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Characterization of Methicillin-Resistant *Staphylococcus aureus* Isolated from Shepherds and Apparently Healthy Goats and Sheep in Egypt

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Abstract

THE OBJECTIVE of this study was to assess the prevalence, antimicrobial susceptibility, and distribution of virulent genes in *Staphylococcus aureus* (*S. aureus*) and MRSA isolates from healthy sheep and goats, as well as their shepherds. The study included 50 sheep, 50 goats, and 32 shepherds. Three types of samples were collected from each animal - milk samples, nasal swabs, and rectal skin swabs, while the shepherds provided thirty-two nasal swabs and 32 hand swabs. Biochemical tests were used to identify *S. aureus* colonies, and cefoxitin disk diffusion was employed to identify MRSA isolates. The isolates were then tested for *nuc*, *mec*A, *PVL*, and *Van*A genes. *S. aureus* was detected in 84.20% of the tested sheep samples, 51.33% in goats and 84% among shepherds. MRSA was present in 54% of milk samples, 58% of nasal swabs, and 48% of skin swabs in sheep. In goats, MRSA was found in 59%, 42%, and 58%, respectively. In shepherds, MRSA isolates were detected in 88% of nose swabs and 90% of hand swabs. All MRSA isolates were multi-drug resistant, with penicillin G showing the highest resistance (100%). In conclusion, sheep, goats, and their shepherds, may play a significant role in the transmission of *S. aureus*. Moreover, the presence of MRSA in raw milk, nose swabs, and skin swabs may contribute to the spread of the bacteria to other individuals.

Keywords: *S. aureus,* MRSA, small ruminants, *mec*A, panton valentine leukocidin, Antibiotics resistance.

Introduction

Sheep are an important source of red meat in Egypt, accounting for 99,322 tons of fresh milk and 6% of the country's total red meat output [1]. Goat rearing has also become a significant aspect of animal production in Egypt, with goats being bred for both meat and milk, which accounts for 2.7% of the country's total meat production [2]. Staphylococcus bacteria are classified into various species and subspecies, with *S. aureus* being one of the most important opportunistic pathogens. This bacterium is the primary cause of nosocomial skin infections and community-associated infections, and its pathogenicity is primarily due to various components such as leucocidins, proteases, hemolysins, and toxins [3, 4]. *S. aureus* strains produce a variety of toxins, including staphylococcal enterotoxins (SEs), enterotoxin-like proteins (SEl), and staphylococcal toxic shock syndrome toxin (TSST) [4].

The close proximity of animals during lambing and kidding creates an ideal environment for infection to spread rapidly. As a result, small ruminants' milk, skin, feces, and nasal cavities are considered potential sources of staphylococcal infections and environmental contamination [5]. This bacterium has been linked to a variety of disorders in humans and animals [6]. *S. aureus* infections in humans can cause arthritis, sepsis, bacteremia, pneumonia, food poisoning, and nosocomial infections [7]. It has also been linked to mastitis in dairy animals, such as cattle, buffalo, sheep, and goats, resulting in significant economic losses in dairy farms due to reduced milk output and poor milk quality [8].

S. aureus has a high degree of variability, allowing it to spread at different periods and locations with varied clonal types and antibiotic resistance profiles across regions and countries [9]. Methicillin Resistance Staphylococcus aureus

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(MRSA) has emerged as a major health hazard for both humans and animals. Excessive and uncontrolled use of antimicrobial drugs causes these issues [10].

Some studies have investigated the prevalence of MRSA in milk from small ruminants, but the consumption of dairy products made from raw goat and sheep milk is still widespread, particularly in the Mediterranean region, where raw milk is used to make traditional cheeses [11]. Despite the limited research on *S. aureus* and MRSA in small ruminants, the current study aimed to provide up-to-date information on the prevalence of these organisms in healthy sheep and goats, as well as their shepherds, and to assess the susceptibility of the identified isolates to antimicrobials.

Material and Methods

Samples Collection and Preparation

The study involved 100 seemingly healthy sheep and goats (50 of each) and their contact shepherds (32 individuals). Each animal provided three types of samples: milk, nasal swabs, and skin swabs (from the rectum area), while the shepherds provided 32 nasal swabs and 32 hand swabs. The study was conducted in accordance with the ethical guidelines of Mansoura University's ethical committee and followed the 3rd edition of the Care and Use of Agricultural Animals in Research and Teaching (<http://www.fass.org/>). The animals were chosen based on convenience, and their owners gave their consent for the sampling procedure and the research plan. Detailed information about the sampling and processing for each type of sample is provided below.

Isolation and Identification of Staphylococcus aureus

The obtained samples were deposited in an enriched broth (Tryptone soya broth, TSB) containing 70 mg of NaCl / ml and incubated at 37°C for 24 hours. After incubation, a loopful (10 µl) of each incubated broth was streaked onto selective media for *S. aureus*, Baird Parker agar base (Oxoid, CM 275) mixed with 5% egg yolk potassium tellurite and incubated at 37°C for 24-48 hours [12]. Colonies with black, shiny, convex surfaces were selected and streaked on Baird Parker agar for purification before incubating for 48 hours at 37°C. Suspected colonies were subjected to a variety of biochemical assays, including catalase, coagulase, and mannitol fermentation tests. The selected colonies were then stored as glycerol stock at -20°C for further identification [13].

Detection of Methicillin-Resistant S. aureus (MRSA)

Cefoxitin disk diffusion test was applied using 30µg discs. A bacterial inoculum was distributed on Muller Hinton agar medium, followed by loading a cefoxitin (30µg) disc and incubating the plates at 37°C for 24 hours. Following incubation, MRSA was detected by measuring the inhibitory zone diameters using the previously reported method [14].

Molecular Characterization of MRSA Strains

Based on biochemical assays, the identified MRSA strains (n = 50) were subsequently screened using PCR targeting the *nuc*, *mec*A, *PVL*, and *Van*A genes.

DNA extraction

Fifty overnight cultures of *S. aureus* were grown on mannitol salt agar. Two to three independent *S. aureus* colonies were harvested using a sterile loop in 200 µl of DNAse/RNAse-free water, vortexed, and boiled to isolate bacterial DNA [15]. The samples were heated at 95°C for 10 minutes before being centrifuged at 13000 rpm for 5 minutes using an iFuge M15K Microcentrifuge. Clear fluids were collected and kept at -20°C for future PCR amplification.

Method of DNA amplification

Amplifications were done using DreamTaq™ Green PCR Master Mix (2X), Thermo Scientific, USA according to manufacturer instructions. The PCR cycle was carried out in the Mini PCR TM Mini16 Thermal Cycler (Amplyus, Cambridge, MA, USA). The PCR reaction was done in a total volume of 50 µl, consisting of 25 µl of 2X Green master mix, 5 µl of DNA templates, and 2 µl of each primer, followed by adding DNA/RNA free water up to 50 µl. *S. aureus* strain was employed as the positive control in each reaction, while nuclease-free water served as the negative control. The positive control strain was isolated in our laboratory and was molecularly characterized using DNA microarray assays [12]. Primers and cycling conditions used for amplification of *nuc* according to Brakstad et al. [16], *mec*A according to Sallam et al. [17], *PVL* gene according to Algammal et al. [8] and *Van*A gene according to Thati et al. [18]. The amplified PCR products were run in 1.5% agarose gel in an electric field using 1X TBE buffer, then visualized and photographed using an ultraviolet transilluminator.

Antibiotic Sensitivity Profiles of S. aureus Strains

The sensitivity of confirmed *S. aureus* isolates was tested using the disc diffusion method in accordance with Clinical and Laboratory Standards Institute guidelines [19]. The antibiotics used were Penicillin G (P, 10 units), Clindamycin (DA, 2 µg), Gentamycin (CN, 10 µg), Kanamycin (K, 30 µg), Trimethoprim-Sulfamethazine (SXT, 1.25/23.75 µg), Ciprofloxacin (CIP, 5 µg), Chloramphenicol (C, 30 µg), Vancomycin (VA, 30 µg), Tetracycline (TE, 30 µg), Fusidic acid (FA, 5 – 10 µg), Erythromycin (E, 15 µg) and Linezolid (LNZ, 30 µg). Multi drug resistance has been defined as single isolate that expressed resistant to three or more antimicrobial agents. The following formula was used to calculate multiple antibiotic resistances (MAR) index for each strain [20]**:**

MAR index = Total no. of resistance / Total no. of tested antibiotics.

Statistical Analysis

The data were analyzed with the Statistical Package for Social Science (SPSS) application for Windows (Standard version 26). Qualitative data were described in terms of numbers and percentages. The Chi-square test was used to assess the correlation between categorical variables. The Chi-square test has a predefined significance level of 5% (p-value). The results were considered significant at $p < 0.05$. The lower the p-value attained, the more significant the results.

Results

Data in Table 1 illustrates the overall prevalence of *S. aureus* and MRSA among healthy sheep, goats, and shepherds. In the current study, *S. aureus* and MRSA were cultivated at different detection rates, regardless of animal species or sample source. For example, sheep had considerably more *S. aureus* (115/150; 77%) and MRSA isolates (62/115; 54%) than goats (77/150; 51%) and (40/77; 52%), respectively. Furthermore, nasal swabs of sheep were the greatest sources of *S. aureus* (45/50; 90%) and MRSA (26/45; 58%), followed by milk (39/50; 78%, and 21/39; 54%), respectively, then rectal skin swabs (31/50; 61%, and 15/31; 48%), respectively, while in goats, the majority of *S. aureus* (33/50; 66%) and MRSA (14/33; 42%) were recovered from nasal swabs, followed by milk (32/50; 64% and 19/32; 59%), respectively. Shepherds had higher detection rates for *S. aureus* (54/64; 84%) and MRSA (48/54; 89%) than the tested sheep and goats. Hand swabs were the most common source of *S. aureus* (29/32; 91%) and MRSA (26/29; 90%), compared to nasal swabs (25/32; 78% and 22/25; 88%), respectively.

Table 2 representing that the majority (90%) of the *S. aureus* isolates (45/50) from various sources expressed *nuc* gene. The *nuc*-positive isolates were examined for *mec*A*, PVL*, and *Van*A genes. The results showed that 25 (56%) isolates carried the *mec*A gene and were identified as MRSA. Furthermore, the *PVL* gene was detected in nineteen (42%) *S. aureus* isolates (10 isolates from sheep, 4 isolates from goats and 5 isolates from human samples). Meanwhile, *Van*A gene wasn't detected in *S. aureus* isolates from different sources.

Table 3 reveals that molecularly identified *S. aureus* isolates (n = 45) are extremely resistant to penicillin G (100%), followed by kanamycin, tetracycline, and fusidic acid (96% each), erythromycin and gentamicin (93% each), sulfamethazine (82%), clindamycin (73%), and ciprofloxacin (60%). Linezolid (98%) was most effective against the tested *S. aureus* strains, followed by vancomycin (82%), and chloramphenicol (67%). In the present study, all *S. aureus* strains exhibited multi-drug resistance (MDR) to more than three antimicrobial drug classes as shown in table 4.

Discussion

In this study, regardless of the animal type or sample source, *S. aureus* and MRSA were determined with various detection rates data presented in (Table 1). A recent study in Egypt reported a low detection rate of *S. aureus* in sheep [21]. The authors identified *S. aureus* in 58% of raw milk and 18% of nasal swabs, however the MRSA recovery rate was slightly higher (51.6% in milk samples and 66.7% in nasal swabs) than in our study. In this investigation, however, MRSA was discovered in 54% (62/115) of sheep samples and 52% (40/77) of goat samples.

Researchers in Tiwan Chu et al. [22], Egypt Fadel [23], Czech Republic Klimešová et al. [24], Italy Macori et al. [25], and Egypt Farag et al. [21] reported detection rates of 58% in goat nasal swabs, 50% in sheep milk, 50% in goat rectum surrounding, 57% in sheep milk, and 52% in sheep milk, respectively. In contrast, researchers from Middle Eastern countries such as Saudi Arabia Al zohairy [26], Egypt Fadel [23] and Farag et al. [21], and even Far-eastern countries such as India Fayaz et al. [27]

have reported a wide variety of MRSA detection rates. The authors found variable detection rates across sample sources, including 68% and 60% from sheep and goat nasal swabs, 71% from goat milk, 67% from sheep nasal swabs, and 100% from teat skin swabs and rectal swabs, respectively. Several European countries, notably Italy Cortimiglia et al. [28], the Czech Republic Klimešová et al. [24] have reported low detection rates of MRSA isolates in goat milk (2%, and 0%), respectively.

Several studies, including Gharsa et al. [29] from Tunisia, Klimešová et al. [24] from the Czech Republic, Jauro et al. [9] from Nigeria, and Venkatvasan et al. [30] from India, found low detection rates (varying from 3% to 26%) using samples originated from small ruminant nasal swabs. However, because each study used different samples and detection methodologies, direct comparisons of the wide prevalence range should be approached with care. Geographic location, the sensitivity of isolation procedures, antibiotic use, farm bio security, manufacturing processes, samples handling, and storage are all possible explanations for the disparity in occurrence between countries.

Interestingly, shepherds had higher detection rates for *S. aureus* (54/64; 84%) and MRSA (48/54; 89%) than the tested sheep and goats. Hand swabs were the most common source of *S. aureus* (29/32; 91%) and MRSA (26/29; 90%), compared to nasal swabs (25/32; 78% and 22/25; 88%), respectively. These findings were higher than those reported in Egypt Fadel [23], where *S. aureus* was detected in 19 of 30 (63%) of the human nose and hand swabs examined. In India, Fayaz et al. [27] discovered *S. aureus* in 11 out of 24 milkers' hand swabs (46%), with all recovered *S. aureus* being MRSA (100%, 11/11). In contrast, in an Italian study, the detection rate of *S. aureus* in nasal swabs from shepherds was 36% (97/275), while MRSA was 1.1% (3/275) [31]. Furthermore, in Nigeria, Jauro et al. [9] discovered *S. aureus* in 40% (40/100) of sheep handlers' nasal swabs, while MRSA was isolated in 17% (17/100). In India, Venkatvasan et al. [30] found *S. aureus* and MRSA in nasal swabs of goat handlers at a rate of 84% (26/31) and 19% (6/31), respectively. Taken together, the high percentages of *S. aureus* in human nose and hand swabs appear to be due to the prevalence of *S. aureus* on skin and nostrils, which are considered *S. aureus*' natural habitat [32]. However, the highest percentage of MRSA in contact humans could be related to the incorrect administration of antimicrobial medications and uncontrollable antimicrobial feed additives [30].

In the current study, the vast majority (90%) of the *S. aureus* isolates (45/50) from various sources expressed *nuc* gene, while the remaining five isolates did not express *nuc* gene specific to *S. aureus*. According to Moustafa et al. [33], several *S. aureus* isolates that tested negative for the *nuc* gene could have been the result of gene mutation or deletion. It is probable that the amount of DNA that can be retrieved could be significantly reduced, or the DNA was destroyed during the boiling process.

The *nuc*-positive isolates were examined for *mec*A, *PVL*, and *Van*A genes. The results showed that 25 isolates (56%) carried the *mec*A gene and were identified as MRSA. Furthermore, the *PVL* gene was detected in nineteen *S. aureus* isolates (42%) (10 isolates from sheep, 4 isolates from goats and 5 isolates from human samples). The presence of *PVL* gene suggests a human origin and a recent, secondary transmission to sheep and goats. This finding may in part agreed with previous report [34].

Surprisingly, no *S. aureus* isolates contained the *Van*A gene, even though 8 isolates exhibited vancomycin resistance. A variety of variables, including inoculum size, pH, medium salt concentration, and incubation length, have been hypothesized to influence the phenotypic expression of antibiotic resistance [35]. In Egypt, Kamel [36] discovered that 64.4% (87/135) of the goats' mastitic milk samples tested positive for the *nuc* gene. Of these, 23 (26.4%) isolates were identified as MRSA using the *mec*A gene. Meanwhile, in Italy, Macori et al. [25] reported that all eight isolates (100%) from sheep bulk tank milk samples were validated phenotypically as MRSA carried *mec*A gene, while *PVL* gene was found in only one isolate (0.1%, 1/831) of sheep bulk tank milk. In Algeria, Agabou et al. [37] detected the *mec*A gene in 6/6 (100%) sheep nasal swabs that were phenotypically characterized as MRSA, as well as the *PVL* gene in 4 isolates out of 19 (21%) *S. aureus* isolates. Dastmalchi Saei and Panahi [38] were unable to detect the *PVL* gene in sheep and goat nasal swabs in Iran. In Tunisia, Ben Slama et al. [39] discovered that 2% (1/55) and 7% (4/55) of *S. aureus* isolates from analyzed nasal swabs of humans in contact with animals had the *mec*A and *PVL* genes, respectively.

Table 3 reveals that molecularly identified *S. aureus* isolates (n = 45) are extremely resistant to penicillin G (100%), followed by kanamycin,

tetracycline, and fusidic acid (96% each), erythromycin and gentamicin (93% each), sulfamethazine (82%), clindamycin (73%), and ciprofloxacin (60%). Linezolid (98%) was most effective against the tested *S. aureus* strains, followed by vancomycin (82%), and chloramphenicol (67%). Antibiotics such as vancomycin and linezolid are commonly used to treat MRSA infections. This is consistent with the findings of Algammal et al. [8], who found that linezolid was more effective than vancomycin in treating MRSA. In Egypt, Kamel [36] discovered that *S. aureus* isolated from raw goat milk samples was extremely resistant to amoxicillin (89.7%), followed by penicillin (88.5%) and ampicillin (86.2%); however, there was minimal resistance to ciprofloxacin (1.2%), levofloxacin (2.3%), and ofloxacin (4.5%).

In this study, all *S. aureus* strains exhibited multi-drug resistance (MDR) to more than three classes of antimicrobial drugs. Another study conducted in Jordan revealed that 87% of MRSA isolates from sheep milk samples and all MRSA isolates from goat milk samples exhibited MDR [11]. Additionally, 18.8-45.45% of human *S. aureus* isolates from Romania showed MDR [40]. The widespread use of antimicrobial agents in humans and animals contributes to the prevalence of MDR.

Conclusion

This study suggests that small ruminants may act as a source of *S. aureus* transmission to humans, and vice versa. MRSA may spread from infected shepherds to small ruminants. Furthermore, the abuse of antimicrobial drugs in small ruminants may increase the risk of MDR pathogen transmission between humans and animals. The presence of MDR *S. aureus* should raise public awareness about the threats these isolates pose to human health. As a result, health and veterinary authorities should enact stringent antibiotic prescription restrictions and laws, as well as prohibit raw dairy consumption.

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Conflict of interest

The authors declare that there is no conflict of interest.

Ethical of approval

This study follows the ethics guidelines of the faculty of veterinary medicine, Mansoura university, Egypt (ethics approval number; PhD/ 96).

Author contributions

Th.S collected the samples, carried out the lab work and conducted data analysis. A. M, A. El-G, M.G and D.N conceptualized the study, planned for the research activity and revised the final version. All authors have read and approved the final version of the manuscript for publication.

TABLE 1. The overall prevalence of *S. aureus* and MRSA in healthy sheep and goats and their shepherds

Subjects	Source of samples	No. of examined samples	*S. aureus*			MRSA		
			No. of identified *S. aureus*	%	Chi-square test (p value)	No. of MRSA	%¨	Chi-square test (p value)
Goats	Milk	50	32	64	χ^2=22.46 P≤0.001 (*)	19	59	χ^2=2.10 P=0.350 (**)
	Nasal swabs	50	33	66		14	42	
	Skin swabs (rectum surrounding)	50	12	24		7	58	
	Total	150	77	51		40	52	
Sheep	Milk	50	39	78	$\chi^{2=}$11.03 P=0.004 (*)	21	54	χ^2=4.26 P=0.119 (**)
	Nasal swabs	50	45	90		26	58	
	Skin swabs (rectum surrounding)	50	31	62		15	48	
	Total	150	115	77		62	54	
Shepherds	Nasal swabs	32	25	78	χ^2 =1.89 P=0.168 (**)	22	88	χ^2=0.037 P=0.847 (**)
	Hand swabs	32	29	91		26	90	
	Total	64	54	84		48	89	
	Total	364	246	68		150	61	

%¨: out of *S. aureus* isolate (*): significant (**): non-significant

TABLE 2. Molecular characterization of some *S. aureus* strains (n= 50) from different sources.

		Type of samples	No. of tested *S. aureus*	*Nuc gene*		*Mec*A *gene*		*PVL gene*	
				No. of positive	¨Ratio	No. of positive	¨ Ratio	No. of positive	¨ Ratio
Animals	Sheep	Milk	6	6	6/6	5	5/6	3	3/6
		Nasal swabs	6	4	4/6	1	1/4	3	3/4
		Skin swabs	6	6	6\6	3	3/6	4	4/6
		Total	18	16	89	9	56	10	63
	Goats	Milk	6	6	6/6	4	4/6	2	2/6
		Nasal swabs	6	5	5/6	-	-	-	-
		Skin swabs	6	5	5/6	3	3/5	2	2/5
		Total	18	16	89	7	44	4	25
	Total number of animal samples		36	32	89	16	50	14	44
Human		Nasal swabs	7	6	6/7	3	3/6	3	3/6
		Hand swabs	7	7	7/7	6	6/7	2	2/7
		Total	14	13	93	9	69	5	38
Total			50	45	90	25	56	19	42

Van A gene wasn't detected in *S. aureus* isolates from different sources.

¨ The ratio of each gene was calculated from positive *S. aureus* by *nuc* gene.

TABLE 3. Antibiotic susceptibility test of PCR positive *S. aureus* strains (n=45).

Antimicrobial agent	S		R	
	No.	%	No.	%
Penicillin G (p)	0	0	45	100
Erythromycin (E)	3	7	42	93
Clindamycin (DA)	12	27	33	73
Gentamycin (CN)	3	7	42	93
Kanamycin (K)	2	4	43	96
Vancomycin (VA)	37	82	8	18
Chloramphenicol (C)	30	67	15	33
Ciprofloxacin (CIP)	18	40	27	60
Trimethoprim-Sulfamethazine (SXT)	8	18	37	82
Tetracycline (TE)	2	4	43	96
Linezolid (LNZ)	44	98	1	2
Fusidic acid (FA)	2	4	43	96

S: Sensitive, R: Resistant

TABLE 4. Antimicrobial resistance profile of *S. aureu*s strains (n=45) with MAR index.

Source	Antimicrobial resistance profile	MAR index
Human nasal swab	P, DA, CN, E, K, C, SXT	0.6
Human nasal swab	P, DA, CN, E, K, C, SXT, CIP, FA, TE	0.8
Human nasal swab	P, DA, CN, E, K, C, SXT, CIP, FA, TE	0.8
Human nasal swab	P, DA, CN, E, K, C, SXT, FA, TE	0.8
Human nasal swab	P, DA, E, K, SXT, CIP, FA, TE	0.7
Human nasal swab	P, CN, E, K, FA, TE	0.5
Human hand swab	P, DA, CN, E, K, C, SXT, CIP, FA, TE	0.8
Human hand swab	P, DA, CN, E, K, C, SXT, CIP, FA, TE	0.8
Human hand swab	P, DA, CN, E, K, SXT, CIP, FA, TE	0.8
Human hand swab	P, DA, CN, E, K, SXT, CIP, VA, FA, TE	0.8
Human hand swab	P, DA, CN, E, K, C, SXT, CIP, FA, TE	0.8
Human hand swab	P, DA, CN, K, SXT, FA, VA	0.6
Human hand swab	P, DA, CN, K, E, SXT, C, CIP, FA, TE	0.8
Sheep milk	P,DA, CN, E, K, SXT, CIP, FA, TE	0.8
Sheep milk	P, DA, E, C, CIP, SXT, FA, TE	0.7
Sheep milk	P, DA, CN, E, K, C, SXT, CIP, FA, TE	0.8
Sheep milk	P, DA, CN, E, K, SXT, CIP, FA, TE	0.8
Sheep milk	P, DA, CN, E, K, SXT, CIP, FA, TE	0.8
Sheep milk	P, DA, CN, E, K, FA, TE	0.6
Sheep nasal swab	P, E, K, SXT, FA, TE	0.6
Sheep nasal swab	P, CN, E, K, SXT, VA, FA, TE	0.7
Sheep nasal swab	P,CN, E, K, SXT, FA, TE	0.7
Sheep nasal swab	P, DA, CN, E, K, SXT, CIP, FA, TE	0.8
Sheep skin swab	P, DA, CN, E, K, SXT, CIP, VA, FA, TE	0.8
Sheep skin swab	P, DA, CN, E, K, SXT, CIP, FA, TE	0.8
Sheep skin swab	P, CN, E, K, SXT, FA, TE	0.6
Sheep skin swab	P, CN, E, K, SXT, CIP, VA, FA, TE	0.8
Sheep skin swab	P, DA, CN, E, K, C, CIP, SXT, FA, TE	0.8
Sheep skin swab	P, CN, E, K, SXT, FA, TE	0.6
Goat milk	P, DA, CN, E, K, C, SXT, CIP, VA, FA, TE	0.9
Goat milk	P, DA, CN, E, K, SXT, CIP, FA, TE	0.8
Goat milk	P, CN, E, K, SXT, VA, FA, TE	0.7
Goat milk	P, CN, E, K, FA, TE	0.5
Goat milk	P, DA, CN, E, K, CIP, FA, TE	0.8
Goat milk	P, DA, CN, K, SXT, CIP, FA, TE	0.7
Goat nasal swab	P, DA, CN, E, K, CIP, FA, TE	0.7
Goat nasal swab	P, DA, CN, E, K, SXT, CIP, FA, TE	0.8
Goat nasal swab	P, CN, E, K, TE	0.4
Goat nasal swab	P, CN, E, K, FA, TE	0.5
Goat nasal swab	P, DA, CN, E, K, C, SXT, FA, TE	0.8
Goat skin swab	P, DA, CN, E, C, SXT, CIP, FA, TE	0.8
Goat skin swab	P, DA, CN, E, K, C, SXT, CIP, FA, TE	0.8
Goat skin swab	P, CN, K, FA, TE	0.4
Goat skin swab	P, DA, CN, K, E, C, SXT, VA, FA, TE	0.8
Goat skin swab	P, DA, CN, E, K, SXT, FA, TE	0.7

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الميكروب العنقودي الذهبي المقاوم للميثيسيلين المعزول من الرعاة والماعز و الأغنام السليمة صحيا ظاهريا في مصر

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الملخص

الهدف من هذه الدراسة كان لتقييم مدي الانتشار، الحساسية لمضادات الميكروبات والمضادات الحيوية وجينات الضراوة في الميكروب العنقودي الذهبي والميكروب العنقودي الذهبي المقاوم للميثيسلين المعزول من الأغنام والماعز السليمة صحيا ظاهريا ورعاتها. الدراسة شملت عدد 50 من الأغنام، 50 من الماعز و32 من رعاة الأغنام. تم تجميع ثلاث أنواع من العينات (مسحات من الأنف، مسحات من الجلد المحيط للمستقيم والألبان) من كل حيوان. بالنسبة لرعاة الأغنام تم تجميع عدد 32 مسحة من الأيدي و 32 مسحة من الأنف منهم. ثم تم عزل الميكروب علي الأوساط البكتيرية النوعية وتم التعرف علي الميكروب باستخدام الاختبارات الكيميائية الحيوية وتم التعرف والتميز علي عترات الميكروب العنقودي الذهبي المقاوم للميثيسلين باستخدام اختبار نشر أقراص السيفوكسيتين. ثم تم اختبار العزلات بواسطة تفاعل البلمرة المتسلسل للكشف عن جينات الضراوة *nuc*, *mec*A, *PVL* and *Van*A

أوضحت النتائج أن الميكروب العنقودي الذهبي تم عزله بنسب 84.20% من عينات الأغنام، 51.33% من عينات الماعز و84% من عينات الرعاة. من ناحية أخري وجد الميكروب العنقودي الذهبي المقاوم للميثيسلين في 54% من الألبان، 58% من مسحات الأنف و 48% من مسحات الجلد المحيط للمستقيم للأغنام في حين أن وجد في 59%، 42% و58% من العزلات المصنفة من الماعز علي التوالي. بالنسبة لعينات والعزلات المصنفة من الرعاة وجد الميكروب العنقودي الذهبي المقاوم للميثيسلين في 88% مسحات الأنف و90 من مسحات الأيدي. أثبتت النتائج أن كل عزلات الميكروب العنقودي الذهبي المقاوم للميثيسلين كانت مقاومة للعديد من المضادات الحيوية المختبرة وكانت أعلاهم مقاومة للبنسلين المائي بنسلين ج بنسبة 100%.

يستخلص من الدراسة أن الأغنام والماعز والرعاة تلعب دورا معنويا في انتقال وانتشار الميكروب العنقودي الذهبي. علاوة علي ذلك وجود الميكروب العنقودي الذهبي في عينات الألبان الخام، مسحات الأنف ومسحات الجلد يساهم في انتشار هذا الميكروب بين الحيوانات والأفراد.

الكلمات المفتاحية: مقاومة المضادات الحيوية، *mec*A, *PVL* الميكروب العنقودي الذهبي المقاوم للميثيسلين، الميكروب العنقودي الذهبي، المجترات الصغيرة.