International Journal of Food Microbiology 336 (2021) 108901

Contents lists available at ScienceDirect

International Journal of Food Microbiology

journal homepage: www.elsevier.com/locate/ijfoodmicro

Resistance profiling and molecular characterization of *Staphylococcus aureus* isolated from goats in Korea

Abraham Fikru Mechesso[a], Dong Chan Moon[a], Gwang-Seon Ryoo[b], Hyun-Ju Song[a], Hye Young Chung[b], Sang Uk Kim[b], Ji-Hyun Choi[a], Su-Jeong Kim[a], Hee Young Kang[a], Seok Hyeon Na[a], Soon-Seek Yoon[a], Suk-Kyung Lim[a,*]

[a] Bacterial Disease Division, Animal and Plant Quarantine Agency, 177 Hyeksin 8-ro, Gimcheon-si, Gyeongsangbuk-do 39660, Republic of Korea
[b] Jeonnam National Veterinary Service Laboratory, 619 Geumgang-ro, Jakcheon-myeon, Gangjingun, Jeonnam 59213, Republic of Korea

ARTICLE INFO

Keywords:
Antibiotics
Carcass
Staphylococcal enterotoxin
spa types
SCCmec types
Nasal cavity
Virulence

ABSTRACT

Staphylococcus aureus is among the most common zoonotic pathogens that cause foodborne illnesses worldwide. The main objectives of the current study were therefore to determine the antimicrobial susceptibility profiles of *S. aureus* isolated from goats in Korea and to investigate the molecular characteristics of identified methicillin-resistant *S. aureus* (MRSA). In the study, 481 *S. aureus* isolates (431 from the nasal cavity and 50 from carcass) were recovered from 1146 carcasses and nasal swabs between July 2018 and January 2019. Approximately 82% and 72.6% of nasal and carcass isolates, respectively, were resistant to at least one antimicrobial agent, with the highest rate of resistance to penicillin, followed by resistance to chloramphenicol and tetracycline. Relatively small proportions of the isolates were resistant to cefoxitin, clindamycin, and erythromycin. However, all *S. aureus* isolates were sensitive to linezolid, rifampin, and vancomycin. Six MRSA isolates were obtained, three each from the nasal cavity and carcass. MRSA isolates were of two sequence types (ST) (ST72 and ST398), three *spa* types (t664, t324, and t571), and two *SCCmec* types (IV and V). The ST72 MRSA isolates had identical PFGE profiles. In addition, ST72 MRSA-*SCCmec* IV isolates carried at least six staphylococcal leukotoxin- and enterotoxin-encoding genes (*lukED*, *seg*, *sei*, *sem*, *sen*, *seo*, and *seq*). The remaining ST398 isolate carried only the *lukED* gene and was additionally resistant to eight non–β-lactam antibiotics. To the best of our knowledge, this is the first report of MRSA from goats in Korea. There is a possibility of transmission of MRSA from goat to human or contamination of food products. Therefore, regular microbiological investigation in goats, farms, and slaughterhouses is critical to determine the existence of virulent and multi-drug resistant (MDR) *S. aureus* and to implement preventive strategies.

1. Introduction

Staphylococcus aureus is an opportunistic pathogen that causes mild-to-severe, life-threatening infections in humans (Sakwinska et al., 2011). It is also one of the leading causes of foodborne diseases worldwide. *S. aureus* colonizes the nares and skin of animals; it may enter the food chain during slaughter and processing of animal products. Staphylococcal food poisoning occurs following ingestion of food, such as meat and dairy products, contaminated with staphylococcal enterotoxins (Fox et al., 2017). *Staphylococcus* spp. is responsible for 2.2% of foodborne and waterborne outbreaks in the EU in 2018 (EFSA, 2019), 2.9% of foodborne illness outbreaks in China between 2008 and 2010 (Luo et al., 2017), and 1.2% of foodborne outbreaks in the US between 2009 and 2015 (Dewey-Mattia et al., 2018). In addition, it was associated with 3.2% of foodborne outbreaks in Japan and the Republic of Korea (Korea) during 2011–2015 (Lee et al., 2019).

The widespread use of antimicrobials for treatment and prophylaxis

Abbreviations: CA-MRSA, Community-associated *S. aureus*; LA-MRSA, Livestock-associated *S. aureus*; MDR, Multi-drug resistance; MLST, Multilocus sequence typing; MRSA, Methicillin-resistant *S. aureus*; PCR, Polymerase chain reaction; PFGE, pulsed-field gel electrophoresis; *SCCmec*, Staphylococcal cassette chromosome *mec*; *spa*, *S. aureus* protein A gene; ST, Sequence type

* Corresponding author at: 177 Hyeksin 8-ro, Gimcheon-si, Gyeongsangbuk-do 39660, Republic of Korea.
E-mail addresses: abrahamf@korea.kr (A.F. Mechesso), ansehdcks@korea.kr (D.C. Moon), rgsun@korea.kr (G.-S. Ryoo), shj0211@korea.kr (H.-J. Song), jeunghy@korea.kr (H.Y. Chung), vetksu@korea.kr (S.U. Kim), wlgus01@korea.kr (J.-H. Choi), kimsujeong27@korea.kr (S.-J. Kim), kanghy7734@korea.kr (H.Y. Kang), nash8090@korea.kr (S.H. Na), yoonss24@korea.kr (S.-S. Yoon), imsk0049@korea.kr (S.-K. Lim).

https://doi.org/10.1016/j.ijfoodmicro.2020.108901
Received 9 March 2020; Received in revised form 28 September 2020; Accepted 29 September 2020
Available online 08 October 2020

of multiple diseases in food-producing animals contributes to the emergence of resistant strains. Shortly after the clinical application of methicillin, methicillin-resistant *S. aureus* (MRSA) was detected in food-producing animals and retail meat in Asia, Europe, and North America (Adesiji et al., 2011; Lim et al., 2010; Miranda et al., 2009). MRSA has become a global public health concern because the pathology of diseases caused by MRSA is multifactorial, involving complex host-pathogen interactions and the production of extracellular hemolysins and toxins. In addition, MRSA strains are frequently multi-drug resistant (MDR), which prolongs therapy, increasing treatment costs and hospitalization rates (Cosgrove, 2006). Hence, screening and molecular characterization of MRSA isolates are vital for the evaluation of the zoonotic potential of MRSA infection and for establishing an effective preventive and control system. Generally, molecular techniques used for the characterization of MRSA have the advantage that they are rapid, less laborious, and more sensitive, specific, and efficient compared to the conventional method (Adzitey et al., 2013).

In Korea, MRSA epidemics have been a common problem in the hospital environment since the 1970s. Liu et al. (2019) revealed a 53% prevalence of MRSA among *S. aureus* isolates from hospitalized patients in Korea. In the past two decades, MRSA has also been isolated from dogs (Kwon et al., 2006), chickens, cattle, and swine (Moon et al., 2007; Moon et al., 2015; Moon et al., 2019) in different parts of Korea.

MRSA isolates are characterized as either community-associated (CA-MRSA), hospital-acquired, or livestock-associated (LA-MRSA) (Conceicao et al., 2017). CA-MRSA sequence type (ST) 72, mainly identified in animals and raw meat, is the most common type of MRSA isolated from humans in Korea (Moon et al., 2019; Song et al., 2011). In addition, ST5 (Kwon et al., 2006), ST692 (Lim et al., 2010), and ST541 (Lim et al., 2012; Moon et al., 2019) MRSA were identified in chicken meat and live pigs in Korea. Similarly, the incidence of LA-MRSA in several animal species is increasing, especially in swine, in Europe, North America, and Korea (Conceicao et al., 2017; Moon et al., 2007; Sorensen et al., 2017). Currently, LA-MRSA is a public health concern and primarily affects people who have frequent contact with animals. ST398 MRSA is one of the most frequent LA-MRSA identified in veterinarians, abattoir, and farm workers worldwide (Cortimiglia et al., 2015; Moon et al., 2019; Sahibzada et al., 2017).

The consumption of goat meat in Korea is increasing, with 584,615 slaughtered in the years 2013–2019. This amount is ten times higher than in 2005–2012 (KOSIS, 2019). With increasing goat meat consumption, concerns about food safety have also increased. Several studies have therefore been conducted in Korea to determine the prevalence and antimicrobial resistance profiles of *S. aureus* isolated from various animal species. To the best of our knowledge, the antimicrobial resistance profiles of *S. aureus* isolated from goats in Korea have not been conducted to date. Consequently, the aim of our study was to determine the antimicrobial susceptibility profiles of *S. aureus* isolated from nasal cavities and carcasses of Korean goats, and to investigate the molecular characteristics of the identified MRSA.

2. Materials and methods

2.1. Sample collection

Swab samples were collected from two slaughterhouses and 51 farms in Jeonnam and Jeonbuk provinces of Korea between July 2018 and January 2019. Samples were randomly collected from two slaughterhouses, from a total of 20, which contributed about 27% (28,350 heads) of the total number of goats slaughtered in Korea in 2018. The numbers of animals and bacterial isolates were determined as described previously (FAO, 2019) Most carcass and nasal swab samples were collected from different goats. A cotton-tipped swab moistened with Stuart's medium (Becton Dickinson, Sparks, MD) was used for nasal sample collection; the back and the chest of carcasses were swabbed using a sterile gauze pad. Samples were placed in ice-cooled containers and immediately transported to the laboratory. All samples were processed within 24 h of arrival.

2.2. Isolation of S. aureus and MRSA

Swab samples were inoculated into Mueller–Hinton broth (Becton Dickinson) containing 6.5% NaCl (v/v) and incubated overnight at 37 °C. One loopful of the broth was then streaked on chrome *S. aureus* agar (CHROMagar, Paris, France) and incubated for 16–20 h at 37 °C. Based on the colony morphology and color, up to five presumptive *S. aureus* colonies were selected from each plate and subcultured on Tryptic Soy Agar (Becton Dickinson). *S. aureus* was then identified by matrix-assisted laser desorption/ionization time-of-flight mass spectrophotometry (Bio Merieux, Lyon, France). A multiplex polymerase chain reaction (PCR) assay specific for the 16S rRNA, *clfA*, and *mecA* genes was used to reconfirm MRSA identity (Mason et al., 2001).

2.3. Antimicrobial susceptibility testing

Antimicrobial susceptibility was determined by the broth dilution method according to the Clinical and Laboratory Standards Institute (2018) guidelines, using antibiotic-containing plates (EUST, TREK Diagnostics Systems, Cleveland, OH). Nineteen antibiotics were tested: cefoxitin (0.5–16 μg/ml), chloramphenicol (4–64 μg/ml), ciprofloxacin (0.25–8 μg/ml), clindamycin (0.12–4 μg/ml), erythromycin (0.25–8 μg/ml), fusidic acid (0.5–4 μg/ml), gentamicin (1–16 μg/ml), kanamycin (4–64 μg/ml), linezolid (1–8 μg/ml), mupirocin (0.5–256 μg/ml), penicillin (0.12–2 μg/ml), quinupristin/dalfopristin (0.5–4 μg/ml), rifampin (0.02–0.5 μg/ml), streptomycin (4–32 μg/ml), sulfamethoxazole (64–512 μg/ml), tetracycline (0.5–16 μg/ml), tiamulin (0.5–4 μg/ml), trimethoprim (2–32 μg/ml), and vancomycin (1–16 μg/ml). Plates were read using the Vizion automated reading device (TREK Diagnostic Systems, Cleveland, OH). Antimicrobial resistance breakpoints were determined based on the Clinical and Laboratory Standards Institute (2018) and European Committee on Antimicrobial Susceptibility Testing (2018) guidelines. *S. aureus* ATCC 25923 was used as a reference strain.

2.4. Characterization of MRSA

2.4.1. Multilocus sequence typing (MLST) and pulsed-field gel electrophoresis (PFGE)

MLST was performed as described by Enright et al. (2000). Specific primers (Genotech, Daejeon, Korea) were used to amplify and sequence the following housekeeping genes: *arcC*, *aroE*, *glpF*, *gmk*, *pta*, *tpi*, and *yqiL*. PCR products were purified (Solgent, Daejeon, Korea) and sequenced using an ABI prism 3100 analyzer (Genotech, Daejeon, Korea). Allele numbers were assigned using the MLST website for *S. aureus* (https://pubmlst.org/saureus/; last accessed [02/08/2019]). In addition, chromosomal DNA was digested with *Sma*I (TaKaRa, Shiga, Japan) and PFGE was performed to determine the genetic relatedness of the isolates, as described by McDougal et al. (2003).

2.4.2. Staphylococcal cassette chromosome mec (SCCmec) and spa typing

SCCmec typing was performed by multiplex PCR as described by Boye et al. (2007). *S. aureus* protein A (*spa*) typing was conducted using Ridom Staph Type server (Ridom GmbH, Wurzburg, Germany) (www.spaserver.ridom.de; last accessed [13/08/2019]) according to Enright et al. (2000) and Harmsen et al. (2003).

2.4.3. Detection of virulence factor-encoding genes

The presence of staphylococcal toxin genes encoding leukotoxins (*lukED*), Panton–Valentine leucocidin toxin (LukF-PV), exfoliatins (*eta* and *etb*), toxic shock syndrome toxin 1 (*tsst1*), and staphylococcal enterotoxins (*sea*, *seb*, *sec*, *sed*, *see*, *seg*, *seh*, *sei*, *selj*, *sek*, *sell*, *sem*, *sen*, *seo*, *sep*, *seq*, and *ser*) was analyzed by PCR, as previously described (van

Table 1
Antimicrobial resistance profiles of *S. aureus* isolated from nasal cavity and carcass of goats in Korea.

(a)

Antimicrobials	Sources of isolates	MIC_{50}	MIC_{90}	Distribution (%) of MICs (μg/ml)															R (%)
				≤0.016	0.03	0.06	0.125	0.25	0.5	1	2	4	8	16	32	64	128	≥256	
Cefoxitin	Carcass	4	4								12.0	82.0		6.0					6.0
	Nasal	4	4							1.2	24.8	73.3	0.5	0.2					0.7
Chloramphenicol	Carcass	8	64									34.0	28.0		26.0	12.0			38.0
	Nasal	4	64									71.0	10.0	0.2	7.2	11.6			18.8
Ciprofloxacin	Carcass	0.25	0.25					100											0
	Nasal	0.25	0.25					97.2	2.1	0.2			0.5						0.5
Clindamycin	Carcass	0.125	0.125				98.0			2.0									0
	Nasal	0.125	0.25				90.0	0.9	0.2			8.8							8.8
Erythromycin	Carcass	0.25	0.5					76.0	24.0										0
	Nasal	0.25	0.5					88.9	2.0		0.2		8.8						8.8
Fusidic acid	Carcass	0.5	0.5						98.0			2.0							2.0
	Nasal	0.5	0.5						99.5	0.2	0.2								0.2
Gentamicin	Carcass	1	1							100									0
	Nasal	1	1							96.3	0.5	2.6	0.2	0.4					0.4
Kanamycin	Carcass	4	4									94.0				6.0			6.0
	Nasal	4	4									95.8		0.5	2.7	0.9			0.9
Linezolid	Carcass	1	2							62.0	38.0								0
	Nasal	1	1							98.4	1.6								0

(b)

Antimicrobials	Sources of isolates	MIC_{50}	MIC_{90}	Distribution (%) of MICs (μg/ml)															R (%)
				≤0.016	0.03	0.06	0.125	0.25	0.5	1	2	4	8	16	32	64	128	≥256	
Mupirocin	Carcass	0.5	0.5						100										ND
	Nasal	0.5	0.5						100										ND
Penicillin G	Carcass	0.5	1				38.0		38.0	18.0	6.0								62.0
	Nasal	0.5	1				38.7	1.4	14.6	39.4	5.8								61.3
Quinupristin/d	Carcass	0.5	0.5						98.0	2.0									0
alfopristin	Nasal	0.5	0.5						98.3	0.9	0.2	0.4							0.4
Rifampin	Carcass	0.016	0.016	100															0
	Nasal	0.016	0.016	99.8	0.2														0
Streptomycin	Carcass	4	32									58.0	14.0	16.0	12.0				ND
	Nasal	4	32									76.8	11.6	0.7	11.0				ND
Sulfamethoxazole	Carcass	64	64													100			ND
	Nasal	64	64													100			ND
Tetracycline	Carcass	0.5	16						62.0					38.0					38.0
	Nasal	16	16						44.5			0.2		55.2					55.2
Tiamulin	Carcass	0.5	0.5						94.0	4.0		2.0							ND
	Nasal	0.5	0.5						99.1			0.9							ND
Trimethoprim	Carcass	2	2								100								0
	Nasal	2	4								99.3	0.2			0.5				0.5
Vancomycin	Carcass	1	1							100									0
	Nasal	1	1							99.8	0.2								0

ND, not determined; R, resistance rate.
The dilution ranges tested are those contained in the white area.
The breakpoints of tested antimicrobial agents are indicated by vertical lines.
MIC_{50} and MIC_{90} are the concentrations at which 50% and 90% of the isolates were inhibited, respectively

Duijkeren et al., 2008; Yamada et al., 2005). The lists of primers and PCR conditions used for molecular characterization of MRSA strains are summarized in Supplement 1.

3. Results

3.1. Antimicrobial resistance of S. aureus isolates

We recovered 481 *S. aureus* isolates (431 from the nasal cavity and 50 from carcasses) from goats. The resistance profiles of the isolates are presented in Table 1a and b. Penicillin, chloramphenicol, and tetracycline resistance were most prevalent in both the nasal and carcass isolates. The chloramphenicol resistance rate was higher among carcass isolates than among nasal isolates, while the converse was noted for tetracycline resistance. The proportions of penicillin-resistant isolates from the nasal and carcass swabs were similar (62 and 61.3%, respectively). Clindamycin- (8.8%) and erythromycin- (8.8%) resistant isolates were detected only in the nasal swabs. Only small numbers of isolates from the carcass or nasal cavity were resistant to ciprofloxacin, fusidic acid, kanamycin, quinupristin/dalfopristin, and trimethoprim. All isolates were sensitive to linezolid, rifampin, and vancomycin. Approximately 72.6 and 82% of isolates from the nasal and carcass cavity, respectively, were resistant to at least one antimicrobial agent (Table 2). In addition, 14.3% of nasal and 22% of carcass isolates were MDR. Resistance to penicillin and tetracycline was the predominant (37.4%) pattern in isolates from the nasal cavity, while resistance to chloramphenicol and penicillin was the predominant pattern in carcass isolates (22%).

3.2. Molecular characteristics of MRSA goat isolates

A total of six (1.2%) isolates were identified as MRSA, three each from the nasal cavity and carcass. The isolates represented two STs (ST72 and ST398), three *spa* types (t664, t571, and t324), and two *SCCmec* types (IV and V) (Table 3). Five (all) MRSA isolates from the farms in Jeonnam province were identified as ST72. The only isolate from farm C-e in Jeonbuk province (nasal) was classified as ST398. The

Table 2
Antimicrobial resistance patterns of *S. aureus* recovered from of goats in Korea.

No. of antimicrobials	Resistance patterns	No. of resistant isolates (%)	
		Carcasses (n = 50)	Nasal swab (n = 431)
0		9 (18.0)	118 (27.4)
1	CHL	–	32 (7.4)
	FUS	1 (2.0)	–
	PEN	7 (14.0)	23 (5.3)
	TET	9 (18.0)	13 (3.0)
2	CHL PEN	11 (22.0)	18 (4.2)
	CHL TET	–	3 (0.7)
	FUS TET	–	1 (0.2)
	PEN TET	2 (4.0)	161 (37.4)
	FOX PEN	–	–
3	CHL PEN TET	8 (16.0)	22 (5.1)
	FOX KAN PEN	3 (6.0)	2 (0.5)
4	CLI ERY PEN TET	–	31 (7.2)
5	CHL CLI ERY PEN TET	–	4 (0.9)
	CLI ERY KAN PEN TET	–	1 (0.2)
9	CHL CIP CLI ERY GEN PEN SYN TET TMP	–	1 (0.2)
10	FOX CHL CIP CLI ERY GEN PEN SYN TET TMP	–	1 (0.2)
MDR	(≥three sub classes)	11 (22.0)	62 (14.3)

CHL, chloramphenicol; CIP, ciprofloxacin; CLI, clindamycin; ERY, erythromycin; FOX, cefoxitin; FUS, fusidic acid; KAN, kanamycin; PEN, penicillin G; GEN, gentamicin; SYN, quinupristin/dalfopristin; TET, tetracycline; TMP, trimethoprim; MDR, Multi-drug resistance.

Table 3
Molecular characteristics of methicillin-resistant *S. aureus* isolates from nasal cavity and carcass of goats in Korea.

Isolates	Sources of isolates	Year/month of sampling	Province	Farm ID	MIC (μg/ml)		Non-beta lactam resistance	MLST	PFGE	*SCC mec*	*spa*	Virulence factors
					PEN	FOX						
N-63	Nasal	2018/11	Jeonnam	B-c	> 2	16	KAN	ST72	I	IV	t324	*lukED, seg, sei, sem, sen, seo, seq*
N-146	Nasal	2018/11	Jeonbuk	C-e	> 2	8	CHL, CIP, CLI, ERY, KAN, GEN, SYN, TET, TMP	ST398	NT	V	t571	*lukED*
N-391	Nasal	2018/12	Jeonnam	E-o	2	8	KAN	ST72	I	IV	t324	*lukED, seg, sei, sem, sen, seo, seq*
C-1-8	Carcass	2018/12	Jeonnam	F-b	> 2	16	KAN	ST72	I	IV	t664	*lukED, seg, sei, sem, sen, seo*
C-49	Carcass	2018/12	Jeonnam	F-d	> 2	16	KAN	ST72	I	IV	t664	*lukED, seg, sei, sem, sen, seo*
C-50	Carcass	2018/12	Jeonnam	F-d	> 2	16	KAN	ST72	I	IV	t664	*lukED, seg, sei, sem, sen, seo*

CHL, chloramphenicol; CIP, ciprofloxacin; CLI, clindamycin; ERY, erythromycin; FOX, cefoxitin; KAN, kanamycin; PEN, penicillin G; GEN, gentamicin; SYN, quinupristin/dalfopristin; TET, tetracycline; TMP, trimethoprim; MLST, multi-locus sequence typing; NT, Untypeable; PFGE, Pulse-field gel electrophoresis; *SCCmec*, Staphylococcal Cassette Chromosome *mec*; *Spa*: *S. aureus* protein; ST, Sequence types.

three ST72 MRSA carcass isolates obtained from two different farms represented *spa* t664-*SCCmec* IV. These isolates carried similar staphylococcal enterotoxin- and leukotoxin-encoding genes (*lukED*, *seg*, *sei*, *sem*, *sen*, and *seo*). The remaining two ST72 MRSA isolates were from other farms (B-c and E-o), and were categorized as *spa* t324-*SCCmec* IV, carrying an additional *seq* virulence gene. ST398 MRSA from Jeonbuk was classified as *spa* t571-*SCCmec* V and carried the *lukED* gene. It was resistant to eight non–β-lactam antibiotics. Of note, all ST72 MRSA isolates exhibited an identical PFGE pattern (Fig. S1).

4. Discussion

The study showed that majority of the isolates were resistant to at least one antimicrobial agent, with the highest rate of resistance to penicillin. Further, we have identified ST72 and ST398 MRSA carrying various virulence factors that are commonly associated with human infections.

The prevalence of *S. aureus* in the nasal cavity of goat determined in our study (82%) was higher than those reported in other countries, e.g., Czechia (40%) (Klimesova et al., 2017), Taiwan (28%) (Chu et al., 2012), Saudi Arabia (18%) (El-Deeb et al., 2018), Switzerland (13%) (Mama et al., 2019), and Norway (10%) (Mork et al., 2010). In the current study, 8% of goat carcasses tested positive for *S. aureus*. To the best of our knowledge, no reports on the prevalence of *S. aureus* in goat carcass are available for comparison. Hence, we compared the prevalence and antimicrobial resistance rate of *S. aureus* from this study with studies conducted mainly in milk samples from dairy goats. The overall prevalence of *S. aureus* in our study (42%) was higher than that noted in Switzerland (32%) (Muehlherr et al., 2003), China (24%) (Qian et al., 2019), Taiwan (17%) (Chu et al., 2012), Czechia (16%) (Klimesova et al., 2017), Saudi Arabia (14%) (El-Deeb et al., 2018), and Norway (7%) (Mork et al., 2010) but, lower than those reported in Norway (96%) (Jorgensen et al., 2005) and Italy (77%) (Spanu et al., 2013). Although the differences might be associated with the variations in sample place, size, type, and the season, the observed prevalence rate in Korea is higher than in other countries.

S. aureus isolates exhibited high rates of resistance to penicillin, tetracycline, and chloramphenicol, in agreement with previous findings in Asia and Europe (Chu et al., 2012; Qian et al., 2019; Virdis et al., 2010). Although the penicillin and tetracycline resistance rates were lower than those reported for Taiwan (Chu et al., 2012), China (Qian et al., 2019), and Italy (Virdis et al., 2010), they were higher than those reported for Brazil (Lira et al., 2016). Ciprofloxacin and gentamicin resistance rate was slightly higher than that reported by the study from Brazil (Lira et al., 2016).

Concurrent with recent reports on *S. aureus* isolates from human and food-producing animals in Korea and other parts of the world (El-Deeb et al., 2018; Hong et al., 2018; Wang et al., 2014), various proportions of *S. aureus* isolates exhibited resistance to cefoxitin, clindamycin, erythromycin, fusidate, gentamicin, kanamycin, and quinupristin/dalfopristin. Interestingly, all isolates were sensitive to linezolid and vancomycin, in agreement with previous reports on isolates from goat in other countries (Chu et al., 2012; Lira et al., 2016; Qian et al., 2019) and human isolates in Korea (Hong et al., 2018). Frequent use of various antimicrobials, including β-lactams, tetracycline, and florfenicol, in food-producing animals is primarily responsible for the emergence of antibiotic-resistant *S. aureus* isolates (Liu et al., 2019).

The proportion of MDR isolates observed in our study (15%) was lower than that recently reported in China (53%) (Qian et al., 2019). The most frequent MDR patterns observed in the current study were slightly different from those reported by El-Deeb et al. (2018) and Wang et al. (2014) from Saudi Arabia and China, respectively. In the current study, penicillin was the predominant resistance trait in both carcass and nasal isolates. Although information on antibiotic usage in goat farms in Korea is scarce, β-lactams are among the most commonly used antibiotics in food-producing animals in the country (APQA, 2016). Of note, the resistance of *S. aureus* isolates to multiple clinically important antibiotics is a grave concern because resistance might be disseminated to humans following frequent contact with infected animals and through the food chain (Chang et al., 2015).

Six (1.3%) MRSA isolates were recovered from our 481 *S. aureus* isolates. The MRSA incidence was lower than those previously reported for goat isolates from milk, nasal, and vaginal swabs in Czechia (33%; 3/33) (Tegegne et al., 2019), Taiwan (41%; 11/27) (Chu et al., 2012), Turkey (Aras et al., 2012) (4.8%; 2/42), Nigeria (2%; 4/200) (Odetokun et al., 2018), and Saudi Arabia (14%; 20/139) (El-Deeb et al., 2018). Although the prevalence of MRSA in our study was lower than that in the above-cited reports, the detection of MRSA in carcasses and nasal cavities of goat emphasizes the public health risks related to the consumption of contaminated goat meat. Having said that, the differences in farm and slaughterhouse management systems, age of goats tested, sample types, sampling methodology, and MRSA detection techniques used should be taken into account while comparing and contrasting findings from different reports.

Regular surveillance of clonal MRSA populations circulating in the food chain is vital to understanding the evolution and dissemination of specific MRSA clones, as well as for implementing appropriate prevention and control measures. Five of the MRSA strains from the current study were classified as ST72, which is the dominant CA-MRSA in humans (Bae et al., 2019; Kim et al., 2019), pig, and cattle (Lim et al., 2010; Moon et al., 2019; Nam et al., 2011) in Korea. The ST72 MRSA isolates represented two *spa* types (t324 and t664) and *SCCmec* type IV cassette, but lacked the *LukF-PV* gene. ST72 MRSA strains with the above characteristics are the most common CA-MRSA in animals in Korea (Bae et al., 2019; Lim et al., 2010; Lim et al., 2012; Moon et al., 2015). Concurrent with the reports of Kim et al. (2019) and Song et al. (2016) on human and bovine MRSA isolates, respectively, ST72 MRSA strains from the current study tested positive for at least the following staphylococcal toxin genes: *seg*, *sei*, *sem*, *sen*, *seo*, and *lukED*. Hence, the detection of MRSA harboring the classical staphylococcal enterotoxin genes in goat carcasses could suggest a potential public health problem. In addition, PFGE analysis revealed the presence of genetically identical ST72 MRSA isolates with identical or different *spa* types and virulence factor genes at the same or different farms in Jeonnam. This suggests clonal spread of ST72 MRSA among goats within and between farms, cross-contamination in the slaughterhouse (mainly for carcass isolates), or the existence of an epidemic clone in the goat industry. Nasal swabs were collected as soon as the goats arrived at the slaughterhouse. Additionally, nasal isolates exhibited different antimicrobial resistance profiles and/or molecular characteristics. Thus, the probability of cross-contamination with nasal isolates was very low.

Our only isolate from farm C-e in Jeonbuk province was identified as ST398 MRSA-t571, one of the most common LA-MRSA strain in Korea and other countries (Moon et al., 2019; Denis et al., 2009; Hau et al., 2017). ST398 MRSA isolates with various *spa* types (predominantly t011, t034, t571, t18102, and t18103) have been detected in pigs and farmers in Korea and other countries (Back et al., 2020; De-Boer et al., 2009; Wendlandt et al., 2013). According to Cuny et al. (2013), few representatives of the major virulence factors are detected in a small proportion of ST398 LA-MRSA. This is in agreement with our findings of only the *lukED* gene in ST398 MRSA. Concordant with previous studies in Korea (Song et al., 2016) and Switzerland (Huber et al., 2009), ST398 MRSA was untypeable by *Sma*I PFGE. To the best of our knowledge, this is the first report of ST398-*spa* t571-*SCCmec* V MRSA from a goat in Korea. This goat originated from a farm that only raises goats and delivers them to the slaughterhouse in a dedicated vehicle. Further, goats are slaughtered therein in a purpose-built house. This might suggest that ST398-*spa* t571-*SCCmec* V MRSA is a unique clone at farm C-e. However, further studies are needed to rule out any cross-contamination from the farm and slaughterhouse workers.

MRSA strains have multiple antimicrobial resistance patterns. All ST72 MRSA strains from the current study were also resistant to

kanamycin, which is a characteristic of most MRSA strains circulating in Korea (Moon et al., 2015) and Europe (Cortimiglia et al., 2015; Feltrin et al., 2016). The emergence of MRSA strains resistant to multiple classes of antibiotics is a major drawback for chemotherapy. In our study, the ST398 MRSA isolate exhibited additional resistance to non–β-lactam antibiotics, including ciprofloxacin and tetracycline. It has been suggested that tetracycline resistance is a potential phenotypic marker for ST398-A-MRSA isolates (Tegegne et al., 2019). Further, resistance to aminoglycosides and chloramphenicol is frequently reported in ST398 MRSA isolated from pig carcasses in Korea (Moon et al., 2015; Moon et al., 2019). These antibiotics are frequently used to treat infectious diseases in ruminants in Korea (APQA, 2016). Accordingly, the MDR-ST398 MRSA identified in the current study may have arisen in response to selection pressure from several antimicrobials.

Multiple studies suggest the possibility of MRSA transmission between humans and animals. ST398 MRSA human carriage following frequent contact with positive animals has been reported in Korea (Moon et al., 2019) and other countries (Fluit, 2012; Verkade et al., 2012). Loncaric et al. (2013) demonstrated a possible goat-to-human transmission of ST398-*spa* t011-*SCCmec* type V MRSA. Cortimiglia et al. (2015) and Stastkova et al. (2009) have suggested ST398 MRSA transmission from goat to human, or vice versa. Hence, ST398-*spa* t571-*SCCmec* V MRSA could be transmitted to humans following frequent exposure to livestock, as well as through the food chain.

Our data were based on a relatively small number of samples collected over a short time period. Therefore, additional studies with a larger number of samples collected over an extended period of time should be performed in the future. Nonetheless, our study is unique in that it is the first report of antimicrobial resistance profiles of *S. aureus* isolates from Korean goats, with an ensuing molecular characterization of the identified MRSA. The obtained findings are important not only for food safety purposes but also to contribute in increasing knowledge regarding the antimicrobial resistance in livestock, that is essential, in the context of the “One Health” approach, to the development of policies and guidelines to tackle antimicrobial resistance (White and Hughes, 2019).

In conclusion, our study showed that goats can act as the reservoir of toxigenic strains of MRSA that are resistant to multiple antimicrobials, including those ranked as medically important. Therefore, frequent screening of goats, farmers, farm and slaughterhouse environments, and thorough cooking of goat meat should be implemented to detect the emergence and persistence of pathogenic *S. aureus* strains, to prevent the dissemination to humans.

Supplementary data to this article can be found online at https://doi.org/10.1016/j.ijfoodmicro.2020.108901.

Funding

This work was supported by the Animal and Plant Quarantine Agency, Ministry of Agriculture, Food and Rural Affairs, South Korea (B-1543081-2020-22-02). The sponsor did not play any role in study design; in the collection, analysis, and interpretation of data; in the writing of the report; or in the decision to submit the article for publication.

Declaration of competing interest

None.

Acknowledgments

Not applicable.

References

Adesiji, Y., Alli, O., Adekanle, M., Jolayemi, J., 2011. Prevalence of *Arcobacter*, *Escherichia coli*, *Staphylococcus aureus* and *Salmonella* species in retail raw chicken, pork, beef and goat meat in Osogbo. Nigeria. Sierra Leone J. Biomed. Res. 3, 8–12.

Adzitey, F., Huda, N., Ali, G.R.R., 2013. Molecular techniques for detecting and typing of bacteria, advantages and application to foodborne pathogens isolated from ducks. Biotech. 3, 97–107.

APQA, 2016. Animal and Plant Quarantine Agency. Korean Veterinary Antimicrobial Resistance Monitoring System. Gimcheon, Korea, APQA.

Aras, Z., Aydin, I., Kav, K., 2012. Isolation of methicillin-resistant *Staphylococcus aureus* from caprine mastitis cases. Small Rumin. Res. 102, 68–73.

Back, S.H., Eom, H.S., Lee, H.H., Lee, G.Y., Park, K.T., Yang, S.J., 2020. Livestock-associated methicillin-resistant *Staphylococcus aureus* in Korea: antimicrobial resistance and molecular characteristics of LA-MRSA strains isolated from pigs, pig farmers, and farm environment. J. Vet. Sci. 21, e2.

Bae, E., Kim, C.K., Jang, J.H., Sung, H., Choi, Y.M., Kim, M.N., 2019. Impact of community-onset methicillin-resistant *Staphylococcus aureus* on *Staphylococcus aureus* bacteremia in a central Korea veterans health service hospital. Ann. Lab. Med. 39, 158–166.

Boye, K., Bartels, M.D., Andersen, I.S., Møller, J.A., Westh, H., 2007. A new multiplex PCR for easy screening of methicillin-resistant *Staphylococcus aureus* SCC mec types I-V. Clin. Microbiol. Infect. 13, 725–727.

Chang, Q., Wang, W., Regev-Yochay, G., Lipsitch, M., Hanage, W.P., 2015. Antibiotics in agriculture and the risk to human health: how worried should we be? Evol. Appl. 8, 240.

Chu, C., Yu, C., Lee, Y., Su, Y., 2012. Genetically divergent methicillin-resistant *Staphylococcus aureus* and sec-dependent mastitis of dairy goats in Taiwan. BMC Vet. Res. 8, 39.

CLSI, 2018. Clinical and Laboratory Standards Institute. Performance Standards for Antimicrobial Susceptibility Testing; Twentieth Informational Supplement. CLSI document M100. Wayne, PA.

Conceicao, T., De Lencastre, H., Aires-De-Sousa, M., 2017. Frequent isolation of methicillin-resistant Staphylococcus aureus (MRSA) ST398 among healthy pigs in Portugal. PLoS One 12, 0175340.

Cortimiglia, C., Bianchini, V., Franco, A., Caprioli, A., Battisti, A., Colombo, L., Stradiotto, K., Vezzoli, F., Luini, M., 2015. Short communication: prevalence of *Staphylococcus aureus* and methicillin-resistant *S. aureus* in bulk tank milk from dairy goat farms in Northern Italy. J. Dairy Sci. 98, 2307–2311.

Cosgrove, S.E., 2006. The relationship between antimicrobial resistance and patient outcomes: mortality, length of hospital stay, and health care costs. Clin. Infect. Dis. 42, 82–89.

Cuny, C., Kock, R., Witte, W., 2013. Livestock associated MRSA (LA-MRSA) and its relevance for humans in Germany. Int. J. Med. Microbiol. 303, 331–337.

De-Boer, E., Zwartkruis-Nahuis, J.T.M., Wit, B., Huijsdens, X.W., de Neeling, A.J., Bosch, T., van Oosterom, R.A.A., Vila, A., Heuvelink, A.E., 2009. Prevalence of methicillin-resistant *Staphylococcus aureus* in meat. Int. J. Food Microbiol. 134, 52–56.

Denis, O., Suetens, C., Hallin, M., Catry, B., Ramboer, I., Dispas, M., Willems, G., Gordts, B., Butaye, P., Struelens, M.J., 2009. Methicillin-resistant *Staphylococcus aureus* ST398 in swine farm personnel. Belgium. Emerg. Infect. Dis. 15, 1098–1101.

Dewey-Mattia, D., Manikonda, K., Hall, A.J., Wise, M.E., Crowe, S.J., 2018. Surveillance for foodborne disease outbreaks-United States, 2009–2015. Surveill. Summ. 67, 1–11.

EFSA., 2019. European Food Safety Authority and European Centre for Disease Prevention and Control. The European Union One Health 2018 Zoonoses Report. EFSA J. 17, 5926.

El-Deeb, W., Fayez, M., Elmoslemany, A., Kandeel, M., Zidan, K., 2018. Methicillin-resistant *Staphylococcus aureus* among goat farms in Eastern province, Saudi Arabia: prevalence and risk factors. Prev. Vet. Med. 156, 84–90.

Enright, M.C., Day, N.P.J., Davies, C.E., Peacock, S.J., Spratt, B.G., 2000. Multilocus sequence typing for characterization of methicillin-resistant and methicillin-susceptible clones of *Staphylococcus aureus*. J. Clin. Microbiol. 38, 1008–1015.

EUCAST, 2018. European Committee on Antimicrobial Susceptibility Testing. Breakpoint Tables for Interpretation of MICs and Zone Diameters. available at: http://www.eucast.org, Version 8.1.

FAO, 2019. Regional antimicrobial resistance and surveillance guidelines. Monitoring and Surveillance of Antimicrobial Resistance in Bacteria From Healthy Food Animals Intended for Consumption. FAO. 1, 63–68.

Feltrin, F., Alba, P., Kraushaar, B., Ianzano, A., Argudín, M.A., Di Matteo, P., Porrero, M.C., Aarestrup, F.M., Butaye, P., Franco, A., Battisti, A., 2016. A livestock-associated, multidrug-resistant, methicillin-resistant *Staphylococcus aureus* clonal complex 97 lineage spreading in dairy cattle and pigs in Italy. Appl. Environ. Microbiol. 82, 816–821.

Fluit, A.C., 2012. Livestock-associated *Staphylococcus aureus*. Clin. Microbiol. Infect. 18, 735–744.

Fox, A., Pichon, B., Wilkinson, H., Doumith, M., Hill, R.L.R., McLauchlin, J., Kearns, A.M., 2017. Detection and molecular characterization of livestock-associated MRSA in raw meat on retail sale in North West England. Lett. Appl. Microbiol. 64, 239–245.

Harmsen, D., Claus, Heike, Witte, W., Rothgänger, J., Claus, Hermann, Turnwald, D., Vogel, U., 2003. Typing of methicillin-resistant *Staphylococcus aureus* in a university hospital setting by using novel software for *spa* repeat determination and database management. J. Clin. Microbiol. 41, 5442–5448.

Hau, S.J., Frana, T., Sun, J., Davies, P.R., Nicholson, T.L., 2017. Zinc resistance within swine-associated methicillin-resistant *Staphylococcus aureus* isolates in the United States is associated with multilocus sequence type lineage. Appl. Environ. Microbiol. 83, e00756-17.

Hong, S.N., Kim, J., Sung, H.H., 2018. Differences in the antibiotic resistance pattern of *Staphylococcus aureus* isolated by clinical specimens in a university hospital in South Korea. Korean J. Clin. Lab. Sci. 50, 85–92.
Huber, H., Koller, S., Giezendanner, N., Stephan, R., Zweifel, C., 2009. Prevalence and characteristics of methicillin-resistant *Staphylococcus aureus* in humans in contact with farm animals, in livestock, and in food of animal origin. Switzerland. Euro Surveill. 15, 1–4.
Jorgensen, H.J., Mork, T., Hogasen, H.R., Rorvik, L.M., 2005. Enterotoxigenic *Staphylococcus aureus* in bulk milk in Norway. J. Appl. Microbiol. 99, 158–166.
Kim, H.J., Choi, Q., Kwon, G.C., Koo, S.H., 2019. Molecular epidemiology and virulence factors of methicillin-resistant *Staphylococcus* aureus isolated from patients with bacteremia. J. Clin. Lab. Anal. 00, e23077.
Klimesova, M., Manga, I., Nejeschlebová, L., Horáček, J., Ponížil, A., Vondrušková, E., 2017. Occurrence of *Staphylococcus aureus* in cattle, sheep, goat, and pig rearing in the Czech Republic. Acta Vet. Brno. 86, 3–10.
KOSIS., 2019. Korean Statistical Information service. Available at: http://kosis.kr Accessed date 2020/01/04.
Kwon, N.H., Park, K.T., Jung, W.K., Youn, H.Y., Lee, Y., Kim, S.H., Bae, W., Lim, J.Y., Kim, J.Y., Kim, J.M., Hong, S.K., Park, Y.H., 2006. Characteristics of methicillin-resistant *Staphylococcus aureus* isolated from chicken meat and hospitalized dogs in Korea and their epidemiological relatedness. Vet. Microbiol. 117, 304–312.
Lee, M.J., Song, K.Y., Lee, W.C., Chon, J.W., Kim, H., Jeong, J., Bae, D., Seo, K.H., 2019. Epidemiological aspects of pathogenic microbial foodborne disease outbreaks in Korea and Japan from 2011 to 2015. J. Prev. Vet. Med. 43, 62–67.
Lim, S.K., Nam, H.M., Park, H.J., Lee, H.S., Choi, M.J., Jung, S.C., Lee, J.Y., Kim, Y.C., Song, S.W., Wee, S.H., 2010. Prevalence and characterization of methicillin-resistant *Staphylococcus aureus* in raw meat in Korea. J. Microbiol. Biotechnol. 20, 775–778.
Lim, S.K., Nam, H.M., Jang, G.C., Lee, H.S., Jung, S.C., Kwak, H.S., 2012. The first detection of methicillin-resistant *Staphylococcus aureus* ST398 in pigs in Korea. Vet. Microbiol. 155, 88–92.
Lira, M.C., Givisiez, P.E.N., de Sousa, F.G.C., Magnani, M., de Souza, E.L., Spricigo, D.A., Gebreyes, W.A., de Oliveira, C.J.B., 2016. Biofilm-forming and antimicrobial resistance traits of Staphylococci isolated from goat dairy plants. J. Infect. Dev. Ctries. 10, 932–938.
Liu, C., Yoon, E.J., Kim, D., Shin, J.H., Shin, J.H., Shin, K.S., Kim, Y.A., Uh, Y., Kim, H.S., Kim, Y.R., Jeong, S.H., 2019. Antimicrobial resistance in South Korea: a report from the Korean global antimicrobial resistance surveillance system (Kor-GLASS) for 2017. J. Infect. Chemother. 25, 845–859.
Loncaric, I., Brunthaler, R., Spergser, J., 2013. Suspected goat-to-human transmission of methicillin-resistant *Staphylococcus aureus* sequence type 398. J. Clin. Microbiol. 51, 1625–1626.
Luo, Q., Li, S., Liu, S., Tan, H., 2017. Foodborne illness outbreaks in China, 2000–2014. Int. J. Clin. Exp. Med. 10, 5821–5831.
Mama, O.M., Gómez-Sanz, E., Ruiz-Ripa, L., Gómez, P., Torres, C., 2019. Diversity of Staphylococcal species in food-producing animals in Spain, with detection of PVL-positive MRSA ST8 (USA300). Vet. Microbiol. 233, 5–10.
Mason, W.J., Blevins, J.S., Beenken, K., Wibowo, N., Ojha, N., Smeltzer, M.S., 2001. Multiplex PCR protocol for the diagnosis of Staphylococcal infection. J. Clin. Microbiol. 39, 3332–3338.
McDougal, L.K., Steward, C.D., Killgore, E.G., Chaitram, J.M., McAllister, S.K., Tenover, F.C., 2003. Pulse-field gel electrophoresis typing of oxacillin-resistant *Staphylococcus aureus* isolates from the United States. Establishing a national database. *J. Clin. Microbiol.* 41, 5113–5120.
Miranda, J.M., Mondragón, A., Vázquez, B.I., Fente, C.A., Cepeda, A., Franco, C.M., 2009. Influence of farming methods on microbiological contamination and prevalence of resistance to antimicrobial drugs in isolates from beef. Meat Sci. 82, 284–288.
Moon, J.S., Lee, A.R., Kang, H.M., Lee, E.S., Kim, M.N., Paik, Y.H., Park, Y.H., Joo, Y.S., Koo, H.C., 2007. Phenotypic and genetic antibiogram of methicillin-resistant Staphylococci isolated from bovine mastitis in Korea. J. Dairy Sci. 90, 1176–1185.
Moon, D.C., Tamang, M.D., Nam, H.M., Jeong, J.H., Jang, G.C., Jung, S.C., Park, Y.H., Lim, S.K., 2015. Identification of livestock-associated methicillin-resistant *Staphylococcus aureus* isolates in Korea and molecular comparison between isolates from animal carcasses and slaughterhouse workers. Foodborne Pathog. Dis. 12, 327–334.
Moon, D.C., Jeong, S.K., Hyun, B.H., Lim, S.K., 2019. Prevalence and characteristics of methicillin-resistant *Staphylococcus aureus* isolates in pigs and pig farmers in Korea. Foodborne Pathog. Dis. 16, 256–261.
Mork, T., Kvitle, B., Mathisen, T., Jorgensen, H.J., 2010. Bacteriological and molecular investigations of *Staphylococcus aureus* in dairy goats. Vet. Microbiol. 141, 134–141.
Muehlherr, J.E., Zweifel, C., Corti, S., Blanco, J.E., Stephan, R., 2003. Microbiological quality of raw goat's and ewe's bulk-tank milk in Switzerland. J. Dairy Sci. 86, 3849–3856.
Nam, H.M., Lee, A.L., Jung, S.C., Kim, M.N., Jang, G.C., Wee, S.H., Lim, S.K., 2011. Antimicrobial susceptibility of *Staphylococcus aureus* and characterization of methicillin-resistant *Staphylococcus aureus* isolated from bovine mastitis in Korea. Foodborne Pathog. Dis. 8, 231–238.
Odetokun, I.A., Ballhausen, B., Adetunji, V.O., Ghali-Mohammed, I., Adelowo, M.T., Adetunji, S.A., Fetsch, A., 2018. *Staphylococcus aureus* in two municipal abattoirs in Nigeria: risk perception, spread, and public health implications. Vet. Microbiol. 216, 52–59.
Qian, W., Shen, L., Li, X., Wang, T., Liu, M., Wang, W., Fu, Y., Zeng, Q., 2019. Epidemiological characteristics of *Staphylococcus aureus* in raw goat milk in Shaanxi Province. China. Antibiotics. 8, 141.
Sahibzada, S., Abraham, S., Coombs, G.W., Pang, S., Hernandez-Jover, M., Jordan, D., Heller, J., 2017. Transmission of highly virulent community-associated MRSA ST93 and livestock-associated MRSA ST398 between humans and pigs in Australia. Sci. Rep. 7, 5273.
Sakwinska, O., Giddey, M., Moreillon, M., Morisset, D., Waldvogel, A., Moreillon, P., 2011. *Staphylococcus aureus* host range and human-bovine host shift. Appl. Environ. Microbiol. 77, 5908–5915.
Song, J.H., Hsueh, P.R., Chung, D.R., Ko, K.S., Kang, C.I., Peck, K.R., Yeom, J.S., Kim, S.W., Chang, H.H., Kim, Y.S., Jung, S.I., Son, J.S., Man-Kit So, T., Lalitha, M.K., Yang, Y., Huang, S.G., Wang, H., Lu, Q., Carlos, C.C., Perera, J.A., Chiu, C.H., Liu, J.W., Chongthaleong, A., Thamlikitkul, V., Hung Van, P., 2011. Spread of methicillin-resistant *Staphylococcus aureus* between the community and the hospitals in Asian countries: an ANSORP study. J. Antimicrob. Chemother. 66, 1061–1069.
Song, J.W., Yang, S.J., Shin, S., Seo, K.S., Park, Y.H., Park, K.T., 2016. Genotypic and phenotypic characterization of methicillin-resistant *Staphylococcus aureus* isolated from bovine mastitic milk in Korea. J. Food Prot. 79, 1725–1732.
Sorensen, A.I.V., Toft, N., Boklund, A., Espinosa-Gongora, C., Græsbøll, K., Larsen, J., Halasa, T., 2017. A mechanistic model for spread of livestock-associated methicillin-resistant *Staphylococcus aureus* (LA-MRSA) within a pig herd. PLoS One 12, 0188429.
Spanu, V., Scarano, C., Virdis, S., Melito, S., Spanu, C., De Santis, E.P.L., 2013. Population structure of *Staphylococcus aureus* isolated from bulk tank goat's milk. Foodborne Pathog. Dis. 10, 310–315.
Stastkova, Z., Karpiskova, S., Karpiskova, R., 2009. Occurrence of methicillin-resistant strains of *Staphylococcus aureus* at a goat breeding farm. Vet. Med. (Praha). 54, 419–426.
Tegegne, H.A., Koláčková, I., Florianová, M., Gelbíčová, T., Wattiau, P., Boland, C., Karpíšková, R., 2019. Genome sequences of livestock-associated methicillin-resistant *Staphylococcus aureus spa* type t899 strains belonging to three different sequence types (ST398, ST9, and ST4034). Microbiol. Resour. Announc. 8, e01351-18.
Van Duijkeren, E., Ikawaty, R., Broekhuizen-Stins, M.J., Jansen, M.D., Spalburg, E.C., de Neeling, A.J., Allaart, J.G., van Nes, A., Wagenaar, J.A., Fluit, A.C., 2008. Transmission of methicillin-resistant *Staphylococcus aureus* strains between different kinds of pig farms. Vet. Microbiol. 126, 383–389.
Verkade, E., Bergmans, A.M.C., Budding, A.E., van Belkum, A., Savelkoul, P., Buiting, A.G., Kluytmans, J., 2012. Recent emergence of *Staphylococcus aureus* clonal complex 398 in human blood cultures. PLoS One 7, 0041855.
Virdis, S., Scarano, C., Cossu, F., Spanu, V., Spanu, C., De Santis, E.P.L., 2010. Antibiotic resistance in *Staphylococcus aureus* and coagulase-negative *Staphylococci* isolated from goats with subclinical mastitis. Vet. Med. Int. 2010, 517060.
Wang, X., Li, G., Xia, X., Yang, B., Xi, M., Meng, J., 2014. Antimicrobial susceptibility and molecular typing of methicillin-resistant *Staphylococcus aureus* in retail foods in Shaanxi. China. Foodborne Pathog. Dis. 11, 281–286.
Wendlandt, S., Kadlec, K., Febler, A.T., Monecke, S., Ehricht, R., Van De Giessen, A.W., Hengeveld, P.D., Huijsdens, X., Schwarz, S., Van Duijkeren, E., 2013. Resistance phenotypes and genotypes of methicillin-resistant *Staphylococcus aureus* isolates from broiler chickens at slaughter and abattoir workers. J. Antimicrob. Chemother. 68, 2458–2463.
White, A., Hughes, J.M., 2019. Critical importance of a One Health approach to antimicrobial resistance. EcoHealth. 16, 404–409.
Yamada, T., Tochimaru, N., Nakasuji, S., Hata, E., Kobayashi, H., Eguchi, M., Kaneko, J., Kamio, Y., Kaidoh, T., Takeuchi, S., 2005. Leukotoxin family genes in *Staphylococcus aureus* isolated from domestic animals and prevalence of *lukM-lukF-PV* genes by bacteriophages in bovine isolates. Vet. Microbiol. 110, 97–103.