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Isolation and Identification of Methicillin Resistant *Staphylococcus aureus* (MRSA) Associated with Infected Wounds

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Abstract

Methicillin-resistant *Staphylococcus aureus* (MRSA) is an important multidrug-resistant pathogen associated with wound infections and poses a significant challenge to effective antimicrobial therapy. This study was conducted to isolate and identify *Staphylococcus aureus* and determine the occurrence of methicillin-resistant strains among infected wound patients in Gusau, Zamfara State, Nigeria. A total of 150 wound abscess samples were collected and processed using standard microbiological techniques. Samples were cultured on nutrient agar and Mannitol Salt Agar, while presumptive *S. aureus* isolates were identified based standard microbiological techniques. Antimicrobial susceptibility testing was performed using the Kirby–Bauer disc diffusion method against oxacillin, vancomycin, tetracycline, levofloxacin and cotrimoxazole. Multidrug-resistant (MDR) isolates were further screened for methicillin resistance using a 30 µg cefoxitin disc. Molecular detection of the *mecA* resistance gene was carried out using polymerase chain reaction (PCR), followed by agarose gel electrophoresis. The results showed that 54 (36.0%) of the 150 samples yielded presumptive *S. aureus*. Of the 41 isolates subjected to antimicrobial susceptibility testing, resistance was highest to cotrimoxazole (70.7%), followed by vancomycin (65.9%), tetracycline (61.0%) and oxacillin (56.1%), while levofloxacin demonstrated the highest susceptibility (87.8%). Twenty-five (61.0%) isolates were classified as multidrug resistant. Among these MDR isolates, 7 (28.0%) were resistant to cefoxitin and were classified as MRSA. Molecular analysis demonstrated the presence of the *mecA* gene in six tested samples, with the expected amplicon observed at approximately 265 bp. It is concluded that the detection of the *mecA* gene further confirms the genetic basis of methicillin resistance in the identified isolates.

Keywords: Antibiotics, Methicillin-resistant *Staphylococcus aureus*, multidrug-resistant, wound infection

Introduction

Methicillin was originally introduced for use in clinical settings in 1961 however, the first clinical methicillin-resistant *Staphylococcus aureus* (MRSA) was also reported in the same year in the United Kingdom (UK). MRSA has evolved resistance to a variety of antibiotic classes; it is also known as the "Super Bug" and is a typical multidrug-resistant strain. MRSA causes infections ranging from mild skin infections to more severe illnesses to potentially fatal conditions such as septicemia, meningitis, endocarditis, and pneumonia (Baorto *et al*., 2014). The MRSA strains induce resistance through a highly transmissible mobile genetic element-Staphylococcal cassette chromosome mec (SCCmec)-which harbors mecA (resistant gene) and its analog mecC (resistant gene) encode penicillin-binding protein 2a (PBP2a) (Paterson *et al.,* 2014). By interfering with the drugs ability to bind to cell wall proteins, both genes provide resistance to methicillin and other beta-lactam antibiotics. Recently, MRSA has emerged as a significant public healthcare concern and a potentially lethal infective agent due to its ineffective response to various antibiotic classes (Kamal *et al.,* 2013). Moreover, it is regarded as the most prevalent pathogen in human nosocomial infections (Silva *et al.,* 2020).

Methicillin Resistant *Staphylococcus aureus* (MRSA) is frequently found in animal-sourced foodstuffs intended for human consumption, especially meat (Costa *et al.,* 2015). Therefore, the presence of MRSA in animal-sourced foodstuffs such as meat, milk, dairy products and fish strongly suggests the potential transmission of these resistant strains to humans which adds to the evidence of its zoonotic potential.Methicillin resistant *Staphylococcus aureus* causes infections ranging from mild skin infections to more severe illnesses to potentially fatal conditions such as septicemia, meningitis, endocarditis and pneumonia (Abdelazeem *et al*., 2020).

Methicillin resistant *Staphylococcusaureus* is significant pathogen causing nosocomial infections with a high prevalence in wound abscesses, sores and burns in Nigerian hospitals (Bilyaminu *et al*., 2025). Antimicrobial resistance is one of the most serious worldwide issues today. It leads to millions of fatalities, long term impairments and higher medical expenditures. It also has a negative influence on livelihoods, poses a danger to food security and causes animal deaths (WHO and UNEP, 2021). This resistant is largely due to indiscriminate use of antimicrobial drugs commonly used in the treatment of these infectious diseases. Synthetic drugs are expensive, not always available the good ones are not available and affordable in rural areas and are also associated with adverse side effect. The study was aimed to isolate and identify of Methicillin Resistant *Staphylococcus aureus* (MRSA) from wound abscess of infected wound patients.

Materials and Methods

Study area

The study area is Gusau the capital city of Zamfara State which lies between latitude 13°34''9'0N, longitude5°14''89'E, and at an altitude of 272m above the sea level. The occupation of the city inhabitants includes farming, trading, fishing and leather works. The town is a dry Sudan savannah surrounded by sandy terrain and isolated hills. Rainfall starts by June and ends early September but might sometime extend to October. The average annual rainfall is 550m with peak in the month of August. The highest temperature of 43-44°C during the hot season is experienced between the month of November and February (Moi, 2008).

Ethical approval

Ethical approval for the study was obtained from Zamfara State Ministry of Health ethics committee with reference number ZSHRECO7052025/290

Isolation of *Staphylococcusaureus*

The wound abscess sample was inoculated into Nutrient broth to promote the growth of test organism. About 1ml from enriched culture was inoculated onto nutrient agar and incubated for 24 hours at 37^0C. Growth from nutrient agar was streaked over sterile Mannitol salt agar (MSA) plates and incubated at 37^oC for 24hours. Isolates that show golden yellow colonies were considered as positive result (Cheesbrough, 2012). The presumptively detected *S. aureus* was subjected to culturing on mannitol salt agar and further identified by Gram stain, catalase and coagulase tests.

Identification of Staphylococcus aureus

Gram staining

A drop of normal saline was placed on a well labelled clean grease-free glass slide using a sterile inoculating loop; a colony of an overnight culture of the bacterial isolate was emulsified with the normal saline to make a thin smear. The smear was allowed to air dried and then heat fixed. The slide was flooded with crystal violet (primary stain) for 30 seconds the stain was rinsed with water. The smear was flooded with Lugol's iodine (mordant) to fix the primary stain. The iodine was then rinsed with water after 60 seconds**.** The slide was flooded with a decolorizer (acetone) and rinsed off almost immediately**.** The counter stain; Safranin was added and left for 30 seconds before being rinsed off. The stained smear was allowed to air dried, and then observed under the microscope using X100 oil immersion objective lens of the microscope (Cheesbrough, 2012).

Biochemical characterization

Catalase test

A drop of 3% hydrogen peroxide was placed on a clean grease-free glass slide. About 2 colonies of the bacteria was picked from a culture plate using a sterile wire loop and placed on the hydrogen peroxide; presence of bubbles indicated a positive Catalase test (Hadwan *et al*., 2024).

Coagulase test

Staphylococcus aureus isolates were distinguished from other staphylococci species by the production of Coagulase an enzyme that clots plasma. About one or two drops of blood plasma was placed on a clean grease-free glass slide and 2 colonies of the organism was picked using a sterile wire loop from 18 hours nutrient agar plate. The colonies were emulsified in the blood plasma and observation of a clot indicated a positive Coagulase test (Sagar, 2025).

Mannitolfermentation test

The pure colonies on nutrient agar were picked using a sterile inoculating loop and sub-cultured onto the surface of Mannitol Salt Agar (Life save Biotech, USA). Then, the plates were incubated at 37^oC for 24 hours. The changes in color of the medium from pink to yellow indicated positive results (Patrick *et al*., 2025).

Preparation of McFarland standard

The McFarland was prepared by dissolving 1% solution of anhydrous barium chloride and 1% solution of sulfuric acid until it forms a turbid suspension, the content was stored in a screw-cap tube at room temperature (25^0C) until when use (Sagar 2025).

Inoculum Standardization

Few colonies of the overnight growth of confirmed isolates to be tested were dispensed in sterile normal saline to match the 0.5 McFarland standards for sensitivity tests as described by Clinical laboratory standard institute, Clinical Laboratory Standard Institute (CLSI, 2020)

Detection of multi-drugs resistant (MDR) isolates

The test was performed using the Kirby Bauer disk diffusion method according to the CLSI interpretive criteria. An Inoculums of the isolates (0.5 McFarland standards) was added onto the surface of Mueller-Hinton agar plate (Oxoid, England). Five different classes of antibiotics discs were placed onto the surface of the agar plates using sterile forceps. The following antimicrobials were used sulfamethoxazole/trimethoprim (SXT 25µg), oxacillin (OX 5µg), levofloxacin (LEV 5µg), tetracycline (TE 30µg), vancomycin (VA 5µg) and the results were recorded in accordance with CLSI guidelines (CLSI 2020).

Screening of Methicillin Resistant *Staphylococcus aureus* (MRSA)

The bacteria suspension adjusted to 0.5 McFarland standard was subjected to antibiotic susceptibility testing using agar disc diffusion method as described by Bauer *et al*. (1996). Mueller Hinton agar (MHA) plates were inoculated with overnight culture of each isolate by streak plating. The 30 µg cefoxitin sensitivity discs was then aseptically placed on the plates and allowed to stand for 30 minutes for pre-diffusion. The plate was incubated at 37°C for 24 hours. Sensitivity pattern of the isolates based on Zone of inhibition was interpreted according to CLSI (2020).

Molecular Identification of MRSA Resistant Gene

DNA Extraction

The bacterial isolates were cultured in nutrient broth tubes and incubated at 37^{o}c for 24 hours; the bacterial cells were harvested through centrifugation at 10,000g for 5 minutes. Genomic DNA was extracted from the harvested cells using a boiling method (95^{o}C for 10minutes) and centrifuged for 10minutes at 12,000 revolutions per minutes (rpm) for 5minutes. Specific primer for MecA (F: CGCCGCATACACTATTCTCAGAATGA, R: ACGCTCACCGGCTCCAGATTTAT) of resistance gene was designed using National Centre for Biotechnology information (NCBI) primer-BLAST (Wayne *et al*., 2021).

PCR Amplification

PCR Amplification was carried out using the Taq PCR Mix 2x (Master Mix). Separate 12.5 µL PCR reactions were set up for mecA detection using the extracted genomic DNA. Each reaction included: Genomic DNA template (1 µL), Forward and reverse primers specific to mecA (0.5µL for each), and Master Mix (6.25µL) and, 3.5 µL PCR-grade water. The PCR reactions were run with the following parameters: Initial denaturation at 95°C for 5 minutes, followed by 35 cycles of Denaturation at 95°C for 30 seconds, Annealing at a temperature of 60°C for 30 seconds, and extension at 72°C for 1 minute, then final extension at 72°C for 5 minutes.

Gel Electrophoresis

To verify the success of PCR amplification and check for the presence of specific amplicons, agarose gel electrophoresis was performed. 1.5% agarose gel was prepared by dissolving agarose powder in 1X TAE (Tris-Acetate-EDTA) buffer, followed by heating in a Microwave oven. The molten agarose gel was stained with 2uL ethidium bromide to aid visualization under UV light. The gel was casted in a gel casting tray and allowed to solidify. Comb slots were inserted at one end of the gel for well formation. After gel solidification, the comb was gently removed, creating wells for sample loading, 4uL of the PCR products were carefully

loaded into the wells. Electrophoresis was conducted at 100V until the DNA bands migrated sufficiently (Wayne *et al*., 2021).

Results

Identification of the Isolates

In this study a total of 150 samples were collected and screened, Initial identification by growth on mannitol salt agar showed that 54(36.0%) isolates were suspected to be *Staphylococcus aureus* based on the formation of golden yellow colonies that indicates fermentation of phenol red in mannitol salt agar as in Table 1.

Table 1: Morphological and Biochemical characteristics of the Isolates

Isolates code	GRR	CAT	COA	MFT	Suspected organism
Isolate 1	+	+	+	+	*Staphylococcus aureus*

Key: + = positive; GRR = Gram reaction; CAT = Catalase; COA = Coagulase; MFT = Mannitol fermentation

Antibiotics Susceptibility results of *S. aureus*

The antimicrobial susceptibility testing observed levofloxacin with (87.8%) activity, and then followed by susceptibility to oxacillin with (43.9%). Lower activity was found in tetracycline and vancomycin with 61% and 65.9% resistant respectively and overall absolute resistant was observed in sulfamethoxazole/trimethoprim (Cotrimoxazole) with (70.7%) activity (Table 2)

Table 2: Summary of Antibiotics Susceptibility profile of *S. aureus* (n = 41)

Antibiotics	Potency (µg/disc)	Resistance (%)	Sensitive (%)
Oxacillin	5	23 (56.1)	18 (43.9)
Vancomycin	5	27 (65.9)	14 (34.1)
Tetracycline	30	25 (61)	16 (39.0)
Levofloxacin	5	05 (12.2)	36 (87.8)
Cotrimoxazole	25	29 (70.7)	12 (29.3)

Multidrug and Non-Multidrug Resistant Isolates

The distribution showed that 25 out of 41 isolates were multidrug resistant which accounted for 61% whereas 16 (39%) were non-multidrug resistant (Table 3)

Table 3: Multidrug and Non-Multidrug Resistant Isolates

Isolates	Number (n)	Percentage (%)
Multidrug	25	61.0
Non-Multidrug	16	39.0
Total	**41**	**100.0**

Screening of MRSA Isolates

The screening of MRSA is presented in Table 4**.** Of the 25 multi-drugs resistant isolates 7 (28.0%) isolates were resistant to cefoxitin

Table 4: Summary of Screened MRSA Isolates

Antibiotics	Potency (µg/disc)	Number (n)	Resistant (%)	Sensitive (%)
Cefoxitin	30	25	07 (28.0)	18 (72.0)

Molecular Characteristics of Resistance Genes

Lanes represent amplified mecA in the samples 1, 2, 3 4, 5, 6, 7 and 8. The presence of DNA band in lane 1, 2, 5 6, 7 and 8 confirm the presence of mecA (at 265bp) in the sample and absence in lane 3. The ladder lane (M) on the left serves as a size reference (at 1500bp) while lane 4 is negative control (Plate 4.1)

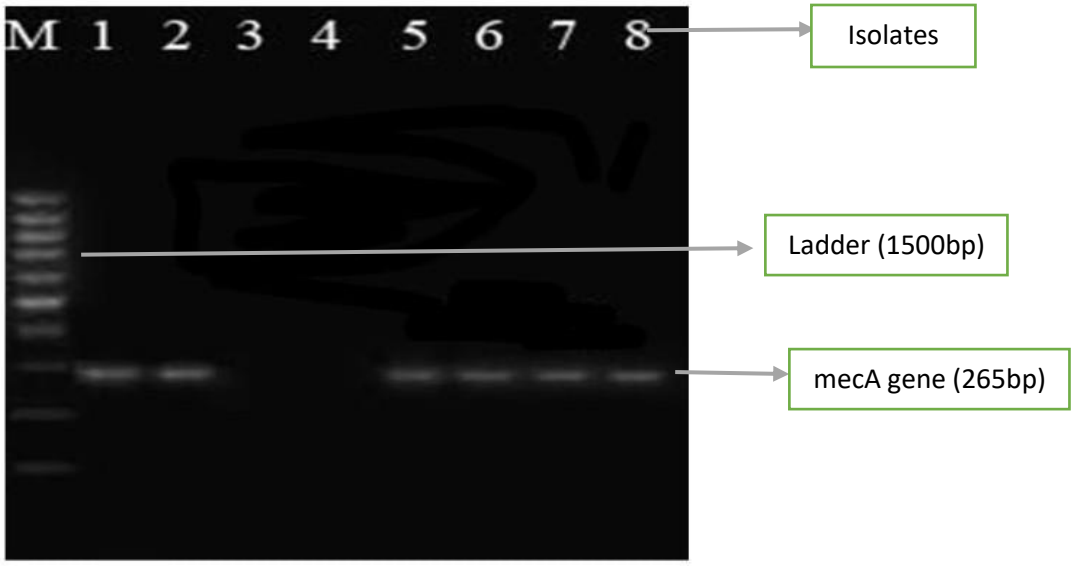


Plate 4.1: Gel Electrophoresis of the amplified MecA gene

KEY: Lanes M= 1500bpMolecular Ladder
Lane 1, 2, 5, 6, 7, 8show bandsof 265bp which indicate presence of MecA gene
Lane 3 shows no band which indicate absence of MecA gene
Lane 4 stands for negative control

Discussion

In the current study, the antibiotic resistance profiling and investigated five different antibiotic classes, pattern of antibiotic resistance demonstrates that Oxacillin resistance was found in 56.1% of isolates, trimethoprim-sulfamethoxazole resistance was found in 70.7% of the isolates, 61% and 65.9% resistance against the isolates were observed in tetracycline and vancomycin respectively. However, there is 12.2% resistance in levofloxacin. This explains that levofloxacin can be use as the antibiotic of choice for the treatment of MRSA in the study area.

The result obtained from the isolation and identification of bacteria revealed that *Staphylococcus aureus* was the most common type of bacteria isolated in wound infections (36.0%) and this is in agreement with the findings of Mahdi *et al*., (2000) which indicated that *Staphylococcus aureus* was the most frequently isolated microorganisms from pus caused by incision to reach pus or fluid collection under the skin surface. Alarmingly, in the present study, it was found that 61% *S. aureus* isolates were phenotypically resistant to three different antimicrobial categories and were defined as multidrug-resistant pathogens; this is

in contrast to the 44% stated by Gaire *et al*., (2021) and a high rate of 84.2% by Wilson *et al*., (2024). Reported 89.7% in South Africa Mkhize *et al*., (2021). Among multi-drugs resistant isolates, 28.0% were resistant to cefoxitin whereas 72% cefoxitin susceptible. However, there is significant susceptibility against levofloxacin, this variation in antibiotic resistance patterns could be due to the differences in the sources of isolates, geographical locations and the overall antibiotics used. Antibiotic resistance develops in bacteria due to horizontal gene transfer between various species of bacteria and mutation (Von Wintersdorff *et al*., 2016). As a result, the greater prevalence of MDR could be attributable to antibiotic overuse and abuse, which is frequent in the study area.

The prevalence rate of MRSA was found to be 28.0% in the current investigation. This conclusion is lower than 63% of (Hanif and Hassan, 2019). In Pakistan and previous report, which found a 52% prevalence rate of MRSA in 2017 in Karachi (Siddiqui *et al*., 2018). And MRSA prevalence was reported to be 50% in Lahore by (Perwaiz *et al*., 2007). It was also reported in Pakistan Punjab Prevalence of 61.8% (Idrees *et al*., 2023). In Europe, however, a frequency of MRSA of 65% was seen in *S. aureus* isolated from Intensive care units (Ullah *et al*., 2016). And 82.7% in kogi Nigeria (Mofolorunsho *et al*., 2022). Whereas, lower prevalence rates of 5.60% and 4.10% were recorded in China by Song *et al.* (2015) and in Algeria by Titouche *et al*., (2019). The study is contrast to research conducted in Ido-Ekiti Nigeria, which discovered 31% MRSA (Musa *et al*., 2023) and high that of 6.60% in Maiduguri, Nigeria (Grema *et al*., 2015). These inconsistencies might be attributed to differences in the laboratory methods employed to screen MRSA, the study's duration, the number of samples used, as well as variations in the situations existing in different countries and hospital settings. Molecular characteristics of the MRSA showed the presence of DNA band in lane 1, 2, 5 6, 7 and 8 confirm the presence of mecA (at 265bp) in the sample and absence in lane 3.

Conclusion

This research revealed that *S. aureus* was the most frequently isolated bacteria from wound samples (36.0%). The antimicrobial susceptibility testing observed levofloxacin has the highest activity, and then followed by susceptibility to oxacillin. Lower activity was found in tetracycline and vancomycin with 61% and 65.9% resistant respectively and overall absolute resistant was observed in sulfamethoxazole/trimethoprim (Cotrimoxazole). Of the 25 multi-drugs resistant isolates 7 (28.0%) isolates were MRSA.Molecular characteristics of the MRSA showed the presence of mecA gene in the sample.

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References

Abdelazeem M. A., Helal F. H., Amr E., Dalal Hussien H. A., Wael N. H., Gaber E. B., Nihal E. N., Mohmoud A. M. (2020). Methicillin-resistant *Staphylococcus aureus* (MRSA): one health perspective approach to the bacterium epidemiology, virulence factors, antibiotic resistance and zoonotic impact. *Infectious drug resistant*, **22**(13): pp 3255-325. doi: 10.2147/idr.s272733.

Baorto E. P., Baorto D., Windle M. L., Lutwick L. I. (2014) *Staphylococcus aureus* infections. WebMD LLC.

Bilyaminu U., Saggah A. M., Abubakar B. M., Moi I. M. (2025). Methicillin-resistant *Staphylococcus aureus* colonization and associated factors in clinical isolates among patients attending a tertiary medical centre in Nigeria. *Journal of infectious diseases,* **11**(25):25-1777 doi: 10.1186/512879-025-12166.

Cheesbrough M. (2012).*District laboratory practice in tropical countries,* Microbiological tests. (2nd Ed): Cambridge University press, pp. 313-327.

CLSI. Performance standards for antimicrobial susceptibility testing, 30th ed. CLSI supplement M100. Clinical and Laboratory Standards Institute: 2020.

Costa, W. L., Ferreira, J., Dos, S., Carvalho, J. S. (2015). Methicillin resistant *Staphylococcus aureus* in raw meats and prepared foods in public hospitals in Salvador, Bahia, Brazil. *Journal of Food Science*. **80**(1): pp. 147-150.

Gaire U García-Lafuente A., Guillamón E., Villares A., Rostagno M. A., Martínez J. A. (2009). Flavonoids as Anti-Inflammatory Agents: Implications in Cancer and Cardiovascular Disease. *InflammatoryResarch*, **58**: 537–552.

Grema H. A., Geidam Y. A., Gadzama G.B, (2015). Methicillin resistant *Staphylococcus aureus* a review. *Advanced Animal Veterinary Science.* **3**(2): 79-98.

Hadwan M. H., Altaee A. H., Mohammed R. M., Hadwan A. M., Al-kawaz H. S., Altalebi Z. A. (2024). An efficient protocol for quantifying catalase activity in biological samples. *Bulletin of the national research centre*, **48**(34): doi: 10.1186/42269.

Hanif E., Hassan S. A. (2019). Evaluation of antibiotic resistance pattern in clinical isolates of Staphylococcus aureus. *Pakistan Journal of Pharmaceutical Science*, **32**(3 (Supplementary)):1219-1223.

Kamal R. M., Bayoumi M. A., Abdel Aal S. F. (2013). MRSA detection in raw milk, some dairy products and hands of dairy workers in Egypt, a mini-survey. *Food Control***33**(1): pp. 49-53.

Paterson G. K., Morgan F. J., Harrison E. M. (2014). Prevalence and properties of mecC methicillin-resistant *Staphylococcus aureus* (MRSA) in bovine bulk tank milk in Great Britain. *Journal of Antimicrobial and Chemotherapy*. **69**(3): 598-602.

Silva V., Capelo J. L., Igrejas G. (2020). Molecular epidemiology of *Staphylococcus aureus* lineages in wild animals in Europe, A *review*. *Antibiotics*. **9**(3): pp. 122. doi: 10.3390/antibiotics9030122.

Mahdi S.E.I., Ahmad, A. O. A., Boelens, H., Abugroun, E. S., Vanbelkum, A., Zijistra E., Verbrugh, H., and Fahal, A. (2000). An Epidemiological study of the occurrence of *Staphylococcus aureus* in superficial abscesses of patients presenting for surgery in teaching hospital in Khartoum, Sudan. *Immunology and Medical Microbiology***29**:155-162.

Mkhize S., Amoako D. G., Shobo C. O., Zishiri O. T., Bester L. A. (2021). Genotypic and Phenotypic Characterizations of Methicillin-Resistant *Staphylococcus aureus,* on Frequently Touched Sites from Public Hospitals in South Africa. *International Journal Microbiology*, **6**(12): 567-781. doi:10.1155/2021/6011045

Musa I., Murtala S., Fatima J. (2023). Antibiogram and detection of mecA gene among MRSA at Specialist Hospital Sokoto, *microbes and Infectious Diseases*. **4**(3): 800-80: doi: 10.21608/MID. 2022.150608.1350

Mofolorunsho K., Emmanuel M., Omatola C., Aminu R., Ocheni H. (2022). Prevalence and antibiotic resistance profiles of Methicillin-Resistant *Staphylococcus aureus* isolated from clinical specimens in Anyigba, Nigeria. *Umar yaradua university Journal of Microbiology Research*, **7**(1):38–46.

Patrick M. S., Samuel H. K., Takeshi Y., Lisa A. B., Donald Y. M. L. (2025). Observations on emergence of mannitol-use-deficient *Staphylococcus aureus, journal of microbiology spectrum.* **14**(2): Pp e03091-25. doi: 10.1128/spectrum.03091-25.

Sagar A. (2025). McFarland standards principle, preparation, uses, and limitations. Accessed online on 12th April, 2026.

Song M., Bai Y., Xu J. (2015). Genetic diversity and virulence potential of *Staphylococcus aureus* isolates from raw and processed food commodities in Shanghai. *International Journal of Food Microbiology*, **195**:1-8.

Titouche Y., Hakem A., Houali K. (2019) Emergence of methicillin-resistant *Staphylococcus aureus* in raw milk and traditional dairy products in the Tizi Ouzou area of Algeria. *Journal Dairy Science*. **102**(8): 6876-6884

Ullah A., Qasim M., Rahman H., Khan J., Haroon M., Muhammad N. (2016). High frequency of methicillin-resistant *Staphylococcus aureus* in Peshawar Region of Pakistan. *Springer Plus*, **5**: 600

Von Wintersdorff C. J., Penders J., Van Niekerk J. M., Mills N. D., Majumder S., Van Alphen L. B. (2016). Dissemination of antimicrobial resistance in microbial ecosystems through horizontal gene transfer, *Frontiers in microbiology.* 7:173.

Wayne, P.A. (2007). Clinical & laboratory standards institute. Performance standards for antimicrobial susceptibility testing, 17, Pp 66

Wilson T. K., Zishiri O. T., El Zowalaty M. E. (2024). Molecular detection of multidrug and methicillin resistance in *Staphylococcus aureus* isolated from wild pigeons (Columba livia) in South Africa, *journal veterinary medicine.* **4**(24): 2352-7714 doi.org/10.1016/j.onehlt.