Journal of Basrah Researches (Sciences) **50**(2), 9 (2024)
DOI: https://doi.org/10.56714/bjrs.50.2. 2

Detection of mecA, icaA, hlα, sea genes, and histological changes in mice for Staphylococcus aureus isolated from vaginosis in Iraqi women

Hawraa Munther Abase*, Enas Abdalhadi Hussain

Department of Biology, College of Education for pure science Ibn-Al Haitham, University of Baghdad, Baghdad, Iraq

ARTICLE INFO

Received 30 March 2024
Revised 3 July 2024
Accepted 15 July 2024
Published 31 December 2024

Keywords:

Staphylococcus Aureus, mecA ,icaA ,hlα, Sea

Citation: H. M. Abase, E. A. Hussain, J. Basrah Res. (Sci.) **50**(2), 9 (2024). DOI:https://doi.org/10.56714/bjrs.50.2.2

ABSTRACT

Staphylococcus aureus causes critical infections in humans such as urinary infections, mastitis, pneumonia, meningitis, endocarditis, and osteomyelitis. It represents the main cause of nosocomial infection in surgical wounds**.** This study aimed to investigate the prevalence of S.aureus resistance and its virulence by using genetic markers. 150 samples were collected from vagina swabs for pregnant and nonpregnant women admitted to Ibn Al-Baladi and Al-Imamain Al-Kadhimain hospitals/Iraq. The study was performed from July to October 2023.The results showed that 13 isolates of S.aureus have mecA genes at (86.7%),11 isolates have icaA gene (73.3%), and 8 isolates have the sea gene (53.3%), while hla gene was found in all 15 isolates (100%). S.aureus isolates showed histopathological changes in liver ,lung and vagina of mice .There was a prevalence of methicillin resistance S. aureus due to the presence resistance gene in most isolates. S.aureus isolates in this study showed their virulence through the occurrence of histopathological changes in liver ,lung and vagina .

1. Introduction

Staphylococcus aureus causes critical infections in humans, such as urinary infections, mastitis, pneumonia, meningitis, endocarditis, and osteomyelitis. It represents the main cause of nosocomial infection in surgical wounds [1,2,3]. Staphylococcus spp. belong to the family of Micrococcaceae. These are gram-positive, non-spore-forming, non-motile, and facultative anaerobic, or aerobic. There are more than twenty species that are known for the genus of Staphylococcus, spread in different habitats. Staphylococcus colonizes the surface of skin, dermal glands, and mucosal membranes in humans and animals [4,5]. Also, in one Iraqi study, it was isolated of Staphylococcus aureus from burn wounds with a high percentage of 25% compared with other bacteria [6]. Other Iraqi studies diagnosed Staphylococcus aureus infection in the urinary system of pregnant women [7]. A previous study detected S.aureus in the nasal cavity of workers in health care. The prevalence of MRSA was 94% among S. aureus [8]. Also, it isolated S. aureus in the nasal cavity from nurses who worked in two hospitals in Baghdad. Where the percentage of infection was 38.4% and 37.5% of S. aureus isolates [9]. The molecular diagnosis applications for pathogenic bacteria have improved the results of septic cases, particularly in synchronism with antibiotics management programs[10]. MRSA

*Corresponding author email: hawraamonther123@gmail.com

ISSN: 1817-2695 (Print); 2411-524X (Online)
Online at: https://jou.jobrs.edu.iq

MRSA (methicillin-resistant Staphylococcus aureus) contagion still to be an important reason for illness and death in the world and forms a challenge to treatment efficiency [11].

The mecA gene detection considers the key mechanism of methicillin impedance in staphylococcus species, enabling the evolution of fast molecular screening to recognize between MRSA colonies and methicillin-sensitive S. aureus (MSSA) via PCR. Whereas, MRSA detection directly in clinical samples represents a challenge, where the mecA gene may exist in the methicillin resistance strain of coagulase-negative staphylococcus, which is found in different types of clinical samples [12]. In the last decades, S. aureus has developed resistance to many drugs worldwide due to the common antibiotics used. The development of S. aureus resistance is referred to by many mechanisms, involving the generation of enzymes that suppress antimicrobial factors, the anti-microbial efflux pump activated, the reduction of permeability in the cell wall of bacteria to antibiotics, and the modulation of target position to the antibiotic [13]. The appearance of virulent and resistant drug strains of S. aureus, especially MRSA, causes a critical challenge to the therapy of staphylococcus infections. The methicillin resistance strains are more resistant to many antibiotics (beta-lactams, macrolides, aminoglycosides,) and therefore difficult to treat infection. The penicillin resistance mechanism is beta-lactamase generation to suppress penicillin via the destroy ring of beta-lactam. Another mechanism related to the existence of penicillin-binding protein 2a encoded via mecA gene, that found on SCCmec (staphylococcus cassette chromosome mec) [14]. S. aureus pathogenicity is associated with different virulence genes, such as S.aureus enterotoxins (SEs), and hemolysins (hlα and hlβ), which contribute to the adhesion, colonization, and invasion tissue , consequently inducing pathogenicity [15]. SEA (Staphylococcal enterotoxin A) is one of the most commonly involved enterotoxins in outbreaks of food poisoning [16]. The icaA (intercellular adhesion gene A) gene responsible for PIA (polysaccharide intercellular adhesin) poly-N-succinyl β-1-6 glucosamine formation has a distinct role in the synthesis of biofilm and cell adhesion. Staphylococcus aureus produces several layers of biofilm firmed within a slime or glycocalyx layer with various protein expressions [17]. One study indicated the occurrence of histological changes in the lungs of mice infected with S.aureus bacteria. The lungs showed pneumonia with pus, moderate to severe, and acute multifocal necrosis with prominent perivascular edema, multifocal hemorrhage, and accumulation of neutrophil and macrophage cells [18].

This study aimed to investigate the prevalence of virulence genes of S.aureus and the detection of histological alteration in mice .

2.Materials and Methods

2.1. Ethical consent

It was obtained oral consent from women to collect samples, and it also obtained approval from the ethics committee at Baghdad University/ College of Education for Pure Science (Ibn Al-Haitham) to conduct this study and from the ethics committee in the Ministry of Health for a sample collection from hospitals (Ref: 1256 / Date 3 March 2023). Moreover, consent was obtained from the Ministry of Health to obtain animals from the National Center for Pharmaceutical Control and Research/ Ministry of Health.

2.2. Study design and Sample collection

Total 150 samples from pregnant and nonpregnant women using vagina swabs. The study was performed from July to October 2023 at Ibn Al-Baladi and Al-Imamain Al-Kadhimain hospitals in Iraq. Inclusion criteria included the ages (15-72 years), symptoms of infection, history of contraception use, and treatment received. There were excluded nonpregnant women and women who suffered from bleeding vaginas. The swab inserted half space between the introitus and the cervix to prevent contamination by uterus mucus. After that the swab is pressed gently on the vagina walls, swirled to collect the sample, and carefully removed to avoid touching another part of the body [19].

2.3. Identification of bacteria

The swabs were cultured on a blood agar plate, and a mannitol agar plate, then incubated for 24 hours at 37^0 C to grow bacteria. The bacteria isolates were identified using the Vitek2 compact system (ID GP card:21342; bioMérieux/France) according to manufacturer instructions. These isolates were re-cultured and stored at 4° C to be used in other analyses.

2.4. Detection of genes by PCR

Genomic DNA in bacteria was extracted using ABIOpure Total DNA/USA. Quantus Fluorometer (Promega /USA) was used to detect DNA concentration. It detected the presence of genes in *S. aureus* using specific primers for these genes (Macrogen company /Korea) as in Table (1). PCR (Polymerase chain reaction) technique was applied to 15 isolates of *S. aureus*, the PCR reaction contents (20 µl) included 10µl GoTaq Green master mix PCR (2X) (Promega, USA), 1 µl for each forward and reverse primer (10 picomoles/µl) (Macrogen/ Korea), 3µl of DNA template, 5µl of free nuclease water. PCR program is shown in Table 2 for genes. Also, electrophoresis was applied using agarose gel (2%) to reveal PCR amplicon using staining with ethidium bromide stain.

Table1. Primers sequences of genes

Gene	5`-3` sequence	Annealing temp(C^0)	Product size(bp)	References
mecA-F	AAAAAA GGT GGT ATC GATTGG C	55	533	[20]
mecA-R	AGT TCT GCA GTA CCG GAT TTG C			
sea-F	TTG GAA ACG GTT AAA ACG AA	55	120	[21]
sea-R	GAA CCT TCC CAT CAA AAA CA			
icaA-F	GAT TAT GTA A TG TGC TTG GA	50	770	[21]
icaA-R	ACT ACT GCT GCG TTA ATA AT			
hla-F	CTG ATT ACT ATC CAA GAA ATT CGA TTG	58	209	[21]
hla-R	CTT TCC AGC CTA CTT TTT TAT CAG T			

Genes	Initial Denaturation	Denaturation	Annealing	Extension	Final Extension	Hold
mecA	95°C(5min) 1cycle	95°C30(sec) 30cycle	55°C(30sec) 30cycle	72°C(30sec) 30 cycle	72°C(7min) 1 cycle	10^0C(10min) 1cycle
sea	95°C(5 min) 1 cycle	95°C(30sec) 30cycle	55°C(30sec) 30cycle	72°C(30sec) 30cycle	72°C(7min) 1cycle	10^0C(10min) 1cycle
icaA	95°C(5 min) 1 cycle	95°C(30sec) 30cycle	50°C(30sec) 30cycle	72°C(30sec) 30cycle	72°C(7min) 1cycle	10^0C(10min) 1cycle
hla	94°C(5 min) 1 cycle	95°C(30sec) 30cycle	58°C(30sec) 30cycle	72°C(30sec) 30cycle	72°C(7min) 1cycle	10^0C(10min) 1cycle

Table 2. PCR programs for genes

2.5. Sequencing of genes

It was conducted using sequence PCR amplicons for studied genes of *S.aureus* isolates by Macrogen DNA sequencing company /Korea. Nucleotide sequences were aligned with global isolates by NCBI's Basic Local Alignment Search Tool Bio Edit program to identify NCBI (http://www.ncbi.nlm.nih.gov).

2.6. Evaluation of ability virulence for S.aureus in mice

It was used in Swiss albino mice Balb/c (8 weeks) with (51-55) grams. The animals were divided into 4 Groups and one control group, the first group was injected with the bacterial suspension in an intraperitoneal membrane with 0.1 ml of S.aureus (~$1x10^4$CFU cell/ml) .The second group was injected with 0.1 ml of S.aureus (~$1x10^8$CFU cell/ml). The third group was injected orally with 0.1 ml of S.aureus (~$1x10^4$CFU cell/ml). The fourth group was injected orally with 0.1 ml of S.aureus (~$1x10^8$CFU cell/ml). It monitored the mortality of mice through 48 hours and 168 hours. Mice were sacrificed and dissection to obtain liver, lung, and vagina for mice. These organs are fixed in 10% formalin and then embedded in paraffin, sectioned, and stained by haematoxylin-eosin stain for histological examination [22].

3.Results

3.1. Identification of bacteria

The results of the Vitek2 compact system showed a probability of 92-99% for *S.aureus* isolates.

3.2. Genes detection

The results showed that 13 isolates of *S.aureus* have *mecA* genes at (86.7%) ,11 isolates have icaA gene (73.3%), and 8 isolates have sea gene (53.3%),while *hla* gene is found in all 15 isolates (100%) as shown in Figures (1,2,3,4).

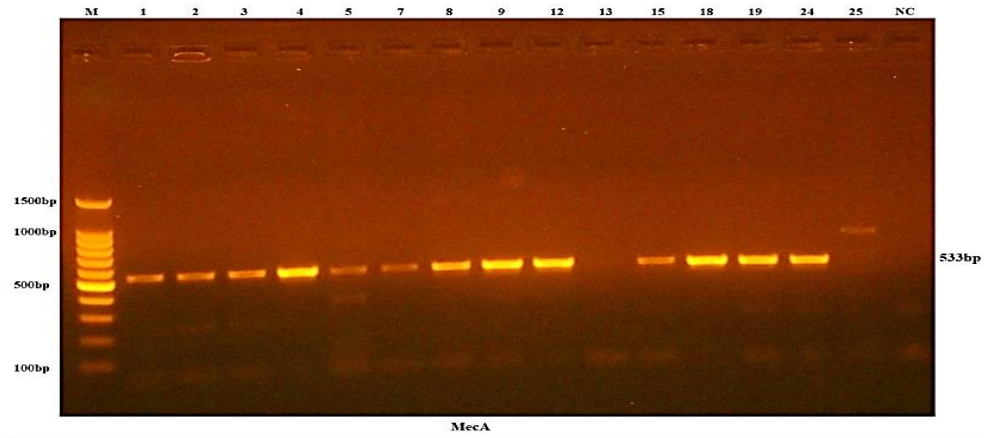

Fig.1. The amplification PCR product of *mecA* gene (533bp) for *S.aureus* isolates was electrophoresed on a 2% agarose gel. M: 100bp ladder marker.

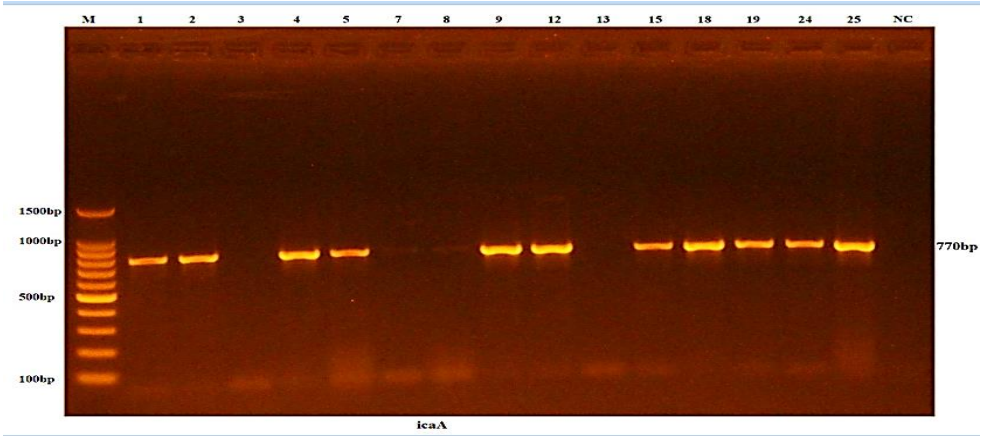

Fig.2. The amplification PCR product of *icaA* gene (770bp) for *S.aureus* isolates was electrophoresed on a 2% agarose gel. M: 100bp ladder marker

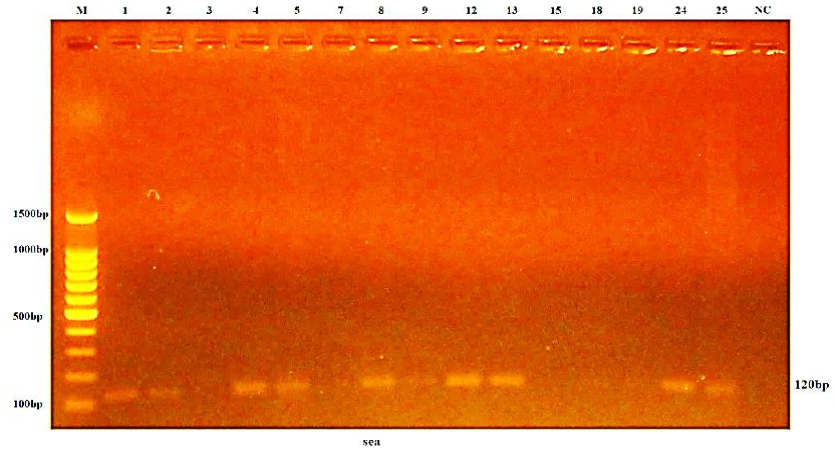

Fig.3. The amplification PCR product of *sea* gene (120bp) for *S.aureus* isolates was electrophoresed on a 2% agarose gel. M: 100bp ladder marker.

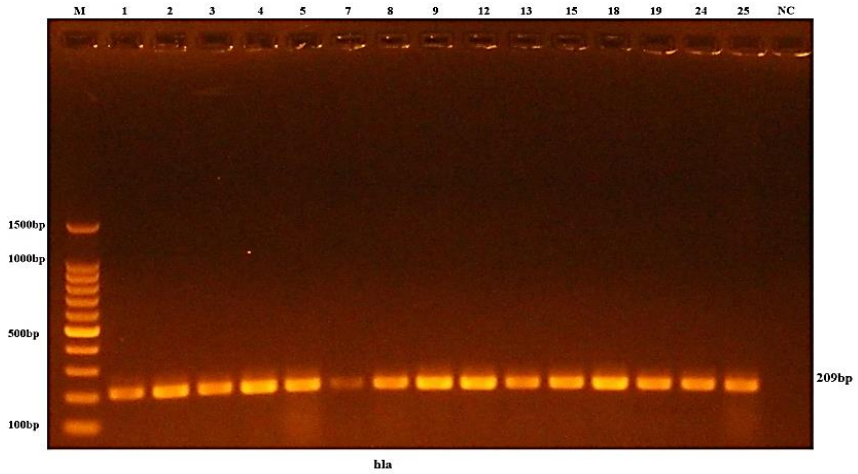

Fig.4. The amplification PCR product of *hla* gene (209bp) for *S.aureus* isolates was electrophoresed on a 2% agarose gel. M: 100bp ladder marker.

3.3. Sequencing of genes

The results of the *mecA* gene in the current study had a similarity of 99% with the reference strain in GenBank (CP133660.1).The *icaA* gene in the current study had a similarity of 99.79% with the reference strain in GenBank (AP028993.1).The *sea* gene had a similarity of 98% with the reference strain in GenBank (LC020109.1). The results sequence of *hla* gene had a similarity of 99.4% with reference stain in the gene bank (EF543163.1).

3.4. Histological examination

The results of histological tissue show the lung in control with normal bronchus, alveolar sac and pulmonary artery(Figure 5). Figure (6) shows the lung of mice infected with *S.aureus* with destructive bronchus, alveolar sac peribronchial lymphatic aggregation with pulmonary artery. Figure (7) shows the hepatic lobule (control) with a normal central vein, normal arrangement of hepatic cords and normal portal triad. Figure (8) shows the hepatic lobule (mice infected with *S.aureus*) with congestion of portal vein , disarrangement of hepatic cords , zonal cellular swelling with granular degeneration and necrosis of hepatocytes.Figure (9)shows the vagina (Control) with normal mucosal folds lined by pseudo-stratified columnar cells, normal submucosal lymphoid aggregates, and smooth muscle of tunica muscularis. Figure (10) shows the vagina (mice infected

with *S.aureus*) with mild hyperplasia (infiltration cells) of stratified epithelium with mild inflammation (vaginitis).

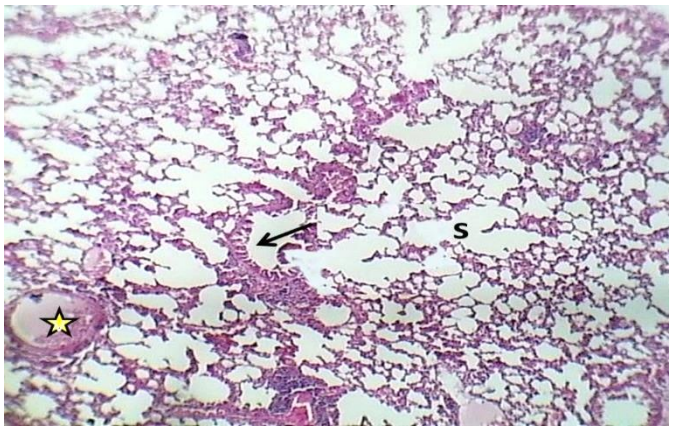

Fig.5. Section of lung (control) shows normal bronchus (Arrow), alveolar sac (S) & pulmonary artery (Asterisk). H&E stain.400x

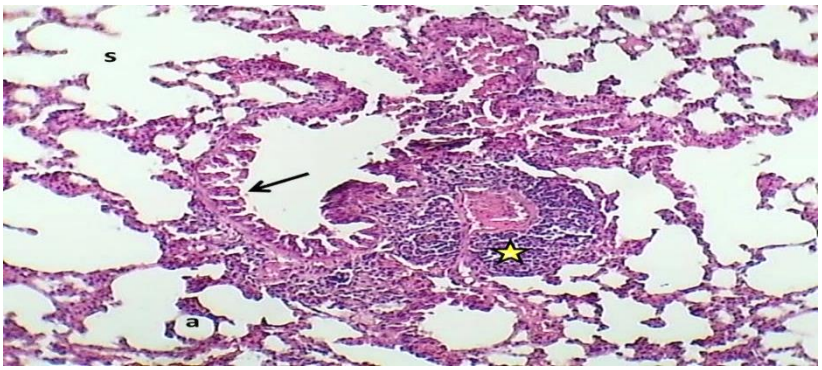

Fig.6. Section of the lung (mice infected with *S.aureus*) shows destructive bronchus (Arrow), alveolar sac (S) peribronchial lymphatic aggregation with pulmonary artery (Asterisk), alveolus (a). H&E stain.100x

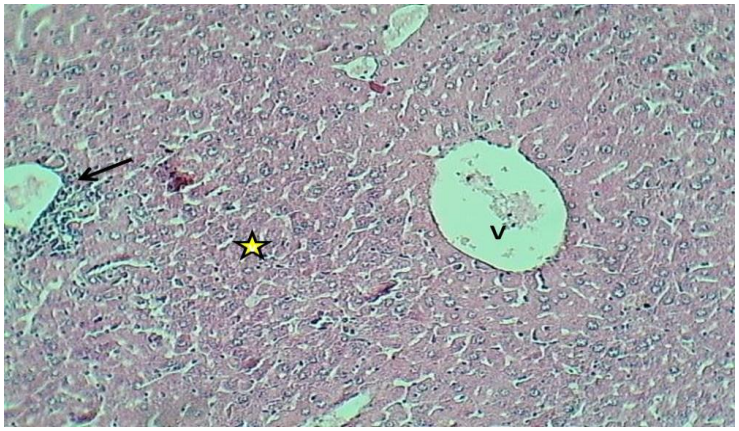

Fig.7. Section of hepatic lobule (control) shows normal central vein (V), normal arrangement of hepatic cords (Asterisk), normal portal triad (Arrow).H&E stain.100x

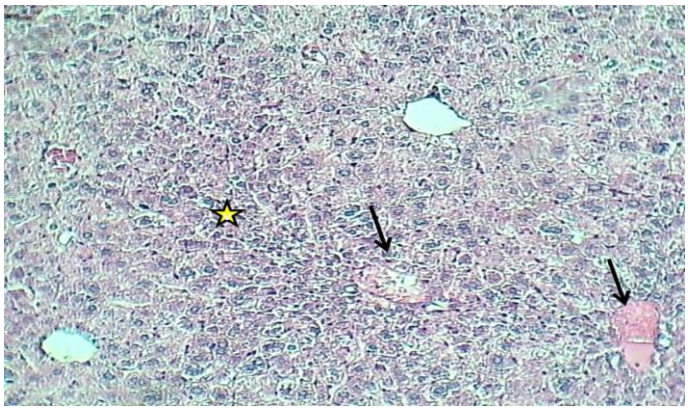

Fig.8. Section of the hepatic lobule (mice infected with *S.aureus*) shows congestion of portal vein (arrows), disarrangement of hepatic cords (Asterisk), zonal cellular swelling with granular degeneration and necrosis of hepatocytes (Asterisk).H&E stain 100x

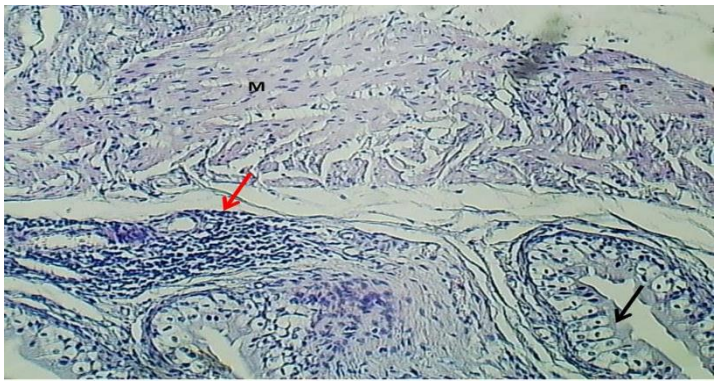

Fig.9. Section of vagina (Control) shows normal mucosal folds lined by pseudo stratified columnar cells (black arrows), normal submucosal lymphoid aggregates (red arrow) & smooth muscle of tunica muscularis (m). H&E stain.100x

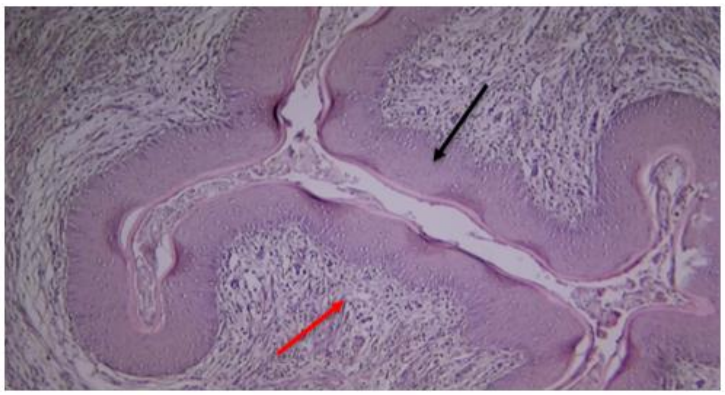

Fig.10. Section of the vagina (mice infected with *S.aureus*) shows mild hyperplasia (Black arrow) (infiltration of cells) of stratified epithelium with mild inflammation (vaginitis)(Red arrow) H & E stain 100x

4. Discussion

Virulence factors like enzymes, adhesin, toxins, and cell surface proteins that are produced by S. aureus have an important role in causing different diseases [21]. Methicillin-resistant S.aureus strains

represent a common reason for the establishment of nosocomial infection and are an important health issue. S. aureus is considered a bloodstream infection in most advanced countries [23].

The outcomes coincide with another study conducted that indicated histological alteration with S. aureus infection. Chen et al. [24] showed in their study that there were histological changes in the liver with focal necrosis of hepatic cells in mice infected with S. aureus. Another study indicated there were histological alterations in the liver with focal necrosis in hepatic cells. Moreover, there were changes in lung tissue showing thickening in the alveolar wall [25]. Also,AL-Zaidi et al.[26] indicated vaginal microbiota cause vaginosis that involves Staphylococcus spp , Enterococcus spp., Acinetobacter spp., Escherichia coli, group B Streptococcus , and Klebsiella spp.

One Iraqi study, that diagnosed Staphylococcus aureus in hospitals by PCR using 16SrRNA found that 100% were diagnosed as S. aureus [27]. Moreover, in one study, mecA gene was detected in 60% of S. aureus isolates that were isolated from Iraqi patients with furunculosis [28].

Abdulmanea et al. [14] showed in their study there is a relation between S. aureus, MRSA, and the presence of icaA, hla genes. Further, the appearance of high resistance in the isolates that carried these genes. Baz et al. [29] recorded in their study that 32.6% were positive for the sea gene in S. aureus that was resistant to ampicillin and amoxicillin.

This variation in resistance could be demonstrated due to the contact degree between the S. aureus strain and antibiotics. Many hypotheses demonstrated the increase in antibiotic impedance not just the excessive utilization of antibiotics in medicinal care but also the deficiency of organization in the marketing and use of antibiotics. This is increased due to self-therapy with high doses. The smuggled traffic of drugs is considered a factor in the appearance of resistant antibiotics [30].

6.Conclusion

The current study found that a large percentage of the isolated Staphylococcus aureus were resistant to methicillin and that these isolates showed histopathological effects on the liver, lung, and vagina of mice.

Recommendations

Study other virulence genes in vaginosis and associated with antibiotic resistance.

Acknowledgment

Thankful to all the participants and the staff of Ibn Al-Baladi and Al-Imamain Al-Kadhimain hospitals/ Iraq. We did not obtain the financial source of the study.

Novelty Statement

The current study represents the survey to monitor these virulence genes in vaginosis.

Conflict interest

The authors declare that they have no known competing financial interests .

Source support

This research received no specific grant from any funding agency in the public, commercial, or not-for-profit sectors.

Authors' contributions

Hawraa Munther Abase: Conceptualization; Data curation; Investigation;Methodology; Project administration; Resources; Software; Writing - original draft; Writing - review and editing.

Enas Abdalhadi Hussain: Supervision; Validation; Writing - review and editing.

7.References

[1] E.D. Salman , A.J.AL-Saedi, A.G.AL-Kazzaz , S.S.Yahya. The Effect of Aqueous Extract and Essential Oils of the Leaves of Eucalyptus incrassate on β-Lactam Resistant Staphylococcus aureus. Ibn al-Haitham J. Pure Appl. Sci.27(1): 76-82(2017). Available: https://jih.uobaghdad.edu.iq/index.php/j/article/view/363/299

[2] A.H. Al-Wandawy , L.A. Zwain. Ability of Staphy-lococcus spp. Isolated from Meningitis Patients to Biofilm Formation. Indian J. Forensic Med. Toxicol. 14(4) :1927-31. (2020). Doi: https://doi.org/10.22092/ ari.2022.357271.2010

[3] A.Hussain , H.Qasim Hameed, A. M. Al-Shuwaikh A, Mز Abdullah. Detection of the aadA1 and aac (3)-1V resistance genes in Acinetobacter baumannii. Arch Razi Inst. 77(3) :959-66. (2022).Doi: https://doi.org/10.22092/ ari.2022.357271.2010

[4] M.K. Abdrabaa, R Abd Aburesha. Gene Expression Evaluation of Intracellular Adhesins and Regulatory Genes among Biofilm Producing MRSA Isolates. Iraqi J Sci. 30:75-83.(2023). Doi: https://doi.org/10.24996/ijs.2023.64.1.8

[5] A.H. Al-Wandawy , L.A. Zwain. Ability of Staphylococcus spp. Isolated from Meningitis Patients to Adhesion. J. Glob. Pharma Technol. 11(7) (2019) 258-2622019.Doi: https://doi.org/10.24996/ijs.2023.64.1.8

[6] M.H.Al-Azzawi , E.J.Alkalifawi. Detection of Bacteria Causing Burn Infection Isolated from Several Hospitals in Baghdad. Ibn al-Haitham J. Pure Appl. Sci.36(3):1-8 (2023). Doi: https://doi.org/10.30526/ 36.3. 3090

[7] H.H.Kadhum, Z.H.Abood ZH. Staphylococcus aureus Incidence in Some Patients with a Topic Dermatitis in Baghdad City. Iraqi J Biotechnol. (2022);21(2):13-20

[8] A.M. Al-Dahbi, H.J.Al-Mathkhur. Distribution of methicillin-resistant Staphylococcus aureus in Iraqi patients and healthcare workers. Iraqi J. Sc. 54(2) 293-300. (2013). Available: https://www.iasj.net/iasj/article/73 640

[9] A.A.Jawad , A.A.Mohammed ,A. Al-Hashimi . Epidemiological Study on the Prevalence of Staphylococcus aureus PVL Gene Among Healthy Community in Al-Karkh and Al-Rusaffa Districts Baghdad, Iraq. Iraqi J. Sc. 441-8. (2022) Doi:https://doi.org/10.24 996/ijs.2022. 63.2.2

[10] S..Y.Tong,J.S. Davis , E.Eichenberger ,T.L. Holland , V.G.Fowler Jr . Staphylococcus aureus infections: epidemiology, pathophysiology, clinical manifestations, and management. Clin. Microbiol. Rev.28(3) :603-61.(2015). Doi:https://doi.org/ 10.1128/cmr.00134-14

[11] S.Lakhundi , K.Zhang . Methicillin-resistant Staphylococcus aureus: molecular characterization, evolution, and epidemiology. Clin. Microbiol. Rev.31(4) :10-128.(2018). Doi: http://doi:10.1128/CMR.00020-18

[12] F.C.Tenover , I.A.Tickler A. Detection of methicillin-resistant Staphylococcus aureus infections using molecular methods. Antibiotics (Basel). 11(2) (2022 (230-239. Doi: https://doi.org/10.3390/antibiotics11020239

[13] B.Mlynarczyk-Bonikowska , C.Kowalewski , A. Krolak-Ulinska ,W. Marusza . Molecular mechanisms of drug resistance in Staphylococcus aureus. Int. J. Mol. Sci.. 23(15)(2022) 8088. Doi: https://doi.org /10.3390/ijms23158088

[14] A.A.Abdulmanea , N.S.Alharbi , A.M.Somily , J.M.Khaled, F.H.Algahtani . The Prevalence of the Virulence Genes of Staphylococcus aureus in Sickle Cell Disease Patients at KSUMC, Riyadh, Saudi Arabia. Antibiotics (Basel).12(7) (2023)117-1221. Doi:https://doi.org/10.3390/antibiotics12071221

[15] S.M.Puah, K.H.Chua, J.A.Tan. Virulence factors and antibiotic susceptibility of Staphylococcus aureus isolates in ready-to-eat foods: detection of S. aureus

contamination and a high prevalence of virulence genes. Int. J. Environ. Res. Public Health 13(2)(2016)190-199. Doi:https://doi.org/10.3390/ije rph13020199

[16] E.L.Fisher , M.Otto, G.Y.Cheung. Basis of virulence in enterotoxin-mediated staphylococcal food poisoning. Front. Microbiol. 9 (2018)430- 436. Doi:https://doi.org/10.3389/fmicb.2018.00436

[17] T.H.Elkhashab ,L.A. Adel , M.S.Nour,M. Mahran, M.Elkaffas. Association of intercellular adhesion gene A with biofilm formation in staphylococci isolates from patients with conjunctivitis. J. Lab. Physicians.10(3) (2018):309-315. Doi:https://doi.org/ 10.4103/ JLP.JLP_122_17

[18] K.Dietert, K. Reppe,L. Mundhenk,M. Witzenrath, &A.D. Gruber. mCLCA3 modulates IL-17 and CXCL-1 induction and leukocyte recruitment in murine Staphylococcus aureus pneumonia. PloS one, 9(7)(2014). Doi:https://doi.org/10.1371/journal.pone.0102606

[19] J.Tumuhamye, H.Steinsland, F.Bwanga, J.K. Tumwine , G.Ndeezi, D.Mukunya , O.Namugga, , A. Kasede,,H. Sommerfelt,and V.Nankabirwa, ,Vaginal colonization with antimicrobial-resistant bacteria among women in labor in central Uganda: prevalence and associated factors, Antimicrob Resist Infect Control. 10(2021):1-11. Doi: https://doi.org/10.1186 /s13756-021-00897-9

[20] J.Wei , K.Ma ,Y. Zhang ,X. Yang ,Q. Tang , Z.Nie . ,Correlation Analysis of Staphylococcus aureus Drug Resistance and Virulence Factors with Blood Cell Counts and Coagulation Indexes, Int. J. Clin. Pract.(2023). Doi:https://doi.org/10.1155/ 2023/ 8768152

[21] A.H.Rasmi, E.F.Ahmed, A.M.Darwish, G.F. Gad , Virulence genes distributed among Staphylococcus aureus causing wound infections and their correlation to antibiotic resistance, BMC Infect. Dis. 22(1) (2022):648-652, Doi:https://doi.org/10. 1186/s12879-022 -07624-8

[22] J.D., Bancroft and C.Layton, C.The Hematoxylin and Eosin. In: S.K.Suvarna, C.Layton, and J.D.Bancroft, Eds., Theory & Practice of Histological Techniques, 7th Edition, Churchill Livingstone of El Sevier, Philadelphia, (Ch. 10 and 11): 172-214.(2013).

[23] F.Yu ,T. Li ,X. Huang ,J. Xie , Y.Xu , J.Tu ,Z. Qin , C.Parsons ,J. Wang , L.HuL, L.Wang , Virulence gene profiling and molecular characterization of hospital-acquired Staphylococcus aureus isolates associated with bloodstream infection. Diagn Microbiol Infect Dis. 74(4))2012) 363-8, Doi:https://doi .org/10.1016/j.diagmicrobio.2012.08.015

[24] H.Chen,J. Zhang, Y.He, Z.Lv, Z.Liang, J.Chen, P.Li, J.Liu, H.Yang, A.Tao, and X. Liu, X ,Exploring the Role of Staphylococcus aureus in Inflammatory, Diseases. Toxins. 14(7) (2022) 440-464,
Doi: https://doi.org/10.3390/toxins14070464

[25] D.A.Hamza , R.M.Abd-Elsalam , S.M.Nader, M.Elhariri, R.Elhelw , H.S.El-Mahallawy. Pathways of methicillin-resistant Staphylococcus aureus in animal model: new insights regarding public health. Infection and Drug Resistance. 4:1593-600.(2020).

[26] M.H AL-Zaidi, W.H.AL-Tamimi , A.A.Salih. Molecular determination of the microbial diversity associated with vaginitis and testing their sensitivity to selected antimicrobials. Biodiversitas Journal of Biological Diversity. 26;24(8).(2023).

[27] A.B. AbdulRazzaq, A.M, Shami, &K.K. Ghaima, Detection of vanA and vanB genes Among Vancomycin Resistant Staphylococcus aureus Isolated from Clinical Samples in Baghdad Hospitals. Iraqi journal of biotechnology, 21(1). (2022).

[28] A.A.Al-Halaq , N.M.Utba. Prevalence of Methicillin-resistant Staphylococcus aureus Carrying lukS-lukF Gene in Iraqi Patients with Furunculosis. Iraqi J.Sc. 3323-3329.(2023). Doi: https://doi.org/10.24996/ijs.2023.64.7.13

[29] A.A.Baz,E.K. Bakhiet ,U. Abdul-Raouf ,A. Abdelkhalek. Prevalence of enterotoxin genes (SEA to SEE) and antibacterial resistant pattern of Staphylococcus aureus isolated from clinical specimens in Assiut city of Egypt. Egypt. J. Med. Hum. Genet.22(1) :1-2.(2021). Doi: https://doi.org/10. 1186/s43042-021-00199-0

[30] H.Chen ,J. Zhang ,Y. He ,Z. Lv ,Z. Liang , J. Chen J, et al. Exploring the Role of Staphylococcus aureus in Inflammatory Diseases. Toxins. ;14(7):464.(2020).

Journal of Basrah Researches (Sciences) **50**(2), 9 (2024)
DOI: https://doi.org/10.56714/bjrs.50.2. 2

كشف عن جينات mecA وicaA وhlα وsea والتغيرات النسجية لبكتيريا Staphylococcus aureus المعزولة من التهاب المهبل لدى النساء العراقيات

حوراء منذر عباس*، إيناس عبد الهادي حسين

قسم علوم الحياة، كلية التربية للعلوم الصرفة ابن الهيثم، جامعة بغداد، بغداد، العراق

معلومات البحث

الاستلام 30 أذار 2024
المراجعة 3 تموز 2024
القبول 15 تموز 2024
النشر 31 كانون الاول 2024

الكلمات المفتاحية

المكورات العنقودية الذهبية، mecA، hlα ،icaA

الملخص

تسبب المكورات العنقودية الذهبية*S.aureus* حالات عدوى خطيرة لدى البشر مثل التهابات المسالك البولية، والتهاب الضرع، والالتهاب الرئوي، والتهاب السحايا، والتهاب الشغاف، والتهاب العظم والنقي. وهو يمثل السبب الرئيسي لعدوى المستشفيات في جروح العمليات الجراحية.هدفت هذه الدراسة إلى معرفة مدى انتشار مقاومة بكتريا المكورة العنقودية الذهبية وضراوتها باستخدام الجينات المسؤولة عن الضراوة . تم جمع 150 عينة من المسحات المهبلية من نساء حوامل وغير حوامل في مستشفى ابن البلدي والإمام الكاظم/العراق. أجريت الدراسة في الفترة من تموز إلى تشرين الاول 2023. أظهرت النتائج أن 13 عزلة من بكتريا *S.aureus* تمتلك جين mecA بنسبة (86.7%)، و 11 عزلة تمتلك جين icaA (73.3%)، و 8 عزلات تمتلك جين sea (53.3%). بينما وجد جين hla في جميع العزلات الـ 15 بنسبة (100%). أظهرت عزلات بكتريا المكورة العنقودية الذهبية تغيرات نسجية مرضية في الكبد والرئة والمهبل في الفئران. وكانت هناك انتشار للمكورات العنقودية الذهبية المقاومة للميثيسيلين بسبب وجود جين المقاومة في معظم العزلات. أظهرت عزلات بكتريا المكورة العنقودية الذهبية في هذه الدراسة ضراوتها من خلال حدوث تغيرات نسجية مرضية في الكبد والرئة والمهبل.

Citation: H. M. Abase, E. A. Hussain, J. Basrah Res. (Sci.) **50**(2), 9 (2024). DOI:https://doi.org/10.56714/bjrs.50.2.2

***Corresponding author email:** hawraamonther123@gmail.com

ISSN: 1817-2695 (Print); 2411-524X (Online)
Online at: https://jou.jobrs.edu.iq