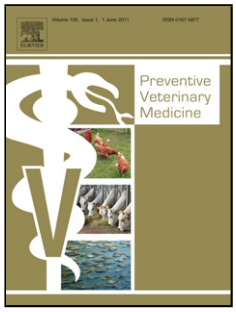

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Methicillin resistant *Staphylococcus aureus* among goat farms in Eastern province, Saudi Arabia: Prevalence and risk factors

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Abstract

A cross sectional study was conducted on 1010 goats from 25 flocks located in the eastern province, Saudi Arabia, to study the prevalence of methicillin resistant *Staphylococcus aureus* (MRSA) among goat farms. A total of 235 milk samples and 775 nasal swabs were collected for bacteriological investigation. Based on resistance to cefoxitin, 20 isolates were permissively identified as MRSA. PCR with specific primers was used to confirm MRSA. The prevalence of MRSA was 2%; with maximum prevalence in mastitic milk (9.2%) and swabs from animals showed respiratory signs (2.6%), while the lowest prevalence was identified in apparently normal milk (0.6). The standard disk diffusion test was used for in vitro evaluation of isolates resistance profile to 13 antimicrobial agents. Multidrug resistance (MDR) was detected in all MRSA and in 23.5% of methicillin sensitive *Staphylococcus aureus* (MSSA). Univariable association between the prevalence of MDR/MRSA strains and management practices indicated a higher prevalence with larger size flocks, where raising animals for both meat and milk production, and where antibiotics were used during the last 30 days, the latter was particularly pertinent to penicillin-streptomycin. Multivariable models indicated that larger flocks (200–400, and >400) were, respectively, 4 and 3.5 fold more likely to have MDR *S. aureus* compared to smaller flocks (<200).

Keywords: MRSA, goat, multidrug resistant, *Staphylococcus aureus*.

Introduction

Antibiotic resistance is a global animal and public health challenge with a significant threat to both human and animal health. Although the problem has accelerated by misuse and over use of antimicrobials, it may be driven by multiple factors including: intrinsic characteristics of bacteria to develop natural antimicrobial resistance over the time through genetic changes; inappropriate use of antibiotic (either through over-prescription, incomplete course of treatment or inadequate dosing), use of antimicrobial agents in agriculture (either as growth promoter or for prophylaxis purposes); mutation and transferable genetic materials (plasmid, transposons and integron) (Meervenne et al 2012, Castro-Sánchez et al 2016).

In USA, antimicrobial resistance is accountable for more than two million of bacterial infections and 23000 human losses (CDC, 2013). Moreover, deaths in the European Union that attributed to drug-resistant bacteria were estimated to be 25000 with economic cost more than US$1.5 billion every year (EMA and ECDC, 2009).

Staphylococcus aureus is considered as a common commensal & pathogenic bacterium in humans and a wide variety of animal species (Sung et al., 2008; Sakwinska et al., 2011). In human, *S. aureus* is a common cause of community-acquired skin infections and a major cause of hospital-acquired infections including surgical and catheter-site infections, bacteremia and life-threatening pneumonia (Lowy, 1998). A variety of infections in livestock could be caused by *Staphylococcus aureus*, most notably the intra-mammary infections in cattle and small ruminants that lead to major economic losses for dairy farmers (Hunter, 1984; Manser, 1986; Vanderhaeghen et al., 2010). Its importance has escalated because of increasing resistance to antibiotics in hospital strains and the emergence of resistant strains in the community (Hiramatsu et al., 2002).

First case of methicillin-resistant *Staphylococcus aureus* (MRSA) was reported in England in 1961 shortly after the introduction of methicillin in clinical practice in the early 1960s (Jevons, 1961), soon became a serious problem challenging hospital infection control throughout the world (Ayliffe, 1997). The methicillin resistance of *S. aureus* is mediated by the mecA gene, which encodes penicillin-binding protein 2a (PBP2a) which has a low affinity for beta-lactam antibiotics (Stryjewski and Corey, 2014).

In the last decades, resistance of *S. aureus* to antimicrobial agents has grown in the Kingdom of Saudi Arabia (KSA) with an increasing prevalence of both nosocomial and community MRSA isolates. A first report on MRSA was published in 1992, in which the antibiotic sensitivity pattern of isolates from KSA and Great Britain was compared (Al-Masaudi et al., 1992). In 1993, the initial epidemic of MRSA was reported in the ICU of the tertiary care hospital in Riyadh (Haddad et al., 1993). Subsequently, the MRSA prevalence was scrutinized in different areas of KSA, including Jeddah (Zaman and Dibb, 1994), Abha (Al-Ghamdi et al., 2002), Al-Ahasa (Panhotra et al., 2005), Taif (Abdel-Fattah, 2005), Riyadh (Baddour et al., 2006) and Mecca (Asghar, 2011).

Isolation of MRSA from animals was first reported in 1972 following its detection in milk from mastitic cows (Devriese et al., 1972). It has now become an increasingly urgent problem in veterinary medicine, with infections been reported in a variety of species, comprising horses, cattle, companion animals, and exotic species, both as a healthy carriers and as a case of infection (Lee, 2003; Strommenger et al., 2006; Anderson et al., 2008; Persoons et al., 2009; Weese, 2010). The transmission of MRSA amongst humans and animals was reported elsewhere (Hanselman et al., 2006; Weese et al., 2006; Wulf et al., 2007; Wulf et al., 2008).

Goats are considered as an important source of meat and milk for human in developing countries. In Saudi Arabia, there are an estimated 3.4 million head of goats producing 30160 tons of meat and 80 000 tons of milk (FAOSTAT, 2013). Mastitis is a serious problem in dairy goats with high economic losses (Leitner et al., 2007). Genus *Staphylococcus*, in particular *S. aureus* is the most important infectious cause of mastitis in dairy goats with isolation frequencies ranged between 4-40% of all isolated microorganisms (White and Hinckley, 1999; Ameh and Tari, 2000; McDougall et al., 2002; Contreras et al., 2007; Hall and Rycroft, 2007; Leitner et al., 2007). MRSA has been isolated from nasal cavities, vagina, mastitic milk, bulk milk and individual milk of goats (Stastkova et al., 2009; Aras et al., 2012; Chu et al., 2012; Cortimiglia et al., 2015).

In KSA, to the best of the author's knowledge, there is no available literature on the prevalence of MRSA in livestock or the risk factors for MRSA infection in animals. Therefore, the main goal of this study was to investigate the prevalence and risk factors associated MRSA in goat flocks in the eastern province, KSA.

Materials and Methods:

Animals:

A cross-sectional study was conducted on 1010 goats from 25 flocks located in Eastern region, KSA over the period between January and December 2015. The examined flocks composed of different breeds of goats (Ardi, Omani, and Damascus) that were mainly raised for meat and milk production. The flock size ranged between 50 and 600 (median=300) animals/flock. The project was ethically approved by Deanship of Scientific Research, King Faisal University, Kingdom of Saudi Arabia (Project No; 17122001).

Sampling process:

Sample size determination

Sample size was determined by using the formula for simple random sampling, with 50% expected prevalence, 5% absolute precision, and 95% confidence level. Due to lack of information on between and within flock variance, the resulting sample size (384) was multiplied by 3 to account for clustering of goats within flocks (Martin et al, 1987). Depending on the relative cost of sampling clusters vs. animals, a total of 25 flocks were sampled with an average of 40 goats sampled per flock.

Flocks and animal selections

A two stage sampling process was carried out. In the first stage, goat flocks were selected at random (using computer-generated random numbers) from a list of producers from agricultural department. If a producer refused to participate, the next producer in the list was contacted. In the second stage, animals within flocks were selected to include any goat with clinical mastitis or respiratory signs, followed by systematic random sampling of 10 % of clinically normal animals from the rest of the flock. A total of 235 (170 clinically normal and 65 mastitic) composite milk samples and 775 nasal swabs (394 apparently healthy and 381 with respiratory symptoms (nasal discharge, cough)) were collected. Milk samples were collected from lactating does, following the standard methods described by the National Mastitis Council (NMC, 1990). All samples were transported cooled to the laboratory in an icebox (4C◦).

Nasal swabs were collected from nostrils after proper cleaning and disinfection of the external nares. The collected swabs were kept in Amies transport medium (Difco) and transported to the laboratory for microbiological examination.

Bacteriological Analysis:

Nasal swabs and 10 µl from each milk sample were plated on 5% sheep blood agar. The plates were incubated aerobically at 37 ºC for 24-48 hours. Suspected colonies were sub-cultured on Braid Parker agar (Difco) supplemented with 5% egg yolk emulsion (Oxoid) and Mannitol Salt Agar (Difco), incubated aerobically at 37 ºC for 24-48 hours. Isolates were presumptively identified as *S. aureus* based on colony morphology, Gram stain, lecithinase activity, haemolysis pattern, catalase and coagulase activities (Quinn et al., 2002). Further confirmation was carried out using commercial biochemical micro-methods (API 32 Staph; BioMérieux, France). The analysis was performed and interpreted according to the manufacturer's recommendations.

DNA Extraction:

Total genomic DNA was obtained as described by Dibbern et al., (2015) using QIAamp DNA minikit (Qiagen SA, Courtaboeuf, France). All isolates were analyzed for *Staphylococcus* 16S rRNA as formerly defined by Jaffe et al., (2000). PCR amplicons (750 bp) were sequenced using a Genetic Analyzer 3500 (Applied Biosystems). Sequences obtained were analyzed for sequence homology against the GenBank database and confirmation of species level was conceded if sequences showed 98% - 100% similarities to the reference gene of *S. aureus*.

Screening for MRSA:

Oxacillin agar (6 µg/ml) was used for screening of methicillin resistance in all isolates (CLSI, 2014).

Antibiotic susceptibility test:

The antibiotic susceptibility of isolates were determined using standard disk diffusion test CLSI (CLSI, 2014), using the succeeding antimicrobial disks: penicillin (10 units), methicillin (5 µg), cefoxitin (30 µg), gentamicin (10 µg), erythromycin (15 µg), tetracycline (30 µg), streptomycin (10 µg), ciprofloxacin (5 µg), clindamycin (2 µg), chloramphenicol (30 µg), trimethoprim/sulfamethoxazole (1.25/23.75 µg) and amoxicillin-clavulanic acid (20/10 µg). Etest® (bioMérieux, France) was used for testing vancomycin susceptibility according to the manufacturer's instructions. *S. aureus* ATCC 12600 was used as a reference strain. Zones of growth inhibition were evaluated based upon interpretative criteria developed by the CLSI (CLSI, 2014). Multidrug resistance was defined as resistance to at least one agent in three or more antimicrobial categories (Magiorakos et al., 2012).

Detection and partial sequencing of methicillin-resistant (mecA) gene:

The mecA gene encoding methicillin resistance was detected using PCR technique (Murakami et al., 1991). ATCC 43300 *S. aureus* strain was used as a mecA positive control.

PCR products were purified using a QIAquick PCR Purification Kit (Qiagen SA, Courtaboeuf, France) for partial sequencing of the mecA gene. Sequencing was conducted by Genetic Analyzer 3500, (Applied Biosystems) using the mecA primer. Partial nucleotide sequences were analyzed using the BLAST program https://blast.ncbi.nlm.nih.gov/Blast.cgi

Statistical analysis:

Three outcomes were evaluated for the occurrence of: (1) *S. aureus* (yes vs. no), (2) multidrug resistance (MDR) strain (yes vs. no), and MRSA (yes vs. no). For each outcome, the mean prevalence and confidence interval for binomial proportion were computed. The association between predictor variables and occurence of MDR and MRSA was evaluated using univariable

and multivariable random effects logistic regression models with random effects for flock. In the initial stage of model building, risk factors for each of the outcomes were initially screened using unconditional associations (P <0.20). Flock size was categorized (<200, 200-400, and >400) due to nonlinear relation with the log odds of the outcome. Spearman correlation coefficients were used to check the variables for collinearity. Subsequently, multivariable analysis was conducted and non-significant variables were removed sequentially using backward elimination at P <0.05. Two-way interactions among predictors that were significant in the final main effect model were evaluated, The multivariable model for MRSA could not be fitted due to the low number of cases. All analyses were conducted using Stata Statistical Software v. 14 (Stata Corp, College Station, TX).

Results:

Overall, 139 (13.7%, 95% CI:11.6 - 15.9) isolates were identified as *S. aureus* by biochemical testing and 16S rRNA gene sequence. Representative sequences were submitted to GenBank as accession numbers KY427940, KY433357, and KY433355. The prevalence of *S. aureus* was highest in mastitic milk followed by nasal swabs from goats with respiratory symptoms. The lowest prevalence was observed in normal milk samples (Table 1).

Out of 139 *S. aureus* isolates, 20 (14.4%, 95% CI: 9.01 - 21.3) isolates showed resistance to oxacillin and cefoxitin after screening with the oxacillin agar screen test and the cefoxitin disc diffusion test. In all MRSA strains, the mecA gene was identified by PCR technique. Sequenced amplicons revealed a great similarity percentage (98%-100%) to the reference gene. Representative sequences of the mecA gene were submitted to GenBank with accession

numbers KY467024, KY490701, and KY467026. The prevalence of MRSA among different samples was illustrated in Table (1).

Antimicrobial susceptibilities of MRSA isolates are reported in Figure (1). All isolates showed 100% resistance to penicillin G, methicillin, cefoxitin, streptomycin and amoxicillin/clavulanic acid. The lowest resistance was detected with trimethoprim/sulfamethoxazole (15%), clindamycin (20%), ciprofloxacin (25%), and chloramphenicol (35%). All isolates showed multi-drug resistance; type and distribution of MRSA multiresistance profiles are shown in Table (2). Among methicillin sensitive *S. aureus* (MSSA) isolates, 80.7% displayed penicillin-resistance, 37.8% to streptomycin, 6.7% to clindamycin, and 5% to amoxicillin/clavulanic acid (Fig. 2).

Twenty-eight (23.5%) MSSA isolates showed multidrug resistance, among them 17 (60.71%) isolates were recovered from goats with respiratory symptoms; the multidrug resistance profile was shown in Table (3). Both MRSA and MSSA isolates were sensitive to vancomycin.

Univariable association (Table 4) between the occurrence of MDR/MRSA strains and management practices indicated a positive association with larger size flocks, raising animals for both meat and milk production, using antibiotics during the last 30 days, or using penicillin-streptomycin during the last 30 days. On the other hand, lower occurrence of MDR/MRSA strains was related to using antibiotics according to veterinary advice, following the recommended dose and time upon antibiotic administration, and using antibiotics based on sensitivity testing.

A multivariable model (Table 5) indicated that larger flocks (200–400, and >400) were, respectively, 4- and 3.5-fold more likely to have multi-resistant *S. aureus* compared to smaller

flocks (<200). On the other hand, flocks that used antibiotics according to antibiotic sensitivity testing were 0.4 times less likely to have multi-resistant *S. aureus* as compared to other flocks.

Discussion:

Human infection with MRSA has been reported in KSA since 1992, yet there is no available literature reporting MRSA in farm animals. The current study was intended to monitor the occurrence of MRSA in goats for the first time in KSA. In this study, goats were chosen because of their economic importance in the study area.

The overall prevalence of *S. aureus* in goat flocks in the eastern region of Saudi Arabia was 13.7% with higher prevalence among goats with clinical mastitis (33.8%) and goats with respiratory symptoms (18%). The occurrence of clinical and subclinical *S. aureus* mastitis in does were ranged from 5.6% to 37% respectively in different countries (Deinhofer and Pernthaner, 1995; White and Hinckley 1999; da Silva et al., 2004; Moroni et al., 2005). Isolates from the nares of goats with respiratory diseases and apparently healthy ones have been previously reported (Vautor et al., 2005, Mørk et al., 2010, Gharsa et al., 2015, Rahimi et al., 2015). Vautor et al., (2005) and Alves et al., (2009) reported that nasal carriage is an important reservoir in ruminants, and a strain of *S. aureus* isolated from ewes showed gangrenous mastitis was found in the nasal cavities of other animals on the same farm (Vautor et al., 2009).

Twenty of 139 isolates (14.4%) were identified as MRSA based on identification of the mecA gene by selected PCR with the highest prevalence in mastitic milk (9.2%). Isolation and identification of MRSA from goat's milk and nares had been stated elsewhere including Czech Republic, (Stastkova et al., 2009), Turkey, (Aras et al., 2012), Taiwan, (Chu et al., 2012), Iran, (Rahimi et al., 2015), and Italy (Cortimiglia et al., 2015). More interestingly, MRSA was

detected in the nostril of 10.9% and 39% of horses and swine (de Neeling et al., 2007; van den Eede et al., 2009).

As expected, results of MRSA isolates susceptibility testing showed 100% resistance to penicillin, methicillin and cefoxitin. Moreover, 100% resistance was reported to streptomycin, 85% to tetracycline, 65% to gentamicin, 55% to erythromycin and 100% sensitivity to vancomycin. Multi-drugs resistance (MDR) is defined as acquired non-susceptibility to at least one agent in three or more antimicrobial categories (Magiorakos et al., 2012). All MRSA isolates showed MDR to 3–5 antibiotic classes. Such profiles of antibiotic resistance occur rather frequently in many of the MRSA isolates from KSA and other countries (Seguin et al., 1999, Al-Humaidan et al., 2015, Wang et al., 2015).Compared to MRSA resistance profile, MSSA exhibited a lower level of resistance and 11 isolates were susceptible to the all antimicrobials. More interestingly, 23.5% of the isolates showed MDR to 3–5 antibiotic classes. Similar results were obtained by other authors (Haran et al., 2012; Zabielinski et al., 2013; Saeed et al., 2014). The Multidrug resistant forms of *S. aureus* strains are a serious concern worldwide and the emergence of MDR strains against advanced antibiotics is a major drawback for chemotherapy.

Penicillin-streptomycin combination, trimethoprim/sulfamethoxazole, oxytetracyclin, gentamicin, ampicillin, and ciprofloxacin are the most common antibiotics for veterinary use in the area of study.

Univariable analysis results showed a positive association between MDR strains and antibiotics usage, especially the penicillin-streptomycin combination. Antibiotic treatment of bacterial infection in animals had been implicated as a catalyst for resistance of isolated bacteria from animals (following treatment), other contact animals within the same flock, and the food derived

from these animals for human utilization (Berghash et al., 1983; Singh et al., 1992; Griggs et al., 1994; Piddock, 1996; Witte, 2000).

Association between occurrence of MRSA and MDR strains and larger flock size as well as milk production farms may be attributed to intensive management may require more for larger flock and so may be expected to administer a greater number of antimicrobial treatments proportionate to the size of the flock, particularly for the treatment or prevention of mastitis as well as to prevent both Escherichia coli infections and navel ill, which would then increase the risk of emergence of resistant organisms. (Lafi et al., 1988, Scott et al 2012).

The northern part of our study area is a communal grazing area where the seasonal movement of livestock flocks for pastoralism is common. There was an association between feeding practice (grazing), and location of herds (north) with a higher incidence of MRSA and MDR strains. This may be attributed to the ability of *S. aureus* to survive in the environment and transmission through the air, and to its commensal nature on skin and mucous membrane of animals (Peton and Loir, 2014). The same authors reported that, skin and mucous membrane of ruminants are the principal reservoir of *S. aureus*.

The performance of antimicrobial susceptibility testing by clinical microbiology laboratories is important to confirm susceptibility to chosen empirical antimicrobial agents, or to detect resistance in individual bacterial isolates. In this study, a lower prevalence of MDR strains was associated with the use of antibiotic susceptibility testing before using antibiotics.

The use of antibiotics under veterinary supervision at recommended doses and duration was associated with a low prevalence of MRSA and MDR strains. With long-term antimicrobial use in a given environment, the microbial ecology will change dramatically, with less susceptible organisms becoming the predominant population (Levy, 1998).

The most obvious limitation of this study included that we were able to sample only 25 flocks due to budget and labor limitations. Because of the relatively small number of flocks included in the study, only variables that were strongly associated with the outcome could be evaluated in the final model. The absence of a particular variable that was significant in the unavailable analyses from the final model may be due to the limited sample size and reduced study power.

Conclusions

Conclusively, isolation of MRSA from goat herds is a public health threat. The use of susceptibility testing of clinical isolates is a cornerstone for prudent use of antimicrobials and for the adequate management of single clinical cases. Further molecular identification of isolates to detect the clone type is recommended. National surveillance programs that assess the extent of the problem are recommended; these will track evolution over time, and evaluate the effectiveness of control measures. There is a great need for diagnostic laboratories to adhere to standards and thus provide reliable and reproducible susceptibility data for clinicians and other users. Veterinary guidance is recommended for shepherds working in a pastoral role in the desert, particularly in the correct use of antibiotics.

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Table 1: Prevalence (%) of *Staphylococcus aureus*, MDR, and MRSA strains by sample type (Estimate and 95% CI) among goat flocks, Eastern region, Saudi Arabia.

Parameter	Nasal swab From respiratory diseased animals N=381	Nasal swab from apparently healthy N=394	Mastitis milk N=65	Normal milk N=170	Overall N=1010
Staphylococcus aureus	17.9 (14.2-22.1)	10.2 (7.4-14.0)	33.8 (22.6-46.6)	4.2 (1.7-8.5)	13.7 (11.6-15.9)
MDR	7.0 (4.7-10.0)	2.3 (1.1-4.3)	15.4 (7.6-26.5)	1.2 0.2-4.3)	4.7 (3.5-6.3)
MRSA	2.6 (1.3-4.7)	0.8 (0.2-2. 2)	9.2 (3.5-19.0)	0.6 (0.02-3.3)	2.0 (1.2-3.0)

MDR: multidrug resistant *S. aureus*

MRSA: Methacilline resistant *S. aureus*

Table 2: Multidrug resistance profile among methicillin resistant *Staphylococcus aureus* (MRSA) isolates in goat flocks, Eastern region, Saudi Arabia.

Resistance profile	Number of isolates	Source of samples			
		Mastitic milk	Normal milk	Nasal swabs from respiratory diseased	Nasal swabs from apparently healthy
PEN MET FOX STR	1	1	0	0	0
PEN MET FOX TCY STR	3	1	0	2	0
PEN MET FOX ERY TCY STR	1	0	0	1	0
PEN MET FOX GEN TCY STR	2	0	0	1	1
PEN MET FOX GEN ERY STR	1	0	0	0	1
PEN MET FOX ERY TCY STR CIP	1	1	0	0	0
PEN MET FOX GEN TCY STR CIP	3	1	0	2	0
PEN MET FOX GEN ERY STR CIP	1	0	0	1	0
PEN MET FOX GEN ERY TCY STR	3	1	0	2	0
PEN MET FOX GEN ERY TCY STR CIP	4	1	1	1	1

Table 3: Multidrug resistance profile among methicillin sensitive *Staphylococcus aureus* (MSSA) isolates in goat flocks, Eastern region, Saudi Arabia.

Resistance profile	Number of isolates	Source of samples			
		Mastitic milk	Normal milk	Nasal swabs from respiratory diseased	Nasal swabs from apparently healthy
PEN ERY TCY	4	0	0	3	2
PEN GEN ERY	2	2	0	0	2
PEN TCY STR CIP	4	0	0	4	0
PEN ERY STR CIP	2	0	0	2	0
PEN GEN TCY CIP	2	0	0	1	1
PEN GEN ERY STR	4	0	0	3	1
PEN GEN ERY TCY	2	0	1	1	0
PEN ERY TCY STR CIP	2	0	0	2	0
PEN GEN ERY STR CIP	2	1	0	1	0
PEN GEN ERY TCY CIP	4	1	0	0	0

Table 4: Univariable association (P<0.20) between multidrug resistant *Staphylococcus aureus* strains, MRSA and management factors among goat flocks, Eastern region, Saudi Arabia.

Variable	Percent	Multi-resistant		MRSA	
		OR[1]	P	OR[1]	P
Flock size			0.006[2]		0.018
<200	28	-	-	-	-
200-400	31	5.53	0.007	6.30	0.086
>400	41	6.21	0.003	8.84	0.036
Location			0.112[2]		
East	17	-	-		
North	55	3.76	0.035		
South	11	1.54	0.610		
West	17	2.52	0.199		
Production					
Meat	57	-	-		
Meat &milk	43	2.49	0.007	5.36	0.003
Feeding practices			0.003[2]		0.007[2]
Concentrates	36	-	-	-	-
Grazing	15	4.62	0.001	10.28	0.003
Both	49	2.50	0.026	3.78	0.087
Antibiotic use last 30 days					
Yes vs. no	79	12.54	0.013	5.28	0.022
Follow recommended dose					
Yes vs. no	59	0.36	0.011	0.16	0.031
Antibiotic sensitivity test					
Yes vs. no	53	0.28	0.001	0.04	0.003
Antibiotic use					
Vet. advice vs. experience	59	0.36	0.011	0.16	0.031
Antibiotic source					
Government vs. private	27	0.17	0.004		
Antibiotic type last 30 days			0.001[2]		
Penicillin-streptomycin	48	-	-		
Oxytetracyclin	9	0.13	0.042		
Gentamicin	3	0.82	0.788		
Ciprofloxacin	7	0.36	0.163		
Cloxacillin	8	0.56	0.289		
Erythromycin	5	0.26	0.189		
No antibiotic use	20	0.06	0.004		

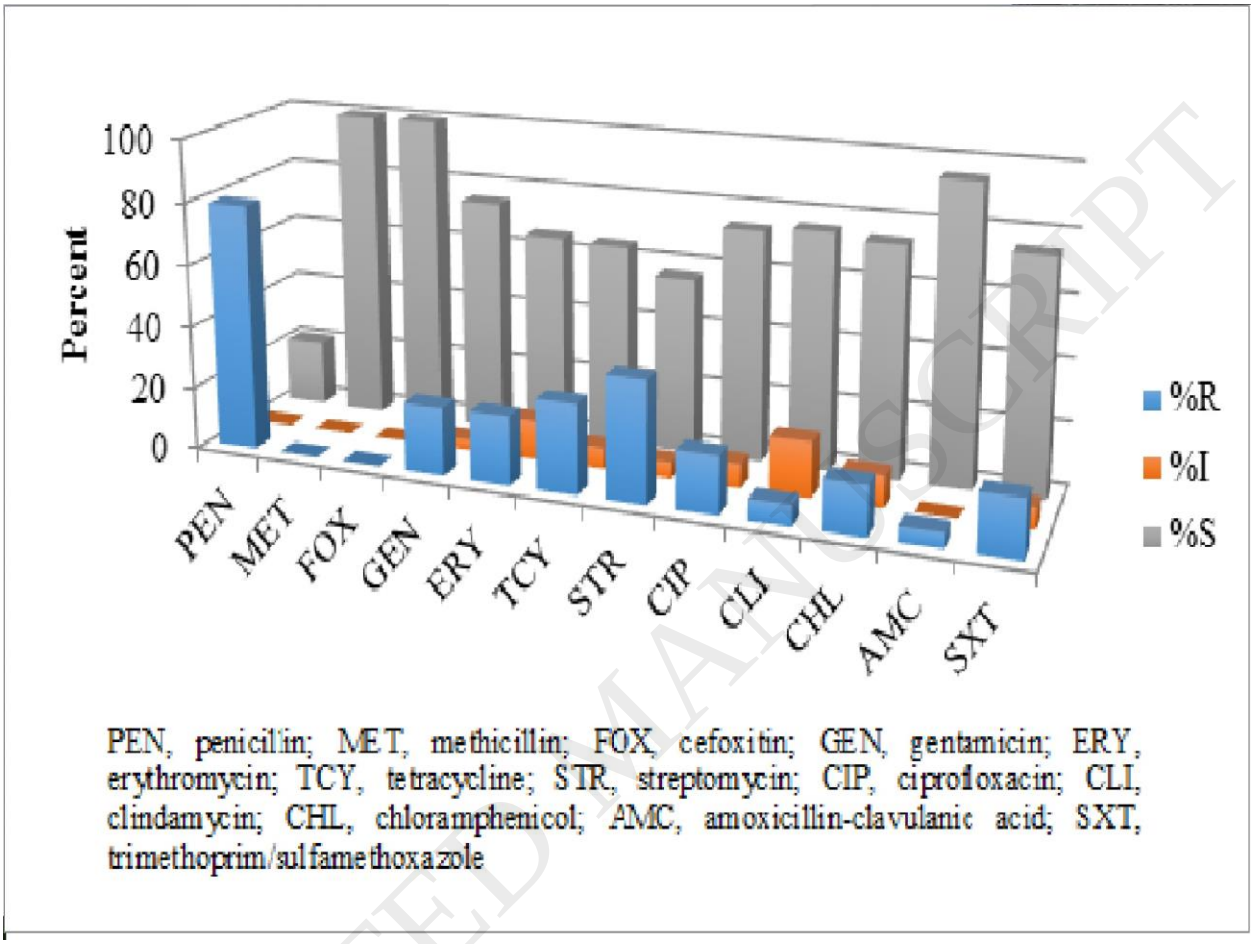
[1] OR: Odds ratio [2] The overall *P*-value for variables with multiple categories.

Table 5: Multivariable association (P<0.05) between multidrug resistant *Staphylococcus aureus* strains and management factors among goat flocks, Eastern region, Saudi Arabia.

Variable	OR[1]	P	95% CI
Flock size		0.049[2]	
<200	-	-	
200-400	4.10	0.028	1.16-14.41
>400	3.52	0.039	1.08-12.60
Antibiotic sensitivity test			
Yes vs. no	0.38	0.009	0.18-0.78

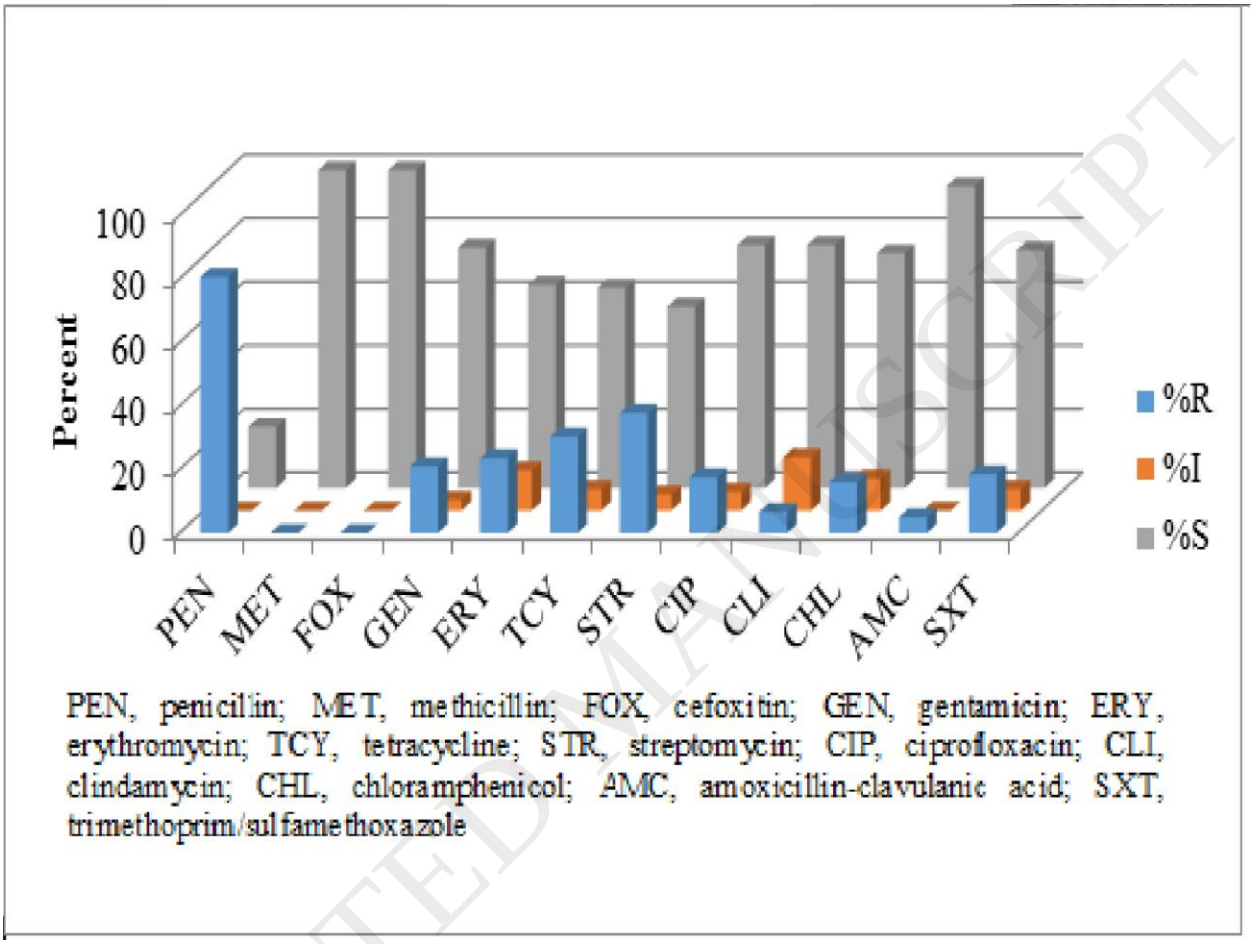
[1] OR: Odds ratio [2] The overall *P*-value for variables with multiple categories.

Figure 1. Antibiotic susceptibility of methicillin-resistant S. aureus (MRSA).



PEN, penicillin; MET, methicillin; FOX, cefoxitin; GEN, gentamicin; ERY, erythromycin; TCY, tetracycline; STR, streptomycin; CIP, ciprofloxacin; CLI, clindamycin; CHL, chloramphenicol; AMC, amoxicillin-clavulanic acid; SXT, trimethoprim/sulfamethoxazole

Figure 2. Antibiotic susceptibility of methicillin sensitive staphylococcus aureus (MSSA) isolates



PEN, penicillin; MET, methicillin; FOX, cefoxitin; GEN, gentamicin; ERY, erythromycin; TCY, tetracycline; STR, streptomycin; CIP, ciprofloxacin; CLI, clindamycin; CHL, chloramphenicol; AMC, amoxicillin-clavulanic acid; SXT, trimethoprim/sulfamethoxazole