The study was aimed to determine and characterize the nasal carriage rate of S. aureus among apparently healthy farm animals including cattle, sheep, and goats using traditional and molecular characterization. The study was conducted in Duhok province during the period from November 2021 to March 2022. Furthermore, the isolates were screened for the presence of MRSA using the standard Kirby-Bauer disk diffusion method (oxacillin discs) and genotypically by PCR targeting the mecA gene. Among the 300 tested nasal swabs, 209 (69.7%) samples were positive for S. aureus isolation using traditional methods. The isolation rate was 62.7% (47/75), 66.7% (100/150), and 82.7% (62/75) in cattle, sheep, and goats, respectively. Amplification of species-specific nuc gene confirmed that 119 of 209 (56.9%) animals carried S. aureus in their nasal cavity. The isolates showed variation toward different antibiotics used in this study and the highest resistance rate was recorded toward penicillin at a ratio of 72.3% (86/119). This study confirms the occurrence of MRSA for the first time in nasal swabs from a healthy animal in Duhok Province. The MRSA isolates were found only in cattle (7/119) and none of the nasal carriages isolates from sheep and goats were carried MRSA isolates. The presence of MRSA and multidrug-resistant MRSA among healthy cattle could be considered as a potential reservoir for transmission of multidrug-resistant MRSA to humans especially farm workers and they could act as a reservoir to spread MRSA in livestock. Further studies are required for a better understanding of pathogenic transmission and for confirming the origin of the strains, whether are of human origin or vice versa.

Keywords: MRSA, Nasal carriage, Healthy animals, Multidrug-resistant MRSA, Duhok

Introduction

Staphylococcus aureus is a commensal and a major opportunistic pathogen causing a wide range of diseases in both humans and animals. It causes a high impact on public health and the livestock industry [1]causing a wide range of infections in various hosts. Objectives: We intended to determine the prevalence of S. aureus in the nasal cavity of healthy ruminants and also to investigate the presence of antibiotic resistance genes. Materials and Methods: In the present study, healthy cattle \( (n = 79) \). S. aureus is a Gram-positive, non-motile, non-spore-forming, facultative anaerobic cocci commensal pathogen that colonizes different parts of the body, including the skin, nares, and mucosal surfaces of humans and animals [2]but pork and beef typically are not. Thus, the risk of methicillin-resistant S. aureus human infection from whole raw poultry carcasses may be greater than that of exposure from pork or beef. The objective of this
study was to isolate and characterize S. aureus from whole retail poultry carcasses and compare the isolates to S. aureus isolates from humans. A total of 25 S. aureus isolates were collected from 222 whole poultry carcasses. The isolates were characterized phenotypically with antibiotic resistance disc diffusion assays and genotypically using multilocus sequence typing. A total of 17 S. aureus isolates obtained from healthy humans were included and characterized in the same way as the poultry isolates. Staphylococcus spp. were recovered from all poultry carcasses. Only 25 poultry carcasses (11.2%). Worldwide, S. aureus is considered a major pathogen causing clinical or subclinical mastitis in lactating sheep, goats, and cows [3]. It has also been suggested that nasal carriage may represent a major reservoir for S. aureus to contaminate the udder and milk in dairy farms [4]. This pathogen has been frequently reported from the nares of farm animals including cattle, sheep, and goats [5-8]. The major concern about S. aureus is the adaptation to the diverse environment and the development of antimicrobial resistance toward multiple antibiotics. The level of resistance is growing very quickly, especially to commonly used antibiotics against staphylococcal infections such as β-lactams, macrolides, and tetracyclines [9]195 nasal swabs from apparently healthy farm animals (52 sheep, 51 goats, 47 cattle and 45 buffalo. Methicillin-resistant S. aureus (MRSA) strains are resistant to all β-lactam antibiotics and the resistance is mediated by the acquisition of mecA, which encodes a penicillin-binding protein (PBP) [10]. mecA is localized within the mobile genetic element known as the staphylococcal cassette chromosome (SCCmec) [10] we identified two novel genes (designated cassette chromosome recombinase genes [crrA and crrB]. One of the public health concerns is MRSA in animals and food and there could be a subsequent transmission of MRSA to humans from animals because they could act as reservoirs of MRSA. Colonization of people in contact with infected or colonized animals has been widely reported for small animals [11]. It has also been shown that MRSA especially multidrug-resistant was distributed among the examined healthy farm animals and could represent a potential reservoir for multidrug-resistant MRSA with public health implications [9]195 nasal swabs from apparently healthy farm animals (52 sheep, 51 goats, 47 cattle and 45 buffalo. Yet, to our knowledge, no studies have been conducted in Duhok Province to investigate the prevalence rate and characterization of S. aureus from the nasal cavity of healthy ruminates. Therefore, this study aimed to determine the prevalence and nasal carriage rate of S. aureus among apparently healthy farms animals; to determine the susceptibility profile to different antibiotics; to detect the occurrence rate of multidrug-resistant S. aureus among the isolates, and investigate the presence of methicillin-resistant Staphylococcus aureus (MRSA) among the healthy animals.

Material and Methods

Sample collection

Three hundred (300) samples of nasal swabs were collected randomly from apparently healthy animals from different areas of Dohuk governorate for the period from November 2021 to March 2022. The sample were distributed as follow: cattle (75), sheep (150), and goats (75). The samples were collected from the nostrils of healthy animals by using sterile cotton swabs. The swab was first moistened with normal saline and inserted into nares and then rotated gently so it can make contact with the nasal septum as mentioned by Hakim et al.[12]. The swabs were directly streaked on mannitol salt agar and then the plates were incubated for 24 h at 37°C.

Phenotypic characterization of S. aureus using standard conventional methods

Isolation and identification of S. aureus were performed using traditional methods. The suspected colonies (mannitol fermenter) were subcultured on MSA to obtain pure culture and incubated for 24 h at 37°C. Colonies with typical morphology including mannitol fermenter colonies were selected and subjected to Gram-staining, catalase, and coagulate test [13]. Phenotypically suspected S. aureus isolates including Gram-positive grape-like cocci, catalase, and coagulate-positive colonies were maintained and stored in 50% glycerol and brain heart infusion broth (BHIB) stocks at -20°C for further processing including molecular characterization and antibiotic susceptibility test.

Molecular detection of S. aureus DNA extraction

Suspected colonies of S. aureus by traditional methods were further confirmed by the detection of the S. aureus-specific thermostable nuclease gene (nuc) by using PCR [14]. DNA was extracted according to the literature [15] we investigated the

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Molecular detection and confirmation of Methicillin-resistant S. aureus (MRSA) isolates among healthy animals

The molecular confirmation of MRSA was carried out through the amplification of a 533-bp mecA gene according to Murakami et al. [18]. The PCR reaction was carried out using mecA1 (AAAATCGATGGTAAAGGTTGGC) and mecA2 (AGTTCTGACATACGGGATTTG) primers. Amplification was performed in a total reaction of 25 µl including 12.5 µl of Add Taq Master (ADDBIO Inc, Korea), 2 µl of each primer, 3 µl of DNA, and 5.5 µl of deionized sterile dH₂O. The following PCR parameters: initial denaturation at 94 °C for 3 min, followed by 40 cycles of denaturation at 94 °C for 30 s, annealing at 55 °C for 30 s, extension at 72 °C for 1 min, and a final extension at 72 °C for 5 min [18]. The PCR reactions were carried out using the standard Kirby-Bauer disk diffusion method according to Clinical and Laboratory Standards Institute (CLSI) [17]. Detection of multidrug-resistant S. aureus strains was confirmed by resistance to three or more three antibiotics. The confirmation was done phenotypically by Kirby-Bauer disk diffusion results based on the size of the inhibition zone according to the guidelines provided by CLSI [17].

Results

Nasal carriage of S. aureus among healthy animals

The results showed that out of the 300 samples of nasal swabs, 209 at the rate of 69.7% were positive for S. aureus by using phenotypic characterization. The recovery rate was different; S. aureus was isolated from 47 of 75 cattle, 100 of 150 sheep, and 62 of 75 goats at the rate of 62.7%, 66.7%, and 82.7%, respectively (Table 1). Based on phenotypic characteristics all the suspected 209 isolates provided typical characteristics of S. aureus where the colonies appeared yellow with yellow background on MSA as a result of mannitol fermentation. Mannitol fermenter isolates were further confirmed by Gram staining and they appeared Gram-positive grape-like cocci. The 209 isolates were catalase positive and finally the results showed that 209 were found to be coagulase positive using slide coagulase test as shown in Table 1
Molecular characterization of S. aureus isolates

Amplification of the nuc gene (226 bp) showed that among 209 suspected isolates, 119 isolates were confirmed as S. aureus (Table 1). The PCR results confirmed that the prevalence of S. aureus was 28/47 (59.6%) in cattle, 50/100 (50%) in sheep, and 41/62 (66.1%) in goats. Therefore, 56.9% (119/209) of the total animals carried S. aureus in their nasal cavity (Table 1).

Antibiotic sensitivity test of S. aureus isolates

Antibiotic susceptibility profiles of the 119 S. aureus isolates from healthy cattle, sheep, and goats were determined against 11 antibiotics, including beta-lactams and non-beta lactams antibiotics. The sensitivity test revealed that none of the isolates were resistant toward rifampin, trimethoprim/sulphamethoxazole, and gentamicin as shown in Figure 1. Furthermore, higher resistance ratios can be seen toward ciprofloxacin 2.5% (3/119), chloramphenicol 4.20% (5/119), clindamycin 5.1% (6/119), oxacillin 5.9% (7/119), vancomycin 6.7% (8/119), erythromycin 22.68% (27/119) and tetracycline 45.37% (54/119). The highest resistance rate was recorded toward penicillin with a ratio of 72.3% (86/119).

The overall susceptibility ratio was the highest for gentamicin (100%), followed by trimethoprim/sulphamethoxazole (99.15%), then two antibiotics that had equal ratios, rifampin, and oxacillin (94.1%). Other isolates showed sensitivity to other antibiotics including ciprofloxacin, chloramphenicol, clindamycin, vancomycin, erythromycin, and tetracycline. However, the sensitivity was with lower ratios as follows ciprofloxacin (88.23%), chloramphenicol (87.39%), clindamycin (78.99%), vancomycin (72.6%), erythromycin (52.1%) and tetracycline (34.45%). Penicillin showed the lowest susceptibility ratio (27.73%) (Figure 1 & Table 2)

Occurrence of multidrug-resistance S. aureus among healthy animals

According to the antibiotic susceptibility test, among 119 isolates, 22 (18.48%) isolates were classified as multidrug-resistant S. aureus (MDR-SA) strains because they were found resistant to at least three or more antibiotics used in this study. The resistant profiles were different among the isolates. Among 22 MDR-SA, 16 isolates were resistant to 3 antibiotics, while 5 isolates were resistant to 4 antibiotics. Only one isolate from sheep was found to be resistant to 5 antibiotics. The results identified 12 different resistant patterns as shown in Table 3.

Screening for methicillin (Oxacillin) resistance S. aureus among healthy animals:

The results showed that among the 119 isolates only 7 isolates from cattle were positive and classified as MRSA isolates as they were positive for the mecA gene. However, none of the isolates from sheep and goats were found to be mecA gene positive and they were classified as MSSA (Table 4). These isolates (7 isolates) from cattle were also found to be resistant to oxacillin phenotypically by antibiotic susceptibility test. Furthermore, the 7 isolates exhibited resistance not only to oxacillin, but they were resistant to several antibiotics, four of the MRSA isolates were resistant to oxacillin, erythromycin, and penicillin, and one of them was resistant to oxacillin, penicillin, and tetracycline. Only one MRSA isolate was resistant to four antibiotics including oxacillin, erythromycin, penicillin, and tetracycline. Therefore, these isolates were

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**TABLE 1. Phenotypic and molecular characterization of S. aureus nasal carriage isolates from healthy cattle, sheep, and goats.**

<table>
<thead>
<tr>
<th>Animals</th>
<th>Species</th>
<th>No. of Samples</th>
<th>Phenotypic characterization</th>
<th>Molecular characterization (PCR)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>Growth on MSA</td>
<td>Gram staining</td>
</tr>
<tr>
<td>Cattle</td>
<td>75</td>
<td>47</td>
<td>47</td>
<td>47</td>
</tr>
<tr>
<td>Sheep</td>
<td>150</td>
<td>100</td>
<td>100</td>
<td>100</td>
</tr>
<tr>
<td>Goat</td>
<td>75</td>
<td>62</td>
<td>62</td>
<td>62</td>
</tr>
<tr>
<td>Total</td>
<td>300</td>
<td>209</td>
<td>209</td>
<td>209</td>
</tr>
</tbody>
</table>

DETECTION AND MOLECULAR CHARACTERIZATION OF *Staphylococcus aureus* AND …

![Antimicrobial sensitivity profile for *S. aureus* nasal carriage isolates](image)

**Fig. 1. Antimicrobial sensitivity profile for *S. aureus* nasal carriage isolates**

**TABLE 2. Antimicrobial sensitivity profile for *aureus* nasal carriage isolates (no: 119)**

<table>
<thead>
<tr>
<th>Antibiotics</th>
<th>Concentrations (µg/disc)</th>
<th>Antimicrobial susceptibility profile</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Sensitive</td>
</tr>
<tr>
<td></td>
<td></td>
<td>No. of isolates</td>
</tr>
<tr>
<td>Vancomycin (VA)</td>
<td>30</td>
<td>86</td>
</tr>
<tr>
<td>Rifampin (RA)</td>
<td>5</td>
<td>113</td>
</tr>
<tr>
<td>Oxacillin (OX)</td>
<td>1</td>
<td>112</td>
</tr>
<tr>
<td>Erythromycin (E)</td>
<td>15</td>
<td>61</td>
</tr>
<tr>
<td>Penicillin (P)</td>
<td>10</td>
<td>33</td>
</tr>
<tr>
<td>Trimethoprim/</td>
<td>25</td>
<td>118</td>
</tr>
<tr>
<td>sulphanethoxazole (SXT)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ciproflaxacin (CIP)</td>
<td>5</td>
<td>105</td>
</tr>
<tr>
<td>Tetracycline (TE)</td>
<td>30</td>
<td>41</td>
</tr>
<tr>
<td>Clindamycin (DA)</td>
<td>2</td>
<td>94</td>
</tr>
<tr>
<td>Gentamicin (CN)</td>
<td>10</td>
<td>119</td>
</tr>
<tr>
<td>Chloramphenicol (C)</td>
<td>30</td>
<td>104</td>
</tr>
</tbody>
</table>

classified as multidrug- resistant MRSA isolates.

**Discussion**

*S. aureus* has been recognized as a major pathogen affecting humans and animals. The prevalence and manifestation rate of this pathogen is increasing worldwide [19, 20]. However, there are significant differences between the rate of *S. aureus* appearance and the rate of MRSA. Moreover, the susceptibility to antibiotics has different outcomes and ratios, and this can be noticed from the difference between the regions utilizing large quantities of antibiotics and regions with lower antibiotic usage [21].

This study is conducted to determine the prevalence of nasal carriage rate of *S. aureus* in healthy farm animals, to investigate the sensitivity profile of *S. aureus* and the occurrence...
TABLE 3. Multidrug-resistance patterns among 22 S. aureus nasal carriage isolates from healthy animals

<table>
<thead>
<tr>
<th>Multidrug-resistance profiles</th>
<th>Pattern</th>
<th>Number of isolates (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>OX, E, P</td>
<td>1</td>
<td>4 (18.2)</td>
</tr>
<tr>
<td>E, P, TE</td>
<td>2</td>
<td>6 (27.3)</td>
</tr>
<tr>
<td>P, TE, DA</td>
<td>3</td>
<td>3 (13.6)</td>
</tr>
<tr>
<td>OX, P, TE</td>
<td>4</td>
<td>1 (4.5)</td>
</tr>
<tr>
<td>P, TE, C</td>
<td>5</td>
<td>1 (4.5)</td>
</tr>
<tr>
<td>VA, P, TE</td>
<td>6</td>
<td>1 (4.5)</td>
</tr>
<tr>
<td>OX, E, P, TE</td>
<td>7</td>
<td>1 (4.5)</td>
</tr>
<tr>
<td>E, P, TE, DA</td>
<td>8</td>
<td>1 (4.5)</td>
</tr>
<tr>
<td>E, P, TE, C</td>
<td>9</td>
<td>1 (4.5)</td>
</tr>
<tr>
<td>P, TE, DA, C</td>
<td>10</td>
<td>1 (4.5)</td>
</tr>
<tr>
<td>VA, P, TE, C</td>
<td>11</td>
<td>1 (4.5)</td>
</tr>
<tr>
<td>VA, E, P, TE, C</td>
<td>12</td>
<td>1 (4.5)</td>
</tr>
<tr>
<td>Total</td>
<td></td>
<td>22</td>
</tr>
</tbody>
</table>

TABLE 4. MRSA and MSSA nasal carriage rate among healthy cattle, sheep, and goats

<table>
<thead>
<tr>
<th>Animal species</th>
<th>No. of nasal swabs</th>
<th>No. of confirmed S. aureus isolates</th>
<th>No. of MRSA isolates (rate %)</th>
<th>No. of MSSA isolates (rate %)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cattle</td>
<td>75</td>
<td>28</td>
<td>7 (25%)</td>
<td>21 (75%)</td>
</tr>
<tr>
<td>Sheep</td>
<td>150</td>
<td>50</td>
<td>0 (0%)</td>
<td>50 (100%)</td>
</tr>
<tr>
<td>Goats</td>
<td>75</td>
<td>41</td>
<td>0 (0%)</td>
<td>41 (100%)</td>
</tr>
<tr>
<td>Total</td>
<td>300</td>
<td>119</td>
<td>7 (5.9%)</td>
<td>112 (94.1%)</td>
</tr>
</tbody>
</table>

MRSA: methicillin resistance S. aureus; MSSA: methicillin-sensitive S. aureus

of (MDR-SA) and to detect the occurrence of MRSA among S. aureus nasal carriage isolates from cattle, sheep, and goats. Both conventional and molecular methods are important for identifying and diagnosing bacteria. Molecular characterization has the advantage of being a more reliable and sensitive methods for diagnosis [22]. In the present study, all the animals were healthy and show no sign of infection. However, they were carriers of S. aureus as it was detected in their nasal cavity. Among 300 nasal swabs using phenotypic characterization, 69.6% (209/300) of the samples tested positive. However, utilizing PCR showed that among 209 isolates, 119 isolates were confirmed as S. aureus.

In the current study, S. aureus isolates were found in 59.6% of cattle, 50% of sheep, and 66.1% of goats. Therefore, 56.9% (119/209) of the total animals carry S. aureus in their nasal cavity. Comparing the results to other studies conducted in Iraq and other countries, it can be noticed that rates of S. aureus prevalence have various rates. For instance, a study conducted in Basra, Iraq by Khudaier et al. [23] showed that the prevalence of S. aureus was lower and the rate was 4%, 12.5%, and 5% in cattle, sheep, and goats, respectively. Furthermore, a previous study conducted in Iran showed lower ratios because the study reported that the ratio of S. aureus in nasal swabs taken from cattle, sheep, and goats 5.06%, 14.1%, and 25%, respectively (1). A study in Pakistan by Anueyiagu et al. [24] included similar farm animals and the results were based on a nasal carriage, revealing that the prevalence rates were 40%, 80%, and 50% in cows, sheep, and goats, respectively. The reason behind the variation in the occurrence of S. aureus in different hosts, might due to various virulence factors that aid
the pathogen in invading and colonizing different hosts [25].

The 119 *S. aureus* isolates were tested against several antibiotics. The antibiotics included were from the beta-lactam group and the non-beta-lactam group. The resistance rate toward the well-known beta-lactam antibiotic, Penicillin, was the highest among all the animals. In the present study, *S. aureus* from cattle resistance rate was 64.28%. The rate from different regions varies. However, penicillin resistance was the highest among all the antimicrobial drugs. A study from Northern Ethiopia by Kalayu et al. [26] including dairy cows. It is the most common cause of intramammary infections in dairy cows. Its public health importance increases inline to the continuous emergence of drug-resistant strains; such as Methicillin-resistant *S. aureus* (MRSA noticed that penicillin showed the highest resistance rate, which was 91.7%. Moreover, another study of cattle isolates in Northern Greece by Kotzamanidis et al. [27] revealed that the resistance toward penicillin was the highest (25%). The resistance toward other drugs in *S. aureus* isolates from cattle was also recorded. The penicillin was followed by erythromycin (42.85%) then tetracycline (17.85%). On the other hand, it has been shown that penicillin was followed by tetracycline (35.4%) and then erythromycin (2.1%) [26] including dairy cows. It is the most common cause of intramammary infections in dairy cows. Its public health importance increases inline to the continuous emergence of drug-resistant strains; such as Methicillin-resistant *S. aureus* (MRSA. However, Kotzamanidis et al. [27], recorded that tetracycline showed a similar rate as penicillin at a rate of 25%. Another study by Kashoma et al. [28] reported higher resistance toward tetracycline (73%) than erythromycin (16.2%).

The nasal carriage *S. aureus* isolates from sheep and goats showed the highest resistance toward penicillin, being 82% for sheep and 65.85% for goats, followed by tetracycline (74% for sheep, 29.6% for goats) then erythromycin (14% for sheep and 19.51% for goats). These results were in agreement with Ünal et al. [29], where the resistance in sheep and goats isolates showed the same descending resistance pattern: the highest for penicillin (19%) followed by tetracycline (4.8%) and erythromycin (4%).

All the isolates from cattle, sheep, and goats were 100% susceptible to gentamicin. These results were in line with Kashoma et al. [28] and *S. aureus* isolates from cattle showed no resistance toward gentamycin. 100% sensitivity to gentamicin was also recorded by Bendahou et al. [30]. A low rate of resistance to gentamycin was recorded and it was only 4.8% (in sheep and goats) [29]. Moreover, all the isolates were not resistant to rifampin and the same results were recorded by Anueyiagu et al. [24] and the total resistance rate to rifampin was 0%. Furthermore, 100% susceptibility to SXT was found in this study, similar results were presented by Abdel-Moein & Zaher [9] 195 nasal swabs from apparently healthy farm animals (52 sheep, 51 goats, 47 cattle and 45 buffalo and they reported that isolates from cattle, sheep, and goats were susceptible to SXT.

Generally, *S. aureus* is susceptible to ciprofloxacin and chloramphenicol. In this study, the resistance rate to ciprofloxacin and chloramphenicol was 2.52% and 4.2%, respectively. Almost similar results were reported by Anueyiagu et al. [24], as being 0% susceptibility in three species) for both antibiotics. Similar results were reported in three species for these both antibiotics and they were found to be 4% resistance to ciprofloxacin and 100% susceptibility to chloramphenicol [23].

Total resistance to clindamycin was also low, as it was 5.04%. Khudaier et al. [23] reported that the total resistance was 8.33%, and Abdel-Moein & Zaher [9] 195 nasal swabs from apparently healthy farm animals (52 sheep, 51 goats, 47 cattle and 45 buffalo showed that all the isolates from cattle, sheep, and goats were highly susceptible to clindamycin. Moreover, it has been reported that *S. aureus* from cattle has a 97.9% susceptibility to clindamycin [26] including dairy cows. It is the most common cause of intramammary infections in dairy cows. Its public health importance increases inline to the continuous emergence of drug-resistant strains; such as Methicillin-resistant *S. aureus* (MRSA.

Susceptibility to vancomycin was noticed to be high as it was 72.26%. However, variation in results was indicated in different studies. For instance, a study showed that the *S. aureus* isolates were 40.28% susceptible to vancomycin [23]. In contrast, it was reported that sensitivity to vancomycin was 100% in all three species [31]. Vancomycin has been selected as an alternative antibiotic of choice for treating *S. aureus* infection mostly MRSA infections and increases in the resistance to vancomycin might cause...
risk for treatment of infection caused by MRSA, especially multidrug-resistance MRSA infection.

The differences among the antimicrobial indicated diversity in resistance rates among different regions in the world. The interpretation of diversity is increased hygienic procedures and risen surveillance measures in some countries more than others [25]. Improved hygienic procedures help with reducing the opportunity for S. aureus to spread. Surveillance helps in the early identification of S. aureus emergence, hence earlier treatment and isolation of infected species [32]. Moreover, high antibiotic usage plays an important role in the resistance rate. For instance, it was believed that vancomycin was highly effective toward S. aureus. However, in developed countries, where there is better access to drugs, the increased usage of vancomycin led to the appearance of vancomycin-resistant strain of S. aureus. In contrast, in developing countries, where vancomycin is barely available, vancomycin resistance is not problematic [33].

Among 119 isolates, 22 isolates demonstrated multidrug-resistance characteristics, and within the 22 isolates only 7 isolates from cattle harbored the mecA gene and none of the sheep and goats isolates contained the mecA gene. All 7 isolates were resistant to oxacillin phenotypically by disc diffusion test and screening for the mecA gene. This is because of the mecA gene function which is a production of PBP 2a, which in turn increase the resistance toward beta-lactams such as methicillin and oxacillin. The results of this study indicated that only (7/119) 5.9% of the animals carried MRSA strains. These findings alert the personnel and owners of the farm because these animals can be possible reservoirs of this pathogen in the farm and the community. Comparing mecA gene results to the other studies, 0% of MRSA strains were detected [23], and also it has been reported that no MRSA was found in the nasal swabs of goats and cattle [12]. It has also been reported only 5/73 (6.84%) nasal swabs from sheep were MRSA [5]. It has been recorded that the mecA gene detection and the occurrence of MRSA were very low among healthy cattle, sheep, and goats [34]. The rate was only 0.49% (1/201) and one MRSA was found only in a nasal swab from sheep [34]. On the other hand, it has been reported the presence of MRSA in 3 species at the rate of 4.3% in cattle, 3.8% in sheep, and 3.9% in goats [9].

The 7 MRSA isolates showed resistance not only to oxacillin but also to other antimicrobials, including penicillin, erythromycin, and tetracycline, making them multidrug-resistant MRSA. Gharsa et al. [5] also reported that MRSA isolates from sheep, presented resistance to more than three antibiotics, in addition to beta-lactams, to streptomycin, kanamycin, erythromycin, and clindamycin, tetracycline thus being multidrug-resistant MRSA as well. It was presented that all the MRSA isolates from sheep, cattle, and goats exhibited resistance to 3-5 antibiotics [9]. The occurrence multidrug-resistant MRSA among apparently healthy cattle, sheep, and goats points out the role of such animals in the epidemiology of multidrug-resistant MRSA strains which may act as a threat to public health [9].

Conclusion

This study showed high nasal carriage of S. aureus among apparently healthy animals. Cattle isolates harbored multidrug-resistant MRSA. The presence of MRSA and multidrug-resistant MRSA among healthy cattle could be considered as a potential reservoir for the transmission of multidrug-resistant MRSA to humans, especially farm workers. None of sheep and goats isolates were found to be positive mecA gene.

Acknowledgments

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Conflict of Interest

The authors declare that no conflict of interest.

References


الكشف والتصنيف الجزيئي لعزلات المكورات العنقودية والسلمية في محافظة دهوك
فين عبدالرحمن رسول و رزيق خالد عبدالله هـ.
فرع الأمراض والأحياء المجهرية - كلية الطب البيطري - جامعة دهوك - العراق.

هدفت هذه الدراسة إلى تحديد وتوصيف نسبة تواجد المكورات العنقودية في الأنف لحيوانات المزرعة السليمة ظاهرياً والتي تشمل الأبقار الضأن والماعز باستعمال التصنيف المظهري والجزيئي. أجريت هذه الدراسة في محافظة دهوك، إقليم كردستان العراق في الفترة ما بين تشرين الثاني 2021 و آذار 2022. عزياً عن ذلك فقد تم استخدام طريقة Kirby-Bauer للكشف عن تواجد MRSA باستخدام طريقة المضادات الحيوية بطريقة PCR وتصنيفها جينياً باستخدام تقنية تفاعل البلمرة المتسلسل وتوصيفها جينياً باستخدام تقنية تفاعل البلمرة المتسلسل (oxacillin discs) للانتشار في الأفراد. وفي دراسة أخرى، تم الكشف عن الحيوانات السليمة تم فحصها كانت عازلة نقدية تم فحصها كانت 300 (69.7%) موجبة للمكورات العنقودية باستخدام المضادات الحيوية المستخدمة في هذه الدراسة. وسجلت نسبة مقاومة وظيفة في الابقار (72.3%)، ولم يوجد المكورات العنقودية ذات المقاومة المتعددة في الابقار وMRSA. إن وجود MRSA من الضأن والماعز حاملة للنوع ذات المقاومة المتعددة للإنسان وخصوصاً العاملين في MRSA المزرعة من أجل لم تتماشى معاً لانتقال العوامل الممرضة سواء كانت من الإنسان أو العكس من ذلك. الكليات الدالة: MRSA: حيوانات السليمة ظاهرياً. MRSA: ذات المقاومة المنحدرة دهوك.