillin Resistance *S. aureus* N(%)	Others N(%)
Number of people in the hostel			
1-2	13(76.5)	17(68)	40(69)
3-4	4(23.5)	8(32)	18(31)
Pvalue	0.812		
Recent surgery			
Yes	0(0)	1(4)	0(0)
No	17(100)	24 (96)	56(100)
Pvalue	0.220		
Recent hospitalization			
Yes	3(17.6)	4(16)	7(12.1)
No	14(82.4)	21(84)	51(87.9)
Pvalue	0.798		
Residence in a long-term care facility			
Yes	5(29.4)	8(32.0)	10(17.2)
No	12(70.6)	17(68.0)	48(82.8)
Pvalue	0.269		
Use of antimicrobial agent last year			
Yes	8(47.1)	16(64)	31(53.4)
No	9(52.9)	9(36)	27(46.6)
Pvalue	0.520		
Contact with a frequently hospitalised person			
Yes	3(17.6)	1(4)	5(8.6)
No	14(82.4)	24(96)	53(91.4)
Pvalue	0.313		
History of chronic illness			
Yes	4(23.5)	0(0)	6(10.3)
No	13(76.5)	25(100)	52(89.7)
Pvalue	0.044		

Table 3 represent the association between Risk factor and Methicillin profile of *S. aureus* among the participants. Based on the number of people in the hostel, group 1-2 has the highest methicillin sensitive *Staphylococcus aureus* (76.5%), and also has the highest methicillin resistance *Staphylococcus aureus* (68%). Based on recent surgery, the participants that had no recent surgery has the highest methicillin sensitive *Staphylococcus aureus* (100%), and also has the highest methicillin resistance *Staphylococcus aureus* (96%). Based on recent hospitalization, the participants that had no recent hospitalization has the highest methicillin sensitive *Staphylococcus aureus* (82.4%), and also has the highest methicillin resistance *Staphylococcus aureus* (84%). Based on residence in a long-term care facility, the participants that had no residence in a long-term care facility has the highest methicillin sensitive *Staphylococcus aureus* (70.6%), and also has the highest methicillin resistance *Staphylococcus aureus* (68.0%). Based on use of antimicrobial agent last year, the participants that had no use of antimicrobial agent last year has the highest methicillin sensitive *Staphylococcus aureus* (52.9%), while the participant that use an antimicrobial agent last year has the highest methicillin resistance *Staphylococcus aureus* (64%). Based on contact with a frequently hospitalised person, the participants that had no contact with a frequently hospitalised person has the highest methicillin sensitive *Staphylococcus aureus* (82.4%), and also has the highest methicillin resistance *Staphylococcus aureus* (96%). Based on history of chronic illness, the participants that had no history of chronic illness has the highest methicillin sensitive *Staphylococcus aureus* (76.5%), and also has the highest methicillin resistance *Staphylococcus aureus* (100%).

Discussion

Methicillin-resistant Staphylococcus aureus (MRSA) constitutes a significant contributor to healthcare-associated infections on a global scale (3). In recent times, instances of MRSA infections have become increasingly prevalent, even among seemingly healthy individuals in the community who do not possess the typical risk factors associated with MRSA infection (4). These infections, acquired within the community, are classified as community-associated MRSA infections. This study aims to assess the presence of methicillin-resistant *Staphylococcus aureus* among individuals appearing to be in good health at Kwara State University, Malete, Nigeria.

In the course of this investigation, a prevalence rate of 42% for *Staphylococcus aureus* was identified among the 100 nasal swab samples examined. This prevalence closely aligns with the rates of 42.9%, 35.0%, and 44.1% reported in studies conducted by (12), (13), and (14), respectively. Conversely, (15) reported a prevalence rate of 34.5%, (16) reported a prevalence rate of 36.7%, and (17) reported a prevalence rate of 52.5%. The study observed a variation in the prevalence rates of *Staphylococcus aureus* recorded in different studies. Notably, higher prevalence rates of 57.8% were reported by (18), and (19) also reported a prevalence rate of 55%. In this research, a total of 42 *Staphylococcus aureus* were isolated from 100 nasal swab samples screened. 25 (59.5%) of the isolates were Methicillin-resistant *Staphylococcus aureus* (MRSA), while the remaining 17 isolates were Methicillin-susceptible *Staphylococcus aureus* (MSSA), and notable differences were observed with other studies identified in this study.

The disparities observed in the prevalence rates among these studies can be attributed to a combination of factors, including variations in the composition of the study populations, the timing at which the studies were conducted, and the diverse methodologies employed for the detection of S. aureus. Differences in age, gender distribution, geographical locations, and the presence of underlying health conditions within the study site could potentially influence the observed prevalence of S. aureus. Furthermore, the temporal aspect plays a crucial role, as shifts in healthcare practices, antibiotic usage patterns, and the emergence of new bacterial strains can impact prevalence rates, resulting in variations over time. Finally, the choice of detection methods, encompassing variances in laboratory techniques, sampling methodologies, and diagnostic criteria, can introduce substantial discrepancies in the identification and quantification of *S. aureus*. Therefore, considering the multifaceted nature of these factors is imperative when interpreting and comparing the prevalence rates reported in different research investigations.

Conclusion

This study has provided valuable insights into the prevalence of *Staphylococcus aureus*, in which 42% of *Staphylococcus aureus* were isolated from 100 nasal swab samples screened, and 25 (59.5%) of the isolates were Methicillin Resistance *Staphylococcus aureus* (MRSA) among university students. The significance of these findings cannot be overstated, highlighting the need for proactive measures such as educational awareness to address MRSA within the university community.

This study underscores the importance of continuous vigilance, education, and preventive strategies to minimize MRSA transmission among university students. Additionally, future research endeavors should aim to expand the sample size and employ molecular techniques to speciate the strains of MRSA to ensure tailored therapeutic interventions.

References

1. World Health Organization. Antimicrobial Resistance [Internet]. World Health Organization. WHO; 2023. Available from: https://www.who.int/news-room/fact-sheets/detail/antimicrobial-resistance

2. Prestinaci F, Pezzotti P, Pantosti A. Antimicrobial resistance: a global multifaceted phenomenon. Pathogens and Global Health [Internet]. 2015;109(7):309–18. Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4768623/

3. Henderson DK. Managing methicillin-resistant staphylococci: A paradigm for preventing nosocomial transmission of resistant organisms. American Journal of Infection Control. 2006;34(5):S46–54.

4. Naimi HM, Tristan A, Bes M, Vandenesch F, Nazari QA, Laurent F, et al. Molecular characterization and antimicrobial resistance of nasal Staphylococcus aureus in the community of

Kabul. Journal of Global Antimicrobial Resistance [Internet]. 2023; 34:18–22. Available from: https://pubmed.ncbi.nlm.nih.gov/37321392/

5. David MZ, Daum RS. Community-Associated Methicillin-Resistant Staphylococcus aureus: Epidemiology and Clinical Consequences of an Emerging Epidemic. Clinical Microbiology Reviews. 2010;23(3):616–687.

6. Kluytmans J, van Belkum A, Verbrugh H. Nasal carriage of Staphylococcus aureus: epidemiology, underlying mechanisms, and associated risks. Clinical microbiology reviews. 1997;10(3):505–20.

7. Turner NA, Sharma-Kuinkel BK, Maskarinec SA, Eichenberger EM, Shah PP, Carugati M, et al. Methicillin-resistant Staphylococcus aureus: an overview of basic and clinical research. Nature reviews Microbiology [Internet]. 2019;17(4):203–218. Available from: https://www.nature.com/articles/s41579-018-0147-4

8. Harkins CP, Pichon B, Doumith M, Parkhill J, Westh H, Tomasz A, et al. Methicillin-resistant Staphylococcus Aureus Emerged Long before the Introduction of Methicillin into Clinical Practice. Genome Biology [Internet]. 2017;18(1):130. Available from: https://www.ncbi.nlm.nih.gov/pubmed/28724393

9. Tenover FC, McDougal LK, Goering RV, Killgore G, Projan SJ, Patel JB, et al. Characterization of a strain of community-associated methicillin-resistant Staphylococcus aureus widely disseminated in the United States. Journal of clinical microbiology. 2006;44(1):108–18. Available from: https://www.ncbi.nlm.nih.gov/pubmed/16390957

10. Turner NA, Sharma-Kuinkel BK, Maskarinec SA, Eichenberger EM, Shah PP, Carugati M, et al. Methicillin-resistant Staphylococcus aureus: an overview of basic and clinical research. Nature reviews Microbiology. 2019;17(4):203–18. Available from: https://www.nature.com/articles/s41579-018-0147-4

11. Hassoun A, Linden PK, Friedman B. Incidence, prevalence, and management of MRSA bacteremia across patient populations—a review of recent developments in MRSA management and treatment. Critical Care. 2017;21(1). Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5557425/

12. Danelli T, Duarte FC, Oliveira TA de, Silva RS da, Frizon Alfieri D, Gonçalves GB, et al. Nasal Carriage by Staphylococcus aureus among Healthcare Workers and Students Attending a University Hospital in Southern Brazil: Prevalence, Phenotypic, and Molecular Characteristics. Interdisciplinary Perspectives on Infectious Diseases [. 2020;2020:e3808036. Available from: https://www.hindawi.com/journals/ipid/2020/3808036/?fbclid=IwAR2GuWMmR96MTvXOSvMquroj4Jqva2aejpcVm020EBh3JMT86uEyo78ioRY

13. Bhatta DR, Hamal D, Shrestha R, Parajuli R, Baral N, Subramanya SH, et al. Nasal and Pharyngeal Colonization by Bacterial Pathogens: A Comparative Study between Preclinical and Clinical Sciences Medical Students. Canadian Journal of Infectious Diseases and Medical Microbiology. 2018; 2018:1–6.

14. Shibabaw A, Abebe T, Mihret A. Nasal carriage rate of methicillin resistant Staphylococcus aureus among Dessie Referral Hospital Health Care Workers; Dessie, Northeast Ethiopia. Antimicrobial Resistance and Infection Control. 2013;2(1):25.

15. Joachim A, Moyo SJ, Nkinda L, Majigo M, Mmbaga E, Mbembati N, et al. Prevalence of methicillin-resistant Staphylococcus aureus carriage on admission among patients attending regional hospitals in Dar es Salaam, Tanzania. BMC Research Notes. 2017;10(1).

16. Kemi Elizabeth Tuta, Abiola Olukemi Okesola, Chukwuma David Umeokonkwo. The Prevalence and Risk Factors Associated with Nasal Methicillin- Resistant Staphylococcus Aureus Colonization among Children in a Tertiary Hospital in Nigeria. Ethiopian journal of health sciences. 1970;29(4).

17. Onanuga A, Temedie T. Nasal carriage of multi-drug resistant Staphylococcus aureus in healthy inhabitants of Amassoma in Niger delta region of Nigeria. African Health Sciences [Internet]. 2011;11(2). Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3158512/

18. Ruimy R, Angebault C, Djossou F, Dupont C, Epelboin L, Jarraud S, et al. Are Host Genetics the Predominant Determinant of Persistent NasalStaphylococcus aureusCarriage in Humans? The Journal of Infectious Diseases, 2022;202(6):924–34. Available from: https://academic.oup.com/jid/article/202/6/924/936964?login=true

19. Phoomphut Sangaphunchai, Chawan Kritsanaviparkporn, Arucha Treesirichod. Association Between Staphylococcus Aureus Colonization and Pediatric Atopic Dermatitis: A Systematic Review and Meta-Analysis. Indian Journal of Dermatology/Indian journal of dermatology. 2023;68(6):619–27. Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10868995/

Citation: Mustapha A, Ogunniyi TJ, Olaide TS, Adekunle CO, Opeyemi AA, Obeagu EI. Nasal Carrier of Methicillin-Resistance *Staphylococcus Aureus* in Apparently Healthy Individuals in Kwara State University, Malete, Nigeria. Elite Journal of Medicine, 2024; 2(6): 10-21