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Molecular characterization of methicillin-resistant *Staphylococcus schleiferi* isolated from canine skin in Korea

한국의 개의 피부에서 분리된 메티실린 내성 *Staphylococcus schleiferi*의 분자학적 특성

2018 년 2 월

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수의학과 임상수의학(피부과학)전공
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이 논문을 수의학석사학위논문으로 제출함

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Molecular characterization of methicillin-resistant *Staphylococcus schleiferi* isolated from canine skin in Korea

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Abstract

Staphylococcus schleiferi can cause infections in dogs and humans, and the methicillin resistance of *S. schleiferi* makes it a particularly

large threat to public health. This study was conducted molecular characterization and the antimicrobial susceptibility of *S. schleiferi* from dogs in Korea and compared the results with those from other countries.

We collected 185 staphylococcal isolates from canine pyoderma and otitis externa. Staphylococci were identified using the microbiology identification system and PCR. Antibiotic susceptibility data were collected using the disk diffusion method, and the SCC*mec* type and direct repeat unit (*dru*) was determined by PCR.

S. schleiferi was the second most prevalent species (17/185, 9.2%). Seven methicillin-resistant *S. schleiferi* (MRSS) (7/17, 41.1%) isolates were detected and confirmed as SCC*mec* type V which is the most prevalent type in MR *Staphylococcus pseudintermedius* from veterinary staff and animals in Korea. *mec*-associated *dru* typing revealed two *dru* types (dt): dt11a and dt9bd. The dt11a type, which is usually observed in *Staphylococcus pseudintermedius*, was found in six MRSS isolates (85.7%), and one isolate was dt9bd type.

This study is the first report on SCC*mec* and *dru* typing of *S. schleiferi* in Korea. SCC*mec* typing and antimicrobial susceptibility tests revealed that MRSS is disseminating and causing skin infections in dogs in Korea. SCC*mec* typing results were the same as those reported in Thailand, but different from those in the USA (SCC*mec* type IV) and India (SCC*mec* type I). The result of SCC*mec* type and *dru* type(dt) 11a suggest that methicillin resistance in MRSS varies with geographical location and have close correlation with

Staphylococcus pseudintermedius. Our results provide important insights into the characteristic and molecular genetics of MRSS strains in Korea and may aid in the monitoring of MRSS spread throughout the country.

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keywords : methicillin-resistant *Staphylococcus schleiferi*,MRSS, antimicrobial susceptibility, SCC*mec*, *dru*-typing, Korea
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CONTENTS

Introduction

Staphylococcus schleiferi was firstly reported from human specimens in 1988 by Freney et al. [1]. However, after the original report about *S. schleiferi* subsp. *coagulans* from canine otitis [2], the species was divided into two subspecies—coagulase-positive (subsp. *coagulans*) and coagulase-negative (subsp. *schleiferi*)—where the two subspecies are defined on the basis of the results of a tube coagulase test. Since then, *S. schleiferi* subsp. *coagulans* has been isolated from several other infection sites in dogs, and *S. schleiferi* subsp. *schleiferi* has been reported as the causative agent of invasive infections such as endocarditis, post-surgical infections, and bacteremia in humans [3-5]. *S. schleiferi* is also a known natural inhabitant of the skin of healthy dogs [6, 7]. Reports on *S. schleiferi* infections have increased in both humans and veterinary medicine [8]. Cross-species transmission of *S. schleiferi* between humans and dogs has therefore been suspected [3, 5, 9].

Methicillin resistance in staphylococcal species has increased substantially in both humans and veterinary medicine in the past decade [10]. This, in addition to the limited antimicrobial treatment options and the potential of zoonotic transmission, makes methicillin-resistant staphylococci a serious public health concern. Methicillin is a semi-synthetic penicillinase-resistant penicillin that was developed to overcome the penicillin resistance mediated by staphylococcal penicillinases [11]. However, soon after the introduction

of methicillin in human medicine, *Staphylococcus aureus* developed resistance to it by acquisition of the *mec*A gene, which codes for a specific penicillin-binding protein (PBP2a) that confers resistance to all β-lactams [11, 12]. Detection of the PBP2a antigen using latex agglutination or detection of the *mecA* gene using PCR provides definitive evidence of methicillin resistance in *Staphylococcus* spp [13].

The *mec*A gene is located within the mobile genetic element, staphylococcal cassette chromosome *mec* (SCC*mec*), which acts as a vehicle for the horizontal transfer of antibiotic resistance genes to other staphylococci [14, 15]. Each SCC*mec* type is associated with a different antibiotic resistance pattern, and the distribution of SCC*mec* types varies depending on the host species and the geographical location [14]. Molecular characterization by SCC*mec* typing of methicillin-resistant *S. schleiferi* (MRSS) is an essential epidemiological tool for studying the evolution of these genetic elements and for obtaining useful information regarding the antibiotic resistance pattern of this species [16].

The prevalence of methicillin resistance in *S. schleiferi* clinical isolates is high in the range of 40–60% [4, 13, 17, 18]. Although methicillin-resistant *S. schleiferi* (MRSS) isolates have been reported to be susceptible to multiple non-β-lactam antimicrobials, the number of MRSS isolates is increasing, thus threatening public health [4, 17, 18].

Sequence analysis of the direct repeat unit (*dru*), a variable number-of-tandem-repeats region, which consists of mostly 40-bp *dru*

repeats and is located downstream of the *mecA* gene and adjacent to IS*431* in SCC*mec* elements of methicillin-resistant staphylococci, has been described [19]. This sequence-based method has advantages of inter laboratory comparison and can be used for typing of MRSS isolates.

Although the importance and concerns regarding *S. schleiferi* infections in humans and veterinary medicine are growing, molecular studies on *S. schleiferi* are few. The present study was designed to investigate the molecular epidemiology and antimicrobial susceptibility of *S. schleiferi* isolated from canine pyoderma and otitis externa in South Korea and to compare the results with those of previous studies conducted in other countries.

Materials and Methods

1. Sample collection and identification

The samples were collected aseptically from the lesions of canine pyoderma (n = 136) and otitis externa (n = 49) from 2010 to 2016 from owner-owned dogs brought to the Veterinary Teaching Medical Hospital of the Seoul National University. Swabs were plated on blood agar (Hangang, Gyeonggi, Korea) and incubated for 24h at 37°C. After incubation, all staphylococcus isolates were identified by colony morphology, Gram stainng and the Vitek II system (Biomerieux, Lyon, France), which included standard biochemical tests.

Multiple PCRs based on *nuc* amplification were conducted for genotypic confirmation of *S. schleiferi* (526 bp) by previously described [20]. Primer sch-F (5'-AATGGCTACAATGATAATCACTAA-3') and sch-R (5'-CATATCTGTCTTTCGGCGCG-3') were used. PCR conditions were as follows: 95°C for 5 min; 35 cycles of 95°C for 30 s, 55°C for 30 s, and 72°C for 1 min 30 S; 72°C for 10 min; and holding at 4°C. All the PCR products were sequenced using ABI PRISM 3730XL Analyzer (Applied Biosystems, Foster, US) to confirm species identification.

To confirm *S. schleiferi* at the subspecies-level, all the *S. schleiferi* isolates were subjected to the coagulase slide test (rabbit plasma, SIGMA-ALDRICH) for clumping factor and to the coagulase tube test for free coagulase (rabbit plasma, SIGMA-ALDRICH) [21-23]. For the

coagulase slide test, one drop of distilled water was placed on a glass microscope slide and a heavy suspension of the *S. schleiferi* organism was mixed. After that, one coagulase disc was added and the disc was rubbed about in the suspension, using the tip of a wire loop. At once, a second drop of distilled water was added and mixed again. Coagulase-negative *S. schleiferi* have remained evenly suspended and macroscopic clumping have occured within 30 seconds in a positive test.

The coagulase tube test was performed with rabbit coagulase plasma containing EDTA (SIGMA-ALDRICH). The lyophilized rabbit plasma was rehydrated with EDTA in 3 ml of distilled water. 0.3 ml of the rabbit plasma and 1/2 an inoculation loop of colony material from blood agar plates (Hangang, Gyeonggi, Korea) were mixed and incubate at 37°C. The tubes were checked every hour for coagulation by gently tipping to the side and the coagulase test was positive if more than 75% of the tube contents has formed a coherent clot. If the test was negative after 4-6 hours, incubating was continued the tube and a final assessment was made after 24 hours.

2. Antimicrobial susceptibility testing and detection of resistance genes

Antimicrobial susceptibility testing was performed on Mueller-Hinton agar using the disk diffusion method according to the CLSI guidelines (performance standard for antimicrobial susceptibility testing, Clinical and Laboratory Standard Institute) [24]. The antimicrobial test included penicillin (10 units), oxacillin (1 μg), amikacin (30 μg), minocycline (30 μg), norfloxacin (10 μg), trimethoprim-sulfamethoxazole (1.25/23.75 μg), chloramphenicol (30 μg).

PCR amplification for the *mec*A gene was performed to identify methicillin resistance in all the *S. schleiferi* isolates [25].

3. Molecular characterization

For SCC*mec* typing, two panels of multiplex PCRs were performed for the *ccr* complex and *mec* complex [25]. M-PCR 1 was used to detect *mecA* and to identify the *ccr* gene complex. M-PCR 2 was used for distinguishing between class A, B, and C *mec*. The primer pairs used for PCR experiments are listed in Table 1.

Table 1. Primers used in this experiment

Primer	Sequence (5′ to 3′)
M-PCR 1	
mA1	TGCTATCCACCCTCAAACAGG
mA2	AACGTTGTAACCACCCCAAGA
A1	AACCTATATCATCAATCAGTACGT
A2	TAAAGGCATCAATGCACAAACACT
A3	AGCTCAAAAGCAAGCAATAGAAT
Bc	ATTGCCTTGATAATAGCCITCT
α4.2	GTATCAATGCACCAGAACTT
β4.2	TTGCGACTCTCTTGGCGTTT
γR	CCTTTATAGACTGGATTATTCAAAATAT
γF	CGTCTATTACAAGATGTTAAGGATAAT
M-PCR 2	
M16	CATAACTTCCCATTCTGCAGATG
IS7	ATGCTTAATGATAGCATCCGAATG
IS2(iS-2)	TGAGGTTATTCAGATATTTCGATGT
mA7	ATATACCAAACCCGACAACTACA

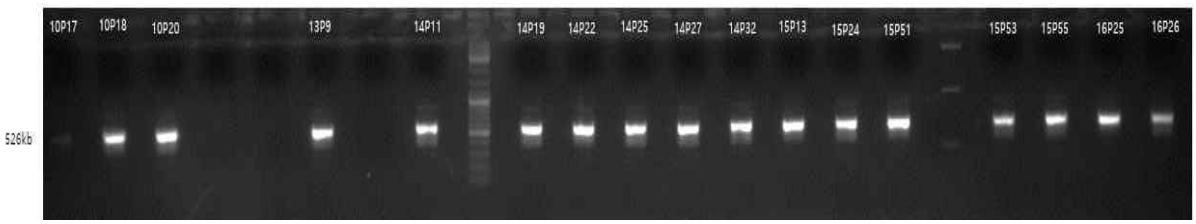
The *mec*-associated direct *dru* VNTR region adjacent to IS*431* in SCC*mec* was sequenced and characterized as described in a previous study [19]. PCR and DNA sequence analysis of the mec-associated *dru* region was performed using the nucleotides 5'-GTTAGCATATTA CCTCTCCTTGC-3' and 5'-GCCGATTGTGCTTGATGAG-3' as forward and reverse primers, respectively. PCR was performed with an initial denaturation step at 94°C for 2 min, followed by 30 cycles of 94°C for 1 min, 52°C for 1 min, and 72°C for 1 min. Sequenced tandem repeats were analyzed using the *dru* database website (http://dru-typing.org).

Results

1. Distribution of Staphylococci

All 185 staphylococcal isolates were collected from the ear and skin infection sites. The most prevalent species were *Staphylococcus pseudintermedius* (144/185, 77.8%), *S. schleiferi* (17/185, 9.2%), and *S. aureus* (13/185, 7.0%). Seventeen *S. schleiferi* isolates were confirmed by PCR for the *nuc* gene. All the PCR products were sequenced (Fig. 1).

Figure 1. PCR for the *nuc* gene in *Staphylococcus schleiferi* isolates. Seventeen *S. schleiferi* isolates were confirmed by PCR.



2. Coagulation test

All 17 *S. schleiferi* isolates were coagulase-positive. Only one of the 17 isolates that yielded positive results in the coagulase tube test was also positive for clumping factor, as determined by slide coagulase testing with rabbit plasma (Table 2).

3. Antimicrobial susceptibility testing and methicillin resistant gene

Results of antimicrobial susceptibility testing for all the *S. schleiferi* isolates identified are summarized in Table 2. Antimicrobial susceptibility testing revealed that 7 of the 17 *S. schleiferi* isolates (41%) were methicillin-resistant by the oxacillin disk diffusion test. These isolates also tested positive for the *mec*A gene in PCR. Six of these MRSS isolates (6/7, 85.7%) showed fluoroquinolone resistance (Table 2).

4. SCC*mec* and *dru* typing of MRSS

All the seven MRSS isolates detected (7/17, 41.1%) were confirmed as SCC*mec* type V (Fig. 2). In *mec*-associated *dru* typing, two *dru* types (dt)were detected: dt11a and dt9bd (Fig. 3). Six of the isolates were dt11a and one was dt9bd (Table 2).

Figure 2A. *Staphylococcus schleiferi mec*A gene and SCC*mec* typing; *mec* A (286 bp)

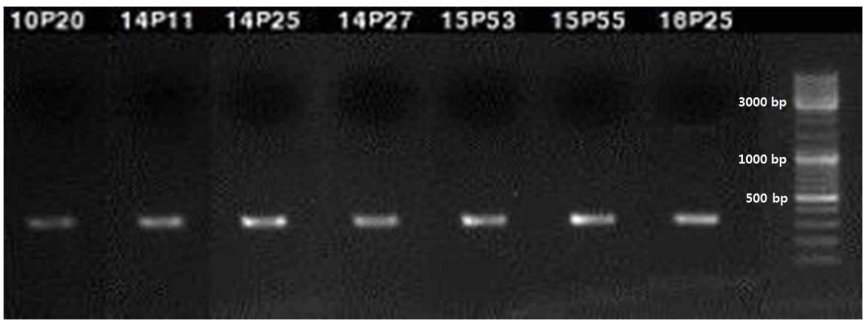


Figure 2B. *Staphylococcus schleiferi mec*A gene and SCC*mec* typing; *ccr* C (531 bp)

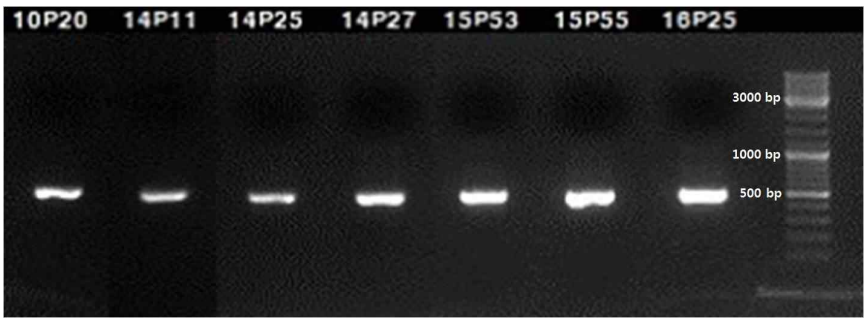


Figure 2C. *Staphylococcus schleiferi mec*A gene and SCC*mec* typing; *mec*A-IS*431* (804 bp)

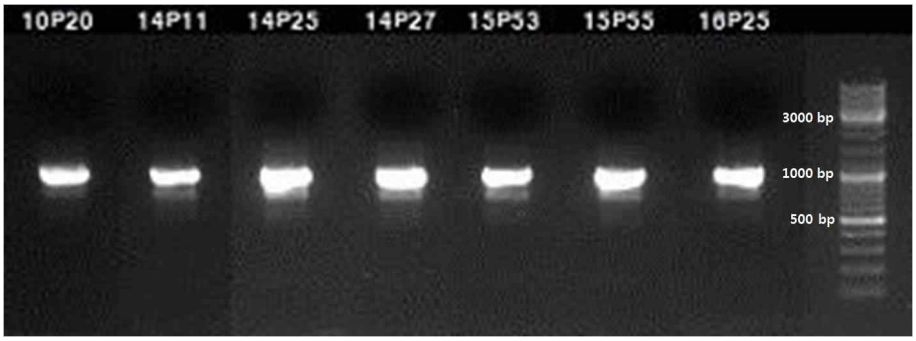


Figure 3. PCR amplification of *Staphylococcus schleiferi* direct repeat unit *(dru)*

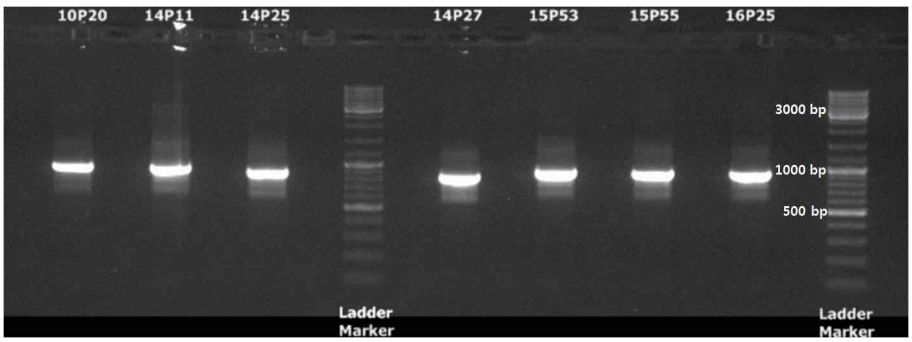


Table 2. Characteristics of the 17 *Staphylococcus schleiferi* isolates in this study

Sample	Origin	Antimicrobial-associated co-resistancepattern[a]	*mec*A	SCC*mec* type	*dru* typing	Slide coagulase test	Tube coagulase test	Urease
10P17	Ear	PEN	−	neg[b]	neg	−	+	+
10P18	Ear	Susceptible to all antimicrobials	−	neg	neg	−	+	+
10P20	Skin	PEN, OXA, NOR	+	V	dt11a	−	+	−
13P09	Ear	Susceptible to all antimicrobials	−	neg	neg	−	+	+
14P11	Ear	PEN, OXA, NOR	+	V	dt11a	−	+	−
14P19	Ear	Susceptible to all antimicrobials	−	neg	neg	+	+	−
14P22	Ear	Susceptible to all antimicrobials	−	neg	neg	−	+	−
14P25	Ear	PEN, OXA, NOR	+	V	dt11a	−	+	−
14P27	Ear	PEN, OXA, NOR	+	V	dt9bd	−	+	−
14P32	Ear	PEN,	−	neg	neg	−	+	+
15P13	Skin	CHL	−	neg	neg	−	+	−
15P24	Ear	Susceptible to all antimicrobials	−	neg	neg	−	+	+
15P51	Skin	Susceptible to all antimicrobials	−	neg	neg	−	+	−
15P53	Skin	PEN, OXA	+	V	dt11a	−	+	−
15P55	Skin	PEN, OXA, NOR	+	V	dt11a	−	+	−
16P25	Skin	PEN, OXA, NOR	+	V	dt11a	−	+	−
16P26	Skin	Susceptible to all antimicrobials	−	neg	neg	−	+	+

[a]PEN, penicillin; OXA, oxacillin, NOR, norfloxacin; CHL, chloramphenicol

[b]neg, Negative.

Discussion

S. schleiferi is a pathogen that causes canine pyoderma and otitis externa [26]. In this study, we isolated *S. schleiferi* from dogs with otitis and pyoderma in South Korea. Although some previous studies have been conducted on the distribution of methicillin-resistant staphylococcus spp. in dogs, humans, and medical equipment, the isolation of *S. schleiferi* from infectious lesions has not been reported previously in Korea [27-29]. In the present study, we also showed that *S. schleiferi* was highly prevalent (17/185, 9.2%) in the otitis and skin infections in the dogs, only second to *S. pseudintermedius*, which is consistent with a previous report [18, 30, 31].

Since *S. schleiferi* subsp. *coagulans* was isolated from canine otitis, it has been mainly associated with dogs, while *S. schleiferi* subsp. *schleiferi* has been mainly isolated from humans [2, 3, 18, 32, 33]. Several studies conducted to distinguish between subspecies of *S. schleiferi* [2, 18, 34] have classified *S. schleiferi* as *S. schleiferi* subsp. *schleiferi* and *S. schleiferi* subsp. *coagulans* based on their coagulase-negative and coagulase-positive results, respectively, which are determined using a tube(free) coagulase test. Coagulase-positive *S. schleiferi* is typically negative for clumping factor (Slide coagulase test), whereas coagulase-negative *S. schleiferi* is positive for clumping factor [32-34]. Some additional biochemical tests such as using urease have also been added to confirm *S. schleiferi* subspecies [21, 34]. Accordingly, *S. schleiferi* subsp. *coagulans* is positive for tube

coagulase and urease [32-34]. However, the 2 subspecies are not genotypically distinct and do not differ in clinical behavior [4, 17]. Isolates from human outbreaks have also been found to be concordant by PFGE, and at the molecular level, both subspecies show the same *nuc* gene [20, 35], which has led to debates about the subspecies of *S. schleiferi* as to whether these two biotypes are genotypically distinct enough to be considered true subspecies [4, 8].

In the present study, all the *S. schleiferi* isolates were found to be coagulase-positive, which indicated that all the isolates could be categorized as *S. schleiferi* subsp. *coagulans*. However, isolate 14P19 was positive for clumping factor, which indicated that it was not *S. schleiferi* subsp. *coagulans*, but *S. schleiferi* subsp. *schleiferi*. Moreover, many results for urease tests were not consistent with characteristics of *S. schleiferi* subsp. *coagulans* (*S.schleiferi* subsp. *coagulans* is tube coagulase and urease-positive) (Table 1). Some previous reports have not been able to distinguish between the subspecies because *S. schleiferi* has pseudocoagulases, which result in false-positive tube coagulase reactions, and because the results of other biochemical tests, such as those for clumping factor and urease, were not consistent with the characteristics of each *S. schleiferi* subspecies [4, 32, 34]. Similarly, results were not reported at the subspecies level in our study due to the challenges associated with differentiating between subspecies. Although an insufficient number of strains have been typed globally to be conclusive, these data suggest that the species may have low diversity and be a single *S. schleiferi* subspecies with

variable coagulase activity instead of 2 biologically distinct subspecies [4, 8].

The overall rate of methicillin resistance in this study was 41%, which is consistent with previous reports. The prevalence of methicillin resistance in *S.schleiferi* clinical isolates has been reported to be in the range of 40–60% in previous reports [4, 17, 36]. However, the results of this study can be an overestimation because the number of samples was not enough and because all the samples were collected from dermatology patients in referral practices. Nevertheless, this is first report on the presence of methicillin resistance in *S. schleiferi* clinical isolates in Korea.

Multidrug resistance is defined as methicillin-resistant staphylococci-acquired resistance to at least two additional antimicrobial classes [37]. In contrast to a previous report in the USA [26], the *S. schleiferi* isolates in our study did not show multidrug resistance. The isolates maintained a susceptibility profile to several antibiotics, but 6 methicillin-resistant *S. schleiferi* isolates (6/7, 85.7%) were resistant to fluoroquinolones. This percentage is higher than reported previously, where *S. schleiferi* isolates showed 35% and 40% susceptibility to fluoroquinolone, respectively [36, 38]. Antimicrobial exposure can be a factor promoting fluoroquinolone resistance in MRSS. Therefore, proper and cautious fluoroquinolone treatment is recommended in veterinary medicine in Korea only when indicated by results of antimicrobial susceptibility testing. Indiscriminate and empirical antimicrobial treatment could be a threat to both human and

animal health, because minor species such as *S. schleiferi* also have high rates of fluoroquinolone resistance.

The reports for SCC*mec* typing of *S. schleiferi* are rare: only 3 have been reported so far [16, 39, 40]. MRSS carrying SCC*mec* type IV was first reported in the USA in 2005 [40]. MRSS carrying SCC*mec* type V has been reported in Thailand and type I has been reported in India [16, 39]. In the present study, all the MRSS isolates obtained from dogs in Korea harbored SCC*mec* V, which is consistent with previously reported SCC*mec* V carriage in humans and dogs in Thailand [39]. Unfortunately there was no report on SCC*mec* type of *S. schleiferi*, but previous studies about SCC*mec* typing for methicillin-resistant staphylococci in Korea have also shown that SCC*mec* V was the most prevalent type in strains originating from dogs [27]. Moreover, among *mec*A-positive *S. pseudintermedius* isolates as well, SCC*mec* V was most prevalent in strains originating from both veterinary staff, hospitalized animals and the lesions of canine pyoderma and otitis externa [28, 41]. While SCC*mec* type V was absent in *S. aureus* isolated from humans and animals in Korea [28, 42]. These results suggest that *S. schleiferi* and *S. pseudintermedius*, which show the most prevalence in canine clinical isolates, have a close relationship due to horizontal transfer of methicillin resistance through the mobile genetic element, SCC*mec*.

Although molecular typing is important for investigating the emergence and dissemination of pathogens, molecular epidemiological tools are limited in MRSS. PFGE has been used for this purpose, but

its results cannot be compared between laboratories. So far, *mec*-associated *dru* typing has been used mainly in the epidemiological analysis of methicillin-resistant *S. aureus* and methicillin-resistant *S. pseudintermedius* [19, 43]. In the present study, we applied this method in MRSS for the first time. Typing by PCR amplification and sequencing was successfully conducted using the *dru* database, and we proved that this tool is very useful in genetic epidemiology studies on MRSS. Furthermore, *dru* type dt11a, which is usually found in canine *S. pseudintermedius* but is rare in *S. aureus*, found in most MRSS isolates (6/7, 85.7%) in our study, which was similar to the trends found in SCC*mec* type [19, 41, 43]. Therefore, we suspect that mutual transfer of methicillin resistance occurs actively between *S. schleiferi* and *S. pseudintermedius* in Korea.

In conclusion, the results from the present study showed that MRSS is disseminating and causing skin infections in dogs in Korea. Further molecular and biochemical characteristics studies are needed in more clinical strains to form definitive conclusions on coagulase activity of *S. schleiferi.* The SCC*mec* results from our study displays that methicillin resistance in MRSS isolates varies with geographical location. Though further studies are needed, we suggest that SCC*mec* type and *dru* type in MRSS have close correlation with *Staphylococcus pseudintermedius* at the interspecies level. Our results provide important insights into the characteristic and molecular genetics of MRSS strains in Korea and may aid in the monitoring and surveillance of MRSS.

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Conflicts of Interest

None to declare.

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국문 초록

한국의 개의 피부에서 분리된 메티실린 내성 *Staphylococcus schleiferi*의 분자학적 특성

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*Staphylococcus schleiferi*는 사람과 개 모두에서 감염을 일으킬 수 있으며, *S.schleiferi*의 메티실린 내성은 공중보건학상 큰 위협이 되고 있다. 이에 본 연구는 한국의 개로부터 분리된 *S. schleiferi*의 항생제 감수성과 그 분자학적 특징에 대해 조사하고 그 결과를 다른 나라의 연구들과 비교해 보았다.

농피증이나 외이염을 앓고 있는 개에서 총 185개의 Staphylococcus 균주가 확인되었다. 균 동정에는 Microbiology identification system과 PCR이 사용되었으며, 항생제 감수성에는 Disk diffusion 방법이 이용되었다. *S. schleiferi*의 분자학적 특징 분석을 위한 SCC*mec* type과 direct repeat unit(*dru*)의 확인은 PCR을 통해서 이루워졌다.

총 185개의 Staphylococcus 균주 중 *S. schleiferi*는 두 번째로 많은 비중을 차지했다(17/185, 9.2%). 이 17개의 *S. schleiferi* 균주 중 41.1%인 7개의 균주에서 메티실린 내성이 확인되었으며, 7개 균주의 SCC*mec*은 모두 SCC*mec* type V로 같았다. SCC*mec* type V는 한국의 동물들과 수의사들에서 분리된 *S. schleiferi* 이외의 메티시린 내성 Staphylococcus 균주들에서도 가장 흔하게 확인되는 type으로 알려져 있다. mec-associated *dru* typing에서는 두 개의 *dru* type(dt), dt11a와 dt9bd가 발견되었다. 6개의 메티실린 내성 *S. schleiferi* 균주는 dt11a type을 가지고 있는 것으로 확인되었는데, dt11a는 *Staphylococcus pseudintermedius*에서 주로 많이 발견되는 *dru* type이다. 나머지 1개 균주의 *dru* 타입은 dt9bd였다.

본 연구는 *S.schleiferi*의 SCC*mec*과 dry typing에 대한 국내 최초의 연구로써, 본 연구를 통해서 한국에 메티실린 내성 *S.schleiferi* 균주가 상재하고 있으며, 개의 피부와 귀에서 감염을 일으키고 있음을 확인할 수 있었다. SCC*mec* type 분석시 모두 SCC*mec* Type V였는데, 이는 이전연구와 비교시, 태국과는 같은 SCC*mec* type V이었으나, 미국(SCC*mec* type IV)과 인도(SCC*mec* type I)와는 다른 type이었다. *dru* type와 SCC*mec* type 결과를 종합시 한국의 *S. schleiferi*의 메티시릴 내성에 대한 분자학적 특성은 지역적인 특성과 더불어 *Staphylococcus pseudintermedius*와 밀접한 연관성을 가지고 있다는 것을 시사하고 있다.

본 실험의 결과는 한국의 메티시린 내성 *S.schleiferi* 균주에 대한 특징과 분자학적 통찰을 제시하며, 추후 메틸시릴 내성 *S. schleiferi* 균주의 확산을 감시하고 모니터링 하는데 조력이 될 수 있을 것으로 판단된다.

주요어 : methicillin-resistant *Staphylococcus schleiferi*, MRSS, antimicrobial susceptibility, SCC*mec*, *dru*-typing, Korea
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