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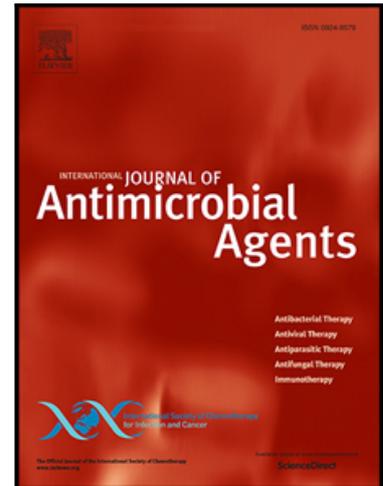
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Detection and characterization of methicillin resistant and susceptible coagulase-negative Staphylococci in milk from cows with clinical mastitis in Tunisia.

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**Highlights**

- Detection of different species of SCN implicated in milk mastitis with predominance of *S. xylosum*.
- MR-CNS isolates harboring *mecA* gene with different resistance genes for erythromycin and tetracycline.
- SCC*mec* type-Iva and recombinase genes *ccrA2/B2* -class B *mec* gene complex were detected in MRSE.
- Low resistance rate in MS-SCN with some resistance gene for erythromycin and tetracycline.
- *tst* genes responsible for toxic shock syndrome is detected only in one methicillin resistant strain.

**Detection and characterization of methicillin resistant and susceptible coagulase-negative Staphylococci in milk from cows with clinical mastitis in Tunisia.**

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## Abstract

The prevalence of methicillin-resistant (MR) and methicillin-susceptible (MS) coagulase-negative staphylococci (CNS) and the implicated mechanisms of resistance and virulence were investigated in milk of mastitis cows. In addition the presence of SCC<sub>mec</sub> type is analyzed in MR *Staphylococcus epidermidis* (MRSE). Three hundred milk samples from bovine with clinical mastitis were obtained from 30 dairy farms in different regions of Tunisia. Sixty-eight of the 300 tested samples contained CNS strains. Various CNS species were identified, being *S. xylosus* the most frequently found (40%), followed by *S. warneri* (12%). The *mecA* gene was present in 14 of 20 MR-CNS isolates. All of them lacking the *mecC* gene. The SCC<sub>mecIVa</sub> was identified in four MRSE isolates. Most of CNS isolates showed penicillin resistance (70.6%) and 58.3% of them carried the *blaZ* gene. MR-CNS isolates (n=20) showed resistance to erythromycin, tetracycline and trimethoprim-sulfamethoxazole harboring different resistance genes such as *erm(B)*, *erm(T)*, *erm(C)*, *mph(C)* or *msr(A)*, *tet(K)* and *dfr(A)* genes. However, a lower percentage of resistance was observed among 48 MS-CNS isolates: erythromycin (8.3%), tetracycline (6.2%), streptomycin (6.2%), clindamycin (6.2%), and trimethoprim-sulfamethoxazole (2%). The *Inu(B)* gene was detected in one *S. xylosus* strain which showed clindamycin-resistance. The virulence gene *tsst-1* was observed in one MR-CNS strain. CNS containing a diversity of antimicrobial resistance genes are frequently detected in milk of mastitis cows. This fact emphasizes the importance of identification of CNS when an intramammary infection is present because of the potential risk of lateral transfer of resistant genes among staphylococcal species and other pathogenic bacteria.

**Keywords:** MR-CNS, MS-CNS, resistance and virulence genes, *mecA*, *SCCmec* MRSE, bovine mastitis.

## 1. Introduction

Coagulase-negative staphylococci (CNS) play a role as opportunistic nosocomial pathogens in human medicine. They are often involved in foreign body infections and catheter-related infections, but also in urinary tract infections and endocarditis, among others [1]. Nowadays, CNS are of great interest in veterinary medicine because they are currently considered emerging pathogens of bovine mastitis. In dairy farms, mastitis remains an important disease with high economic effect. Among the etiologic agents of mastitis bovine, staphylococci is the main type of microorganisms, with some coagulase-positive species (*S. aureus*) associated with more severe illness than CNS [2]. CNS form a heterogeneous group of over 50 species and subspecies that are traditionally considered to be minor pathogens. However, CNS are increasingly being recognized as an important cause of clinical and subclinical bovine mastitis worldwide [3,4]. These microorganisms can cause persistent infections leading to an increased number of somatic cells, changes in milk composition and reduction of production [3]. The treatment of mastitis by extensive use of antibiotics in dairy cows induce antimicrobial resistance that staphylococci might acquire and is considered one of the main reasons for low cure rate of mastitis [5]. It is known that CNS species tend to be more resistant to antimicrobials than *S. aureus*, and they easily develop multi-resistance [3]. The production of  $\beta$ -lactamase is an important acquired resistance mechanism among bovine CNS which confers resistance to aminopenicillins. Resistance also to aminoglycosides, tetracyclines, and macrolides has been described [6,7]. Interestingly, MR in staphylococci is mainly conferred by the spreading of *mecA* gene that complicate the treatment of the infection related to MR-CNS, representing a public health risk [8]. The *mecA* gene, which encodes

PBP2a, is carried by a mobile genetic element, the staphylococcal cassette chromosome *mec* (SCC*mec*), which contains the *mec* complex genes, its regulators and the *ccr* gene complex, which encodes site-specific recombinases that are responsible for the mobility of the element. In fact, 11 types of SCC*mec* (I–XI) have been defined in *Staphylococcus* isolates [10]. Recently, a new divergent *mecA* homolog (*mecC*) was described in a novel SCC*mec* designated as type XI [10]. Furthermore, *mecA*-positive CNS may act as potential donors for the creation of new MR *Staphylococcus aureus* (MRSA) clones [9]. The pathogenicity of CNS could be associated to the production of several virulence factors such as the enterotoxins, the Panton-Valentine leukocidin (PVL) or the toxic shock syndrome toxin 1 (TSST-1) [3]. Biofilm production, a recognized virulence factor in staphylococci, has been proposed as a significant element in the persistence of bovine intra-mammary infections [11]. Methicillin-resistant staphylococci are increasingly being isolated in bovine mastitis and the use of antimicrobials can be an important tool in the mastitis control programs. The close contact of humans and animals in dairy farms can present a great risk for the transmission of bacteria between animal and human hosts [8]. Therefore, surveillance of antimicrobial resistance and surveillance of CNS is important to minimize the risk for development and spread of antimicrobial resistance and virulence genes. The goal of this study was to determine the incidence of antibiotic resistance and virulence determinants among different species of CNS isolated from cows with clinical mastitis in Tunisia.

## **2. Materials and methods**

### **2.1. Origin of Samples**

Three-hundred milk samples were collected from 300 cows that showed clinical mastitis symptoms (one sample/cow). Samples were obtained of 30 farms with intensive breeding across different regions in North and South of Tunisia, during October 2013 to September 2014. The farms included in this study were involved in the production of milk for self-

consumption, cheese production, and milk bottling. Each cow was clinically diagnosed by the appearance of general clinical signs related to udder and teats and the presence of any of the gross abnormalities such as fibrosis, inflammatory swellings, pain, visible injury or lesion, atrophy of the tissue and teat blindness. The milk sample was observed for changes regarding color, odor and consistency. The presence of clots, flakes, blood and other consistent changes were indicators of clinical mastitis along with udder and teat morphological changes. A milk sample of one infected quarter was obtained from the 300 tested mastitis cows by veterinarians. Before taking the milk samples, teats were washed thoroughly and dried. They were then sprayed with 70% ethanol, the first few squirts of milk were discarded, and 30 ml milk samples were collected in sterile tubes. The milk samples were transferred to the laboratory in cooler and immediately processed. It is important to note that the studied cows did not receive any antibiotic therapy.

### **2.2. Isolation and identification of staphylococcus species**

One ml of each milk sample was suspended in sterile saline solution for serial dilutions and then they were seeded on Baird Parker (BP, Biolife) for *Staphylococcus* recovery. All the plates were incubated at 37 °C for 24-48 h. Isolates with typical staphylococci morphology were selected (one per sample) and identified by classical biochemical methods [Gram staining, oxydase, catalase, DNase, and ability to coagulate rabbit plasma (Bio-Rad)] [12]. The CNS strains were submitted to molecular identification by amplification and sequencing of *sodA* gene [13].

### **2.3. Antimicrobial susceptibility testing**

Antimicrobial susceptibility testing for 15 antimicrobial agents was performed using the disk-diffusion method in accordance with the Clinical and Laboratory Standards Institute (CLSI) recommendations [14]. Antimicrobial agents tested ( $\mu\text{g}/\text{disk}$ ) were as follows: penicillin (10),

oxacillin (1), ceftiofloxacin (30), kanamycin (30), gentamicin (10), tobramycin (10), tetracycline (30), chloramphenicol (30), trimethoprim–sulfamethoxazole (1.25/23.75), erythromycin (15), clindamycin (2), ciprofloxacin (5), vancomycin (30), and teicoplanin (30). Methodology and guidelines for streptomycin (10µg/disk) were as recommended by the European committee on antimicrobial susceptibility testing [15].

#### **2.4. Detection of antimicrobial resistance genes**

Detection of antimicrobial resistance genes was performed by PCR, according to the resistance phenotype [*bla*(Z), *ant*(4)-Ia, *dfr*(A), *catp*C221, *tet*(K), *tet*(M), *tet*(L), *erm*(A), *erm*(B), *erm*(T), *erm*(C), *mph*(C), *lnu*(A), *lnu*(B), *lnu*(C), *vga*(A), *vga*(B), *vga*(C), *msr*(A)/*msr*(B) genes] [16,17].

#### **2.5. Detection of *mecA* and *mecC* genes**

Methicillin-resistance was detected by oxacillin and/or ceftiofloxacin susceptibilities by the disk-diffusion agar according to CLSI, 2015. Confirmation of methicillin resistance was performed by conventional PCR targeting the *mecA* gene [18], and *S. aureus* ATCC 43300 was used as control strain. All *mecA* negative CNS isolates with oxacillin or ceftiofloxacin resistance were tested for the presence of *mecC* gene by PCR [19]. A positive control MRSA strain (C7697) of *mecC* gene from the collection of the University of La Rioja (Logroño, Spain) were used in each PCR assay [19].

#### **2.6. SCC*mec* typing in MRSE isolates**

The presence of SCC*mec* types I to V was investigated in MRSE isolates by PCR of the *ccr* recombinases (1–5) and the *mec* gene complex type (A to C), as recommended by the International Working Group on the Classification of Staphylococcal Cassette Chromosome Elements (IWG-SCC) [20]. An additional PCR was performed to differentiate the subtypes of SCC*mec* IV (a–d) [18].

### ***Detection of staphylococcal toxin genes and biofilm production***

All isolates were tested by PCR for the presence of the toxic shock syndrome toxin 1 (*tsst-1*), leukocidin of Pantone Valentine (PVL, *lukF-lukS-PV*) and exfoliative ETA/ETB toxins (*etA* and *etB* genes). Furthermore, the presence of genes coding for the formation of biofilm (*icaA*, *icaB*) was determined by PCR [21].

## **3. Results**

### **3.1 Distribution of CNS species**

Isolates were collected from milk samples of cows with symptoms of clinical mastitis across different regions in North and South of Tunisia. Of the 300 samples tested, 83 milk samples showed the growth of staphylococci and one isolate per sample was further characterized. Sixty-eight of these strains (82%) were presumptively identified as CNS according to their morphology in BP media. The remaining fifteen staphylococci were identified as *S. aureus* isolates and were previously characterized [22]. The molecular identification by amplification and sequencing of *sodA* gene of the 68 CNS isolates in this study revealed the presence of 11 different species (number of isolates): *S. xylosus* (27), *S. warneri* (8), *S. chromogenes* (6), *S. sciuri* (5), *S. epidermidis* (5), *S. pasteurii* (5), *S. haemolyticus* (4), *S. succinus* (3), *S. equorum* (2), *S. saprophyticus* (2) and *S. cohnii* (1).

### **3.2. Identification of methicillin resistance among CNS isolates**

Screening of MR was performed by oxacillin and/or cefoxitin disc diffusion. Twenty of 68 CNS isolates (29.41%) showed oxacillin and/or cefoxitin resistance and 14 of them carried the *mecA* gene (1 *S. sciuri*, 1 *S. warneri*, 4 *S. epidermidis*, 2 *S. haemolyticus*, 4 *S. pasteurii*, 1 *S. chromogenes*, and 1 *S. cohnii*); the remaining 6 MR-CNS isolates were *mecA* and *mecC* genes negative (all of them were cefoxitin-resistant) (Table 1).

### 3.3. Detection of antimicrobial resistance phenotypes and genotypes in MR-CNS and MS-CNS

Eleven of 20 MR-CNS strains showed erythromycin-resistance and harbored the *erm*(B), *erm*(T), *erm*(C), *mph*(C) or *msr*(A) genes; four strains were tetracycline-resistant (with *tet*(K) gene), and eight strains trimethoprim-sulfamethoxazole-resistant (with *dfr*(A) gene in three of these isolates). The *blaZ* gene was detected in 15/17 MR-CNS. Other resistances detected were as follows: clindamycin (n=14), gentamicin (n=4), ciprofloxacin (n=5), streptomycin (n=6), tobramycin (n=2), and chloramphenicol (n=1). No resistance genes for tetracycline and erythromycin were detected in some of the isolates (Table 1). Ten MR strains showed a resistance to 3 or 4 different antibiotics families.

Concerning the 48 MS-CNS isolates, most of them showed penicillin resistance (31 isolates, 13 of them with *blaZ* gene). Tetracycline resistance was detected in only three strains, encoded by *tetK* gene. Macrolide resistance was noted in four strains with the presence of *erm*(C) (n=2), *erm*(T) (n=1) and *msr*(A) (n=2) genes. It is noted that these three genes are present in one strain. The *Inu*(B) gene was detected in one clindamycin-resistant *S. xylosus* strain.

### 3.4. Detection of virulence genes in CNS isolates

Virulence trait characterization revealed that only one MR-CNS isolate (*mecA*-positive *S. chromogenes*) harbored the virulence gene *tsst-1*, and none of them were positive for enterotoxins, *pvl*, *etA*, *etB* or the *icaA*, *icaB* genes.

### 3.5. Molecular typing of *S. epidermidis* isolates

The SCC*mec* type-IVa was identified in all four MRSE isolates which also exhibited the recombinase genes *ccrA2/B2* -classe B *mec* gene complex.

## 4. Discussion

To the best of our knowledge, there is no published information regarding MR-CNS from bovine mastitis in Tunisia and in Africa. Only very limited data on the prevalence and molecular characterization of MR-CNS isolated from hospital, animals and food are available in Africa (Tunisia, Egypt and Nigeria) [23,24,25]. CNS is an important etiological agent of mastitis in cattle worldwide, including South Africa [26,20,27,3,28]. Staphylococcal species were detected in 27.7% of bovine clinical mastitis milk samples, in most of the cases of the CNS group (82%). Our investigation revealed a high diversity of staphylococcal species among CNS (*S. xylosus*, *S. warneri*, *S. chromogenes*, *S. scuri*, *S. epidermidis*, *S. pasteuri*, *S. haemolyticus*, *S. succinus*, *S. equorum*, *S. saprophyticus* and *S. cohnii*). The CNS species most often isolated in our survey were *S. xylosus* (39.7%) followed by *S. warneri* (11.8%). This observation confirms the previous studies reported by Kot et al. [29] and Bochniarz et al. [30], who showed that *S. xylosus* was the most frequently species isolated of milk samples of bovine mastitis. *S. xylosus* seems to be a versatile organism, but little is known about its epidemiology in mastitis [31]. *S. warneri* was also reported by Klimiene et al. [4], which is the second species isolated and described as a minor pathogen of intra-mammary infection. According to Mork et al. [32], *S. warneri* cannot survive in the udder for a long period of time and thus cannot cause persistent mastitis [33]. A low number of other species was detected, in fact, the distribution of staphylococcal species varies between studies, but *S. chromogenes*, *S. epidermidis*, *S. haemolyticus* and *S. simulans* are commonly found [6]. The resistance to methicillin was confirmed by the presence of the *mecA* gene in 14 isolates, constituting 20.6% of all CNS isolates. Methicillin-resistance among CNS was similar to that found in Poland (20%) and in China (17.1%) [30,27]. However, low percentages of MR-CNS isolates from bovine mastitis was reported in Portugal (9.3%) and Brazil (4.6%) [34,20]. It is important to note that the presence of *mecA* gene has been detected in diverse CNS species (*S. scuri*, *S. warneri*, *S. epidermidis*, *S. haemolyticus*, *S. pasteuri*, *S. chromogenes* and *S.*

*cohnii*), which is similar to what was reported previously [35]. Methicillin-resistant staphylococci have been reported in milk samples from dairy cattle and surveillance of this resistance trait is important for public health and veterinary medicine [36]. *MecA*-positive *S. epidermidis* isolates have been found in this study, a putative zoonotic pathogen; these strains carried the SCC*mec* type-IVa, what is in agreement with the report of Silva et al. [20]. In fact, the relatively smaller size of this cassette (20–24 kb) compared with other types of SCC*mec* may facilitate its transference among staphylococci [10]. However, the presence of MRSE strains in bovine milk samples is a matter of concern as they may act as a reservoir of genetic elements carrying antimicrobial resistance. Because of their mobile nature, the SCC*mec* elements can be transferred to other species of staphylococci including *S. aureus* [37]. A possible mechanism to explain the phenotype of resistance to oxacillin and/or ceftiofur in the absence of the *mecA* gene would be the overproduction of  $\beta$ -lactamase, the production of a new methicillinase, or the change in the penicillin-binding proteins [37]. Our results showed that resistance to penicillin was observed frequently among CNS isolates (n=48) and 28 isolates (58.33%) harbored the *blaZ* gene. The higher prevalence of this gene may be due to the frequent use of penicillin for dairy cow therapy in Tunisia. The *blaZ* gene in CNS isolates from mastitis milk was also reported in Switzerland (90.7%), Lithuania (66%) and China (30.3%) [7,27,4]. MR-CNS isolates showed resistance to other antibiotics such as erythromycin, tetracycline, clindamycin, gentamicin, ciprofloxacin, streptomycin, tobramycin, chloramphenicol and trimethoprim-sulfamethoxazole, and they harbored the *erm*(B), *erm*(T), *erm*(C), *mph*(C), *msr*(A), *tet*(K) or *dfr*(A) genes. On the other hand, the MS-CNS isolates showed susceptibility to the tested antimicrobials, with some exceptions due to the presence of *erm*(B), *erm*(C), *erm*(T), *msr*(A), *mph*(C) and *tet*(K) genes. It's important to note, that tetracycline resistance was encoded only by the *tet*(K) gene in both groups, being this resistance gene very frequent in staphylococci species [29]. According to our study, the

simultaneous presence of two or more macrolide resistance genes in the CNS isolates is well known and has been reported previously in *S. aureus* or in CNS isolates from bovine mastitis [38].

Virulence trait characterization revealed that only one isolate MR-CNS (*S. chromogenes* *mecA* positive) harbored the virulence gene *tsst-1* and none of them were positive for enterotoxins genes, the exfoliative toxin genes (*etA*, *etB*), the intracellular adhesion genes (*icA*, *icB*) and the *lukF-lukS-PV* gene. The presence of enterotoxin and *lukF-lukS-PV* genes in CNS isolated from bovine mastitis has been previously described [12]. Compared to *S. aureus*, only few studies were focused on the prevalence of virulence genes in CNS isolated from cows with mastitis [39,40].

## 5. Conclusion

Antimicrobial resistance in CNS, mainly for beta-lactams and tetracycline, is high in isolates recovered from milk of mastitis cows, what may be caused by the use of these compounds in Tunisian farms. The identification of *Staphylococcus* species and the surveillance of antimicrobial resistance are important to minimize the risk of the spread of antimicrobial resistance but also the possible risk of transmission of these microorganisms between cows and in-contact humans. Moreover, the potential transmission of antibiotic resistance could affect not only to Tunisian cattle breeding but also in neighboring countries across the exportation of milk products or Tunisian breed cows.

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**Declarations**

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**Competing Interests:** No

**Ethical Approval:** The study underwent ethical review and was given approval by the Bio-Medical Ethics Animal Committee at Pasteur Institute of Tunis, ref 2016/16/1/LR11IPT03/V0

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**Table 1** Phenotypes and genotypes of antimicrobial resistance and types of SCC<sub>mec</sub> in MR-CNS recovered from milk samples of clinical mastitis

Strain	species	Resistance to OXA or FOX	<i>mecA</i>	<i>mecC</i>	Resistance phenotype	Resistance genes	Virulence gene	SCC <sub>mec</sub> , class <i>mec</i> , <i>ccr</i> type
EC70	<i>S. scuri</i>	OXA	<i>mecA</i>		ERY, CLI	<i>blaZ</i> , <i>erm(B)</i>	-	
EC186	<i>S. warneri</i>	OXA, FOX	<i>mecA</i>		PEN, CLI, CIP	<i>blaZ</i> ,	-	
EC196	<i>S. epidermidis</i>	OXA, FOX	<i>mecA</i>		PEN, TET, SXT	<i>blaZ</i> , <i>dfr(A)</i>	-	IVa, (B, <i>ccrA2/B2</i> )
EC201	<i>S. epidermidis</i>	OXA, FOX	<i>mecA</i>		PEN, ERY, SXT	<i>blaZ</i> , <i>msr(A)</i> , <i>dfr(A)</i>	-	IVa, (B, <i>ccrA2/B2</i> )
EC207	<i>S. epidermidis</i>	OXA, FOX	<i>mecA</i>		PEN, ERY, TET, GEN, TOB, STR, SXT, CIP	<i>blaZ</i> , <i>erm(T)</i>	-	IVa, (B, <i>ccrA2/B2</i> )
EC134	<i>S. epidermidis</i>	OXA, FOX	<i>mecA</i>		PEN, ERY, CLI, TET, GEN, SXT, CIP	<i>blaZ</i> , <i>tet(K)</i>	-	IVa, (B, <i>ccrA2/B2</i> )
EC200	<i>S. haemolyticus</i>	OXA, FOX	<i>mecA</i>		PEN, ERY, CLI, TET, GEN, CIP,STR,SXT,CHL	<i>blaZ</i> , <i>msr(A)</i> , <i>tet(K)</i> , <i>erm(C)</i> , <i>dfr(A)</i>	-	
EC195	<i>S. haemolyticus</i>	OXA, FOX	<i>mecA</i>		PEN, ERY, CLI, GEN, SXT, CIP, TOB, TET	<i>blaZ</i> , <i>tet(K)</i>	-	
EC 6	<i>S. pasteurii</i>	OXA, FOX	<i>mecA</i>		PEN, ERY, CLI, STR, SXT, TET	<i>blaZ</i> , <i>msr(A)</i> , <i>tet(K)</i>	-	
EC84	<i>S. pasteurii</i>	OXA, FOX	<i>mecA</i>		PEN, ERY, CLI, STR, SXT	<i>blaZ</i>	-	
EC53	<i>S. pasteurii</i>	OXA, FOX	<i>mecA</i>		PEN, STR	<i>blaZ</i>	-	
EC199	<i>S. pasteurii</i>	OXA	<i>mecA</i>		-	-	-	
EC39	<i>S. chromogenes</i>	OXA	<i>mecA</i>		-	-	<i>tsst-1</i>	
EC60	<i>S. cohnii</i>	OXA, FOX	<i>mecA</i>		PEN, CLI	<i>blaZ</i>	-	
EC22.1	<i>S. xylosus</i>	OXA, FOX	-	-	PEN, CLI, ERY	<i>blaZ</i> , <i>erm(B)</i> , <i>msr(A)</i>	-	
EC119	<i>S. xyosus</i>	OXA, FOX	-	-	PEN, CLI, ERY	<i>mph(C)</i>	-	
EC104	<i>S. scuri</i>	OXA, FOX	-	-	PEN, ERY, CLI	<i>blaZ</i> , <i>erm(T)</i> , <i>,msr(A)</i>	-	
EC136	<i>S. warneri</i>	OXA, FOX	-	-	PEN, CLI	-	-	
EC161	<i>S. warneri</i>	OXA, FOX	-	-	PEN, CLI, STR	-	-	
EC193	<i>S. equorum</i>	OXA, FOX	-	-	PEN, CLI	<i>blaZ</i>	-	
<b>Total</b>	20		14	0				

OXA oxacillin, FOX cefoxitin, PEN penicillin, STR streptomycin, TET tetracycline, CLI clindamycin, ERY erythromycin, TOB tobramycin, GEN gentamicin, CIP: ciprofloxacin, SXT trimethoprim-sulfamethoxazole, CHI chloramphenicol, *tst-1*: toxic shock syndrome toxin 1 gene

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**Table 2** Antimicrobial resistance phenotype and genotype of MS-CNS recovered from milk samples of clinical mastitis in Tunisia.

Strain	Species	Phenotype resistance	Resistance gene detected	Virulence gene detected
EC15	<i>S. xylosus</i>	TET	<i>tet(K)</i>	-
EC16	<i>S. xylosus</i>	PEN	<i>blaZ</i>	-
EC19.1	<i>S. xylosus</i>	PEN	-	-
EC27	<i>S. xylosus</i>	PEN	-	-
EC29.1	<i>S. xylosus</i>	PEN	-	-
EC31.1	<i>S. xylosus</i>	PEN	-	-
EC31.2	<i>S. xylosus</i>	PEN, STR	<i>blaZ</i>	-
EC32	<i>S. xylosus</i>	PEN	-	-
EC43	<i>S. xylosus</i>	PEN	<i>blaZ</i>	-
EC55	<i>S. xylosus</i>	PEN	-	-
EC105	<i>S. xylosus</i>	PEN, ERY	<i>blaZ</i>	-
EC106	<i>S. xylosus</i>	PEN	-	-
EC45	<i>S. xylosus</i>	PEN	<i>blaZ</i>	-
EC165	<i>S. xylosus</i>	PEN	-	-
EC150	<i>S. xylosus</i>	PEN	-	-
EC157.1	<i>S. xylosus</i>	PEN, CLI	<i>blaZ, Inu(B)</i>	-
EC157.2	<i>S. xylosus</i>	PEN	-	-
EC162	<i>S. xylosus</i>	PEN	<i>blaZ</i>	-
EC163	<i>S. xylosus</i>	PEN	-	-
EC172	<i>S. xylosus</i>	-	-	-
EC177	<i>S. xylosus</i>	PEN, STR, SXT	<i>blaZ</i>	-
EC195	<i>S. xylosus</i>	PEN	<i>blaZ</i>	-
EC199	<i>S. xylosus</i>	PEN	-	-
EC205	<i>S. xylosus</i>	PEN	-	-
EC209	<i>S. xylosus</i>	PEN	<i>blaZ</i>	-
EC68	<i>S. scuri</i>	PEN	-	-
EC78	<i>S. scuri</i>	-	-	-
EC99	<i>S. scuri</i>	PEN	-	-
EC10	<i>S. warneri</i>	PEN, ERY, CLI	<i>blaZ, erm(C), msr(A)</i>	-
EC12	<i>S. warneri</i>	ERY, CLI	<i>erm(C), msr(A), erm(T)</i>	-
EC23	<i>S. warneri</i>	-	-	-
EC93	<i>S. warneri</i>	-	-	-
EC103	<i>S. warneri</i>	-	-	-
EC17	<i>S. epidermidis</i>	PEN, STR, TET	<i>blaZ, tet(K)</i>	-
EC24	<i>S. heamolitycus</i>	-	-	-
EC101	<i>S. heamolitycus</i>	-	-	-
EC19.2	<i>S. chromogenes</i>	-	-	-
EC72	<i>S. chromogenes</i>	-	-	-
EC155.1	<i>S. chromogenes</i>	ERY	-	-
EC155.2	<i>S. chromogenes</i>	-	-	-
EC187	<i>S. chromogenes</i>	-	-	-
EC34	<i>S. saprophyticus</i>	PEN	-	-
EC212	<i>S. saprophyticus</i>	-	-	-
EC52	<i>S. succinus</i>	PEN	-	-
EC64	<i>S. succinus</i>	PEN	<i>blaZ</i>	-
EC191	<i>S. succinus</i>	PEN	-	-
EC208	<i>S. pasteurii</i>	-	-	-
EC102.1	<i>S. equorum</i>	TET	<i>tet(K)</i>	-

PEN penicillin, STR streptomycin, TET tetracycline, CLI clindamycin, ERY erythromycin,

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