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Antibiotic resistance of *Staphylococcus aureus* isolates from intensive care unit patients in Wasit province, Iraq

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Abstract

Background: This study examines the antibiotic resistance of *Staphylococcus aureus* isolates from patients in critical care units in Wasit Province, Iraq, with a focus on methicillin-resistant strains.

Material and Methods: For this study, 125 clinical specimens from patients in the critical care unit were collected between September 2023 and January 2024. The isolates were first identified by culture, microscopic examination, and biochemical testing.

Results: According to the biochemical data, 24 out of 30 *S. aureus* isolates had an 80% MRSA designation. Urine samples had the highest prevalence of *S. aureus* (50%), followed by skin abscesses (37.5%) and sputum (12.5%). According to antibiotic susceptibility testing, all MRSA isolates showed resistance to penicillin and amoxicillin, while sensitivity was highest for rifampicin (91.7%), clindamycin (80%), and trimethoprim (75%).

Conclusion: These findings highlight the critical necessity for efficient infection control protocols and antibiotic management in ICU environments to address the escalating threat of MRSA. Continuous surveillance is crucial for monitoring the dissemination of resistant strains and guiding treatment approaches. This study provides significant data regarding MRSA epidemiology in Iraq, emphasizing the crucial public health ramifications of antibiotic resistance in healthcare settings.

Introduction

Staphylococcus aureus is a Gram-positive bacterium that produces coagulase and can form clusters resembling grapes: it is usually present in the human body without causing harm. However, due to its ability to thrive in different hosts and environments, *S. aureus* can lead to various infections; this bacterium is a significant pathogen in humans and is a common cause of infections acquired in hospitals and communities [1]. *Staphylococcus aureus* has the potential to cause various infections such as bloodstream, skin, soft tissues, lower respiratory tract, medical instrumentation-related infections (CLABSI), osteomyelitis, and endocarditis; the virulence factors and toxins of *S. aureus* can lead to toxin-induced diseases like scalded skin syndrome, staphylococcal toxic shock syndrome, and foodborne diseases [2].

Staphylococcus aureus, a bacterial pathogen, is a notorious and widespread bacterial strain in an intensive care unit (ICU) that causes an incredulous number of superficial skin infections and potentially hundreds of thousands to even more severe invasive infections worldwide each year; it is a primary comorbidity responsible for causing pneumonia, respiratory tract infections, surgical site, prosthetic joint, and cardiovascular infections, as well as nosocomial bacteremia [3]. Other infections, such as furuncles, abscesses, and wound infections, are

usually not life-threatening but may involve significant morbidity and pain, particularly in moderately severe skin infections, such as furuncles, abscesses, and wound infections; *S. aureus* can generate a broad spectrum of virulence factors, including toxins, immune evasion factors, and protein factors that help in colonizing the host during infection [4].

Staphylococcus aureus is a highly adaptive organism that employs various mechanisms of antibiotic resistance, making it extremely challenging to treat; one mechanism is enzymatic inactivation, where beta-lactamase enzymes hydrolyze beta-lactam antibiotics such as penicillin, rendering them ineffective; another mechanism is efflux pumps that actively pump out antibiotics from the bacterial cell, preventing therapeutic concentrations from accumulating. [5]. Target site alterations are a frequent resistance mechanism in *Staphylococcus aureus*; mutations in genes responsible for the bacterial cell wall or protein synthesis can lead to modifications in antibiotic binding sites, making them ineffective; in certain instances, bacteria can develop new binding sites to avoid the antibiotic's effects [6].

Methicillin-resistant *Staphylococcus aureus* (MRSA) is a bacteria that is resistant to the antibiotic methicillin; it can cause serious infections that spread in hospitals, healthcare facilities, and the community, MRSA responsible for difficult-to-treat infections in humans and cause over 100,000 deaths worldwide due to antimicrobial resistance in 2019 [7]. MRSA infections are caused by a strain of staph bacteria called *Staphylococcus aureus* that can reside on the skin, in the nose, armpits, groins, and other body areas; the increase in antibiotic-resistant bacteria like MRSA is attributed to prolonged and unnecessary use of antibiotics over the years, leading to the emergence of drug-resistant strains [8]. Methicillin-resistant *Staphylococcus aureus* MRSA, resistant to multiple antibiotics, presents a significant risk to ICU patients due to its resistance to commonly prescribed antibiotics; MRSA is known for its capability to survive and flourish in hospital and healthcare settings; it is a significant factor in healthcare infections, resulting in more extended hospital stays, higher morbidity, and death [9].

Patients who have recently undergone surgery are at a higher risk of developing MRSA infections while in the ICU are on prolonged antibiotic treatment, or have weakened immune systems; other risk factors include lengthy hospital stays and close contact with MRSA carriers, MRSA can spread rapidly within the ICU through contact with contaminated surfaces, equipment, or healthcare workers; patients with indwelling catheters, ventilators, or surgical wounds are particularly vulnerable to MRSA infections in the ICU [10]. Methicillin-resistant *Staphylococcus aureus* (MRSA) is usually transmitted through direct or indirect contact with infected individuals or contaminated objects; in the ICU, medical equipment and invasive devices can harbor MRSA and serve as sources for spreading the bacteria [11].

Methicillin-resistant *Staphylococcus aureus* (MRSA) is a serious threat to patients in the intensive care unit (ICU), leading to poor clinical outcomes and impacting infection control practices; the prevalence of MRSA in the ICU varies, with studies reporting rates around 8.7% to 34.2% in different settings [12]. The risk of acquiring MRSA in the ICU is primarily associated with the length of stay; it can be transmitted within the ICU environment, including through patient-healthcare worker interactions and environmental contamination; preventive measures, including comprehensive sampling for MRSA, isolation policies, and

additional infection control strategies, are necessary to address the challenges posed by MRSA in the ICU [13].

Understanding MRSA prevalence, risk factors, and transmission dynamics in the ICU is crucial for guiding empirical antibiotic choices, enhancing infection control, and reducing mortality and morbidity; effective control of MRSA infection requires a thorough knowledge and analysis of its risk factors [14]. As well as the development of future strategies to combat its spread and impact in the ICU; the search results provide insights into the prevalence, transmission dynamics, and challenges associated with MRSA in the ICU, emphasizing the importance of preventive measures and strategic allocation of healthcare resources to address this issue [15].

The *Staphylococcus aureus* bacteria are inherently weak to almost all antibiotics; while chromosomal mutation and antibiotic selection play significant roles, horizontal gene transfer is a common way for bacteria to develop resistance; consider this remarkable sensitivity of *S. aureus* [16]. However, penicillin enabled the eradication of invariably lethal illnesses; penicillin resistance was already a problem in hospitals by the mid-1940s, just a few years after it was first used in clinical practice; within a decade, it had spread across the community; it is pretty astounding how *S. aureus* may develop resistance to any medication [17]. Worldwide, the prevalence of infections caused by *Staphylococcus aureus* strains that are resistant to antibiotics has reached epidemic proportions; community and healthcare-associated staphylococcal infections, especially those caused by methicillin-resistant *Staphylococcus aureus* (MRSA), are on the rise in many nations [18].

The causes of healthcare-associated infections (HAIs) might be either internal or external infectious pathogens; local microbial flora is commonly found in the nose, skin, mouth, gastrointestinal tracts, and other patient-specific regions, making them endogenous sources [19]. These bacteria may invade and cause sickness under the right conditions; *staphylococcus aureus* can come from sources outside the patient, such as other people, equipment, or even the surrounding environment; the antimicrobial resistance (AMR) poses a significant health hazard, leading to over 700,000 deaths annually, and is projected to cause up to 10 million deaths globally by 2050 [20]. Prolonged antibiotic medication can cause bacteria that are initially susceptible to develop resistance; as the microorganism adapts and gains resistance, the drugs lose their effectiveness; when an antibiotic attacks bacterial cells, the sensitive ones will die off while the relatively resistant ones will survive [21].

Resistance genes carried by plasmids can quickly transmitted to all members of a bacterial species and even other bacterial taxa; bacteria that have resistance genes in their DNA will multiply and become antibiotic-resistant *Staphylococcus aureus* [22]. Understanding the prevalence and mechanisms of antibiotic resistance in *Staphylococcus aureus* is crucial for developing effective treatments and preventing the emergence of resistant infections; by delving into the molecular mechanisms of drug resistance in *S. aureus*, we can gain insights that will inform the development of new therapies and strategies to combat these challenging infections. [23]. *Staphylococcus aureus*, particularly methicillin-resistant *S. aureus* (MRSA), has developed various mechanisms of resistance to antibiotics; the primary reason behind MRSA's resistance to beta-lactam antibiotics is the presence of the *mecA* gene; this gene

Annals of R.S.C.B., ISSN:1583-6258, Vol.28, Issue1, 2024 Pages: 499 - 513

Received 30 July 2024; Accepted 15 August 2024

produces a protein called *PBP2a*, which is a transpeptidase, *PBP2a* has a much lower affinity for beta-lactam antibiotics compared to the normal transpeptidases found in non-resistant strains, making MRSA resistant to the effects of these drugs [24].

This resistance is usually conferred by the acquisition of a nonnative gene encoding a penicillin-binding protein with a significantly lower affinity for β-lactams; additionally, MRSA strains have evolved resistance mechanisms to almost all antimicrobial drugs used in the treatment of Gram-positive bacteria, including beta-lactams, glycopeptides, and oxazolidinones.[25]. These mechanisms include target modification, enzymatic drug inactivation, and decreased antibiotic uptake or efflux; understanding these resistance mechanisms is crucial for developing new anti-infective drugs and mitigating the evolution of MRSA [26]. The *mecA* gene is essential for methicillin-resistant *Staphylococcus aureus* (MRSA); it produces an alternative penicillin-binding protein, *PBP2a*, which has a much weaker attraction to beta-lactam antibiotics like methicillin, this weakened binding makes these antibiotics less effective against MRSA [27]. The presence of the *mecA* gene is a crucial mechanism of resistance to β-lactam antibiotics in MRSA; additionally, the *mecA* gene is widely disseminated in the *Staphylococcus aureus* population and is associated with multi-resistance to non-β-lactam antibiotics, the development of a modified penicillin-binding protein (*PBP*), known as *PBP 2a* or *PBP 2′*, has a reduced binding affinity for β-lactams, leading to resistance to almost all β-lactam medications that are now available [28].

Materials and methods

The patients

In total, 125 samples were collected from patients in the intensive care unit and some isolates from a private clinic in Kut city who were admitted to Zahra and Al-Karama Teaching Hospital in Wasit province from 1 September 2023 to 1 January 2024. This dataset encompassed detailed information for each patient, including their details such as name, age, and gender, their medical histories like underlying health conditions and prior antibiotic use, their admission dates to both the Intensive Care Unit (ICU) and the hospital, the treatment received during their ICU stay, and ultimately, the outcome of their clinical care.

Culture media

Table (1): Cultural media employed in the present study

No.	Media	Companies	Origins
1	Brain heart infusion Broth	Himedia	India
2	Blood Agar	Himedia	India
3	Muller-Hinton Agar	Himedia	India
4	Mannitol Salt Agar	Oxoid	England

Antibiotics

Table (2): The Antibiotics required in this work

Classes	Antibiotic	Symbol	Disk content	Company

Annals of R.S.C.B., ISSN:1583-6258, Vol.28, Issue1, 2024 Pages: 499 - 513

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			(µg)	
Aminoglycosides	**Amikacin**	**AK**	**30**	**Liofilchem (Italy)**
Penicillins	**Penicillin**	**P**	**10**	
β -lactamase inhibitor	**Methicillin**	**MET**	**5**	
	Amoxicillin-calvulinc acid	**AUG**	**30**	
Cephalosporins	**Cefoxitin**	**FOX**	**30**	
	Ceftriaxone	**CRO**	**30**	
Fluorquinolones	**Ciprofloxacin**	**CIP**	**5**	
Glycopeptides	**Vancomycin**	**VA**	**30**	
Diaminopyrimidines	**Trimethoprim**	**SXT**	**25**	
Lincosamides	**Clindamycin**	**CD**	**2**	
Refamycin	**Rifampicin**	**RD**	**5**	
Macrolides	**Erythromycin**	**E**	**15**	

Preparing the culture media

Table (1) lists the various media used in this study; the media were made precisely as instructed by the manufacturer, and each container bore the correct label to ensure sterility, to ensure sterility; the media used in the study was autoclaved at 121 degrees Celsius for 15 minutes under a pressure of 15 pounds per square inch. For the preparation of blood agar plates, a 5-7% concentration of human blood was added to the cooled blood agar base (45°C). This mixture was then poured into sterile Petri dishes, with approximately 20 ml per dish. These plates were further incubated for 24 hours at 37°C to verify sterility. Lastly, for later usage, the labeled plates were kept in a refrigerator at 4°C [29].

Bacterial isolation and characterization

The samples were grown on blood agar and Mannitol salt agar medium, and after a 24-hour aerobic incubation period at 37°C, the bacteria were positively identified by morphological and biochemical tests.

Gram stain method

A few drops of normal saline were applied to disperse a bacterial colony sample onto a clean slide, the sample was then fixed using heat, and crystal violet was spread evenly on the slide, followed by treatment with iodine; the crystal violet was subsequently removed using alcohol; finally, the sample was counterstained with safranine and examined under a 100X oil immersion lens. [30].

Annals of R.S.C.B., ISSN:1583-6258, Vol.28, Issue1, 2024 Pages: 499 - 513

Received 30 July 2024; Accepted 15 August 2024

Biochemical tests

Catalase test

A single bacterial colony was isolated from a culture plate and placed on a glass slide using a sterile loop. To test for the presence of the enzyme catalase, a small amount of 3% hydrogen peroxide solution was added to the bacterial colony. The appearance of oxygen bubbles was interpreted as a positive result for the presence of the enzyme catalase [31].

Coagulase Test

A sterile loop was used to gently pick a few colonies from a Petri plate in order to encourage bacterial growth, and the colonies were then put into a test tube holding five milliliters of brain heart infusion broth. After securing the tube snugly to avoid contamination, the bacteria were allowed to proliferate for 12 hours at a regulated temperature of 37 degrees Celsius. Subsequently, the tube underwent centrifugation following thorough mixing. After incubation, 0.5 ml of the clear liquid (supernatant) above the settled bacterial growth was carefully removed from the tube. After that, 0.5 ml of rabbit plasma was added, and the tube was incubated for the predetermined amount of time at 37°C in a water bath.

The formation of a clot in the plasma indicated a positive coagulase test, suggesting the bacterial organism's ability to induce blood clotting, certain coagulations occurred within 30 minutes, but others took many hours to appear; the evaluation of the coagulase test involved observing the formation of clots at different time points, the formation of clots in the rabbit plasma was observed over time. The results of the test showed varying degrees of clot formation in the rabbit plasma. Observations ranged from a loose, suspended clot to a completely solid and immobile clot after 24 hours. A specific observation, which occurred after 24 hours, was noted and recorded [32].

Detection of MRSA *S. aureus*

The susceptibility of the *S. aureus* isolates was determined using the agar diffusion technique on Muller Hinton agar with Cefoxitin (30µg) sensitivity discs, the isolates were standardized to a 0.5 McFarland standard, and then a suspension of the isolates was cultured into the Muller Hinton agar plates using aseptic techniques. The plates were cultured for 24 hours at a temperature of 37 degrees Celsius; isolates that exhibit resistance or decreased sensitivity to cefoxitin (≤ 18 mm) are classified as MRSA and are then analyzed through molecular studies.

Antimicrobial Sensitivity Test

The antibiotic susceptibility test was performed using Mueller Hinton agar. A bacterial suspension was prepared by gently mixing colonies from an overnight culture in a sterile normal saline solution. The suspension was adjusted to a specific turbidity level, matching the 0.5 McFarland standards, ensuring a consistent bacterial concentration. This standardized bacterial suspension was then spread evenly onto a Mueller Hinton agar plate using a clean swab and allowed to dry thoroughly before proceeding to the next step. Using sterile forceps, antibiotic discs were carefully deposited on the agar's surface. The inoculated plates were placed in an incubator set at 37°C for 24 hours to allow the bacteria to grow and for the antibiotics to diffuse into the agar. The diameter of the clear zone encircling each antibiotic

Received 30 July 2024; Accepted 15 August 2024

disc was meticulously measured after the incubation time. This "zone of inhibition" represents the area where the antibiotic prevented bacterial growth, indicating the effectiveness of the antibiotic against the bacteria being tested. The results of these measurements were then interpreted using the guidelines established by the Clinical and Laboratory Standards Institute (CLSI) in 2023 to determine the bacteria's susceptibility or resistance to each antibiotic.

Ethical approval

Following the principles outlined in the Declaration of Helsinki, this research investigation was carried out ethically. All participants gave their written and verbal informed consent prior to any samples being taken, guaranteeing they were aware of the risks and nature of the study. A local ethics committee examined and approved the consent form, study information, and study protocol. Approval document number 1851, dated August 21, 2023, and contains the documentation of this approval.

Statistical analysis

The collected data underwent statistical analysis using SAS software, version 9.1. To determine if there were significant differences in proportions between different groups, the chi-square test was employed; a statistically significant p-value was less than 0.05, indicating that the observed changes were probably the result of a meaningful effect rather than a random variation, this threshold suggests a strong likelihood that the differences in proportions are fundamental and not just a result of random variation.[33].

The results

The Patient's age groups and samples:

The study analyzed 125 clinical specimens (urine, sputum, and pus) obtained from patients hospitalized in the ICU in Wasit hospitals and some isolates from a private clinic in Kut city; *S. aureus* was identified in 30 isolates (26) isolates from the ICU and four isolates from the community. The MRSA was identified in 24 isolates; urine samples contained the highest proportion of *S. aureus* 12 (50%) compared to skin abscesses 9 (37.5%) and sputum 3 (12.5%) samples. As shown in Table (3 and 4). The ability to ferment mannitol aerobically was assessed in 30 isolates through catalase and coagulase production assays. Results of the P. value test revealed that there is no significant association between gender and type of sample.

(**Table 3): Types of collected samples**

Samples	**Percentage %**	**Male %**	**Female%**	**Median age (years)**
Urine (12)	50%	41.6 (5)	58.4 (7)	31
Abscesses (9)	37.5%	66.6 (6)	33.4 (3)	35
Sputum (3)	12.5%	33.3 (1)	66.7 (2)	42

Annals of R.S.C.B., ISSN:1583-6258, Vol.28, Issue1, 2024 Pages: 499 - 513

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Samples	Male %	Female%	P-value
Urine (12)	41.6 (5)	58.4 (7)	0.43
Abscesses (9)	66.6 (6)	33.4 (3)	
Sputum (3)	33.3 (1)	66.7 (2)	

Table (4): The distribution of patient samples according to sex

Isolation of *Staph aureus*

Bacterial isolates that were obtained from the intensive care unit patients were initially characterized based on cultural morphology and biochemical tests. Results of culture showed colonies on blood agar appeared as round, spherical, light to golden yellow colonies with a diameter of 0.8-1.0μm; they were soft, convex, brilliant, with a sharp border, and produced zones of obvious β-hemolysis on the agar.[34].

The isolates were stained with Gram stain to analyze the morphology of bacterial colonies; they were then studied using an oil immersion microscope lens, revealing round Gram-positive purplish-blue color cells; these cells were found in clusters organized in grape-like formations.[35].When *S. aureus* is streaked on mannitol salt agar to isolate the bacteria, the bacteria ferment the mannitol and create yellow zones in the reddish agar because it produces fermentation acids that lower the medium's pH and change the color of the phenol red to yellow, as reported by [36].

The coagulase test results for every isolate were positive; this test is used to differentiate between *Staphylococcus* species that are coagulase-negative and those that are coagulase-positive in the tube coagulase test; the coagulase test was also crucial to note and was used to detect free coagulase that secreted extracellularly and reacted with thrombin in plasma; additionally, the bound coagulase, often referred to as clumping factor and cell wall-associated coagulase, was found using a slide coagulase test.[37]. Also, they identified the bacterial isolates and confirmed that the diagnosis is consistent with previous studies conducted in Iraq [38] and studies by [39].

Detection of Methicillin Resistance *Staphylococcus aureus*

The results of the present study, MRSA showed the highest resistance for cefoxitin with 100% *Staphylococcus aureus* mainly MRSA has spread to all parts of the world and is becoming of significant concern in public health as one the most common causes of nosocomial infections [40]. The results of the present study are similar to those of other researchers, including [41] and [42], who found that all the isolates revealed complete resistance to cefoxitin at 100%, respectively. Methicillin resistance *S.aureus* is most noteworthy because it is responsible for an increased number of hospital and community-acquired infections worldwide and because of its association with multidrug resistance, colonization by *staphylococcus aureus* , especially involving a multi-resistant strain by hospitalized patients and health professionals, represents a severe problem for public health.[34]. In our study, the criteria for identification of MRSA were the presence of resistance to the antibiotic cefoxitin.

Annals of R.S.C.B., ISSN:1583-6258, Vol.28, Issue1, 2024 Pages: 499 - 513

Received 30 July 2024; Accepted 15 August 2024

Antibiotics sensitivity profile

Methichlin-resistant *S. aureus* causes infections with high morbidity and mortality, especially in hospitalized patients, because it carries genes that confer resistance to various antibiotics.The maximum resistance level of this study for Penicillin and Amoxicillin was (100%), Ceftriaxone and Erythromycin (75%), respectively, Vancomycin (58%), while the maximal sensitivity of the Methicillin-resistant *Staphylococcus aureus* has been to the Rifampicin (91.7%), Clindamycin (79 %), Trimethoprim (75%), Ciprofloxacin (71%) . as shown in the Figure (1).

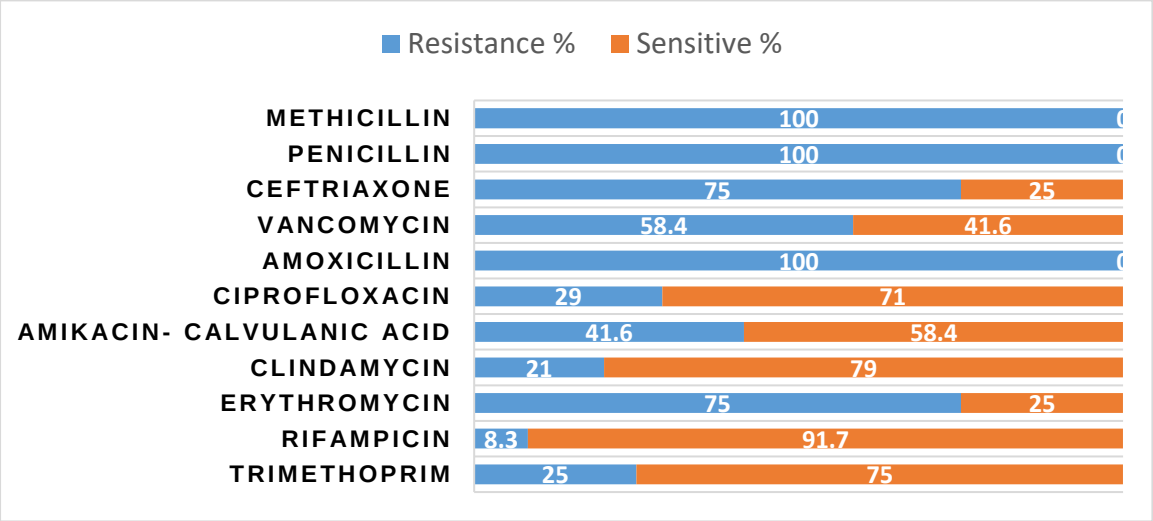

Figure (3-1): Antibiotic susceptibility of Methicillin-resistant *Staphylococcus aureus* isolates.

Multidrug resistance in MRSA typing isolates

The isolate (M201 urine sample is resistant to 10 antibiotics except vancomycin. In comparison, the isolate (M202 abscess sample) is sensitive to 7 antibiotics and resistant to 4 antibiotics (Augmentin, vancomycin, penicillin, and methicillin). The isolate (M91 abscesses sample) is sensitive to (Trimethoprim/sulfamethoxazole, Rifampicin, clindamycin, and Ciprofloxacin), and resistant to (Erythromycin, Amicacin, Augmentin, Vncomycin, Carbapenem, penicillin, and methicillin). (Table 5).

Also, the antibiotic sensitivity results show that the isolate M32 abscesses sample is resistant to three antibiotics and sensitive to eight antibiotics, while the isolating M212 urine sample is resistant to four antibiotics and sensitive to seven (Table 5).

Annals of R.S.C.B., ISSN:1583-6258, Vol.28, Issue1, 2024 Pages: 499 - 513

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Table (5): antibiotic sensitivity

Sample ID	Sample type	Trimethoprim	Rifampicin	Erythromycin	Clindamycin	Amikacin-calvulanic acid	Ciprofloxacin	Amoxicillin	Vancomycin	Ceftriaxone	Penicillin	Methicillin
M 21	urine	15	0	0	0	0	12	16	21	0	12	3
M32	abscess	23	30	0	28	17	28	0	16	18	10	15
M57	urine	25	29	29	26	20	30	0	21	17	6	0
M59	abscess	23	28	15	7	14	15	0	11	23	18	7
M63	sputum	24	30	7	25	18	25	0	16	14	6	14
M80	urine	25	28	9	25	20	29	0	19	12	0	16
M91	abscess	24	30	7	25	12	29	0	13	13	7	10
M95	abscess	29	23	25	26	20	26	0	23	19	8	0
M103	abscess	25	29	22	22	18	25	0	15	10	7	13
M127	abscess	24	32	25	24	24	29	0	16	14	8	13
M128	urine	28	33	10	24	21	30	0	18	12	7	0
M140	abscess	24	33	12	26	20	29	11	21	20	12	15
M186	sputum	10	25	7	14	18	14	11	20	20	10	4
M200	urine	0	26	0	0	12	0	15	23	13	12	7
M201	urine	0	0	0	0	0	7	0	18	0	0	3
M202	abscess	28	27	22	21	18	26	7	15	16	7	11
M203	urine	27	30	8	27	26	33	0	28	12	9	8
M211	urine	26	23	0	26	27	27	0	24	17	0	10
M212	urine	26	23	0	26	27	27	0	24	17	0	10
M213	abscess	26	22	8	20	19	30	0	17	13	0	11

Dissections:

Numerous factors have contributed to the increase in antimicrobial resistance rates, including the overuse/misuse of antibiotics by the general public and healthcare professionals [44, 45] and [46]. Insufficient systems of surveillance and independence from reliable microbiological methods result in incorrect antibiotic prescriptions [47].

The results showed that 100% of *S.aureus* isolates were resistant to penicillin; this result agreed with the results obtained in the other local study done by [48]. This also aligns with the results of [49] and [50].

Similarly, all MRSA isolates from a study in Dessie, Ethiopia, were resistant to penicillin, whereas 84.8% of all *S. aureus* isolates were resistant to penicillin [51]

Other studies conducted by [52] from Egypt did not match the present study about resistance to ciprofloxacin (60%). The study agrees with [52], which found sensitivity of clindamycin (88.5%). However, other studies conducted in Ethiopia have reported the prevalence of clindamycin-resistant MRSA ranging from 7 to 17.1%. Moreover, Iran reported a high clindamycin-resistant MRSA rate of 58.5% [53]. The high proportion of antibiotic resistance observed in our study could be due to the extensive use of antibiotics to treat infection caused by *S. aureus* without appropriate prescription. In keeping with earlier research indicating a high proportion of multidrug resistance in MRSA, the current investigation demonstrated that a significant portion of MRSA was MDR; according to [54], the observed MDR rates in hospitals show that pathogenic bacteria circulating in hospitals become increasingly resistant to all current medicines, and antibiotic resistance is rising at an alarming rate.

The absence of an antibiotic resistance surveillance and management program in Iraq may be the first factor. According to enough evidence, an antibiotic resistance surveillance and stewardship program helps to understand the pattern of resistance better and improve the use of antibiotics to avoid antibiotic resistance. The absence of a comprehensive national antibiotic policy and issues related to its execution may be the second factor. Purchasing antibiotics without a prescription from private drug dealers and pharmacies is a frequent practice in Iraq. Studies conducted in other nations have found a lower prevalence. For example, Ullah *et al*. discovered that 15.84% of people had MDR [55]. The time required to conduct molecular typing tests is a significant challenge for the establishment of a trustworthy infection control system in hospitals. Accurate and quick typing techniques are necessary to track the transmission of MRSA strains in a hospital environment.

Conclusion

This study demonstrates how common methicillin-resistant Staphylococcus aureus (MRSA) is among patients in Iraq's Wasit Province's intensive care units. The results show a concerning degree of antibiotic resistance, especially when it comes to popular medications like amoxicillin and penicillin. In healthcare settings, effective infection control strategies and antibiotic stewardship are critically needed, as 80% of S. aureus isolates have been identified as MRSA. The high resistance rates, coupled with a notable sensitivity to rifampicin and clindamycin, underscore the need for continuous monitoring and tailored treatment strategies. Effective infection management protocols are essential to mitigate the spread of MRSA and improve patient outcomes in critical care settings. Furthermore, the study emphasizes the importance of establishing comprehensive surveillance systems and antibiotic policies to combat the rising threat of antibiotic resistance. Addressing these challenges is crucial for public health, particularly in healthcare environments where vulnerable populations are at risk.

Annals of R.S.C.B., ISSN:1583-6258, Vol.28, Issue1, 2024 Pages: 499 - 513

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