

AperTO - Archivio Istituzionale Open Access dell'Università di Torino

Isolation of methicillin-resistant *Staphylococcus pseudintermedius* from breeding dogs.

This is the author's manuscript

Original Citation:

Availability:

This version is available <http://hdl.handle.net/2318/85272> since 2015-09-16T11:39:29Z

Published version:

DOI:10.1016/j.theriogenology.2010.07.016

Terms of use:

Open Access

Anyone can freely access the full text of works made available as "Open Access". Works made available under a Creative Commons license can be used according to the terms and conditions of said license. Use of all other works requires consent of the right holder (author or publisher) if not exempted from copyright protection by the applicable law.

(Article begins on next page)

1
2



UNIVERSITÀ DEGLI STUDI DI TORINO

3
4

This Accepted Author Manuscript (AAM) is copyrighted and published by Elsevier. It is posted here by agreement between Elsevier and the University of Turin. Changes resulting from the publishing process - such as editing, corrections, structural formatting, and other quality control mechanisms - may not be reflected in this version of the text. The definitive version of the text was subsequently published in

Theriogenology, 75 (1), 2011 doi: 10.1016/j.theriogenology.2010.07.016.
<http://www.sciencedirect.com/science/article/pii/S0093691X1000409>

You may download, copy and otherwise use the AAM for non-commercial purposes provided that

your license is limited by the following restrictions:

(1) You may use this AAM for non-commercial purposes only under the terms of the CC-BY-NC-ND license.

(2) The integrity of the work and identification of the author, copyright owner, and publisher must be preserved in any copy.

(3) You must attribute this AAM in the following format: Creative Commons BY-NC-ND license

(<http://creativecommons.org/licenses/by-nc-nd/4.0/deed.en>),

<http://dx.doi.org/10.1016/j.amc.2013.11.030>

25

26

27 **Isolation of methicillin-resistant *Staphylococcus pseudintermedius* from breeding**
28 **dogs**

29

30 **Ada Rota^{a*}, Chiara Milani^b, Ilenia Drigo^c, Michele Drigo^d, Michela Corrò^c**

31

32 ^aDipartimento di Patologia Animale, Facoltà di Medicina Veterinaria, via Leonardo da
33 Vinci 44, 10090 Grugliasco (TO), Italy e-mail: ada.rota@unito.it

34 ^bDipartimento di Scienze Cliniche Veterinarie, Facoltà di Medicina Veterinaria,
35 Agripolis, 35020 Legnaro (PD), Italy e-mail: chiara.milani@unipd.it

36 ^cIstituto Zooprofilattico Sperimentale delle Venezie, Agripolis, 35020 Legnaro (PD),
37 Italy e-mail: mcorro@izsvenezie.it

38 ^dDipartimento di Sanità Pubblica, Patologia Comparata ed Igiene Veterinaria, Facoltà di
39 Medicina Veterinaria, Agripolis, 35020 Legnaro (PD), Italy e-mail:
40 michele.drigo@unipd.it

41

42

43 *Corresponding author

44 Tel + 39 11 6709051

45 Fax +39 11 6709097

46 e-mail:

47 ada.rota@unito.it

48 **Abstract**

49 The overuse of antimicrobials can select resistant bacteria strains; staphylococci have
50 the ability to become resistant to all beta-lactam antimicrobials and are a significant
51 concern in human medicine and a growing issue for veterinary medicine. Since in
52 breeding kennels antimicrobials are sometimes incorrectly used, the objective of the
53 work was to assess the occurrence of methicillin-resistant coagulase-positive
54 staphylococci in breeding dogs. The research was carried out in 13 kennels that were
55 allotted to three categories according to the intensity of antimicrobial use. Vaginal and
56 milk swabs were taken from 87 healthy bitches around parturition and also from
57 multiple organs of 27 of their pups that died within the first 2 weeks. Standard
58 bacteriological examinations were carried out and coagulase-positive staphylococci
59 were identified. All the coagulase-positive staphylococci resulted to be *Staphylococcus*
60 *pseudintermedius*. Susceptibility to oxacillin and the presence of the *mecA* gene were
61 tested. Nine out of 89 strains (six isolated from the bitches' milk and three from dead
62 puppies, all belonging to kennels characterized by an excessive use of antimicrobials)
63 were multidrug-resistant, methicillin-resistant and *mecA* positive.
64 Our results confirm that excessive use of antimicrobials entails the risk of selecting
65 resistant staphylococci strains. Our data also indicate that the bacterial flora of healthy
66 dogs belonging to specific populations may act as a reservoir of resistance genes.

67

68

69

70 **Keywords:** *Staphylococcus pseudintermedius*; methicillin-resistance; *mecA* gene; dog

71 1. Introduction

72 Coagulase-positive staphylococci, (*Staphylococcus aureus*, *S. intermedius*, *S.*
73 *pseudintermedius* and *S. delphini*) are commensal bacteria and opportunistic pathogens
74 in most animal species [1]. Resistance to methicillin appeared in *S. aureus* in 1960 [2]
75 and originated because of widespread use of beta-lactam antibiotics in nosocomial
76 settings; the frequency of infections due to methicillin-resistant *S. aureus* has steadily
77 increased over the years, representing a serious problem in human medicine [3].
78 Resistance to methicillin is due to the presence of the *mecA* gene, which encodes the
79 altered penicillin-binding protein 2a (PBP2a) that has a reduced affinity for all beta-
80 lactam antimicrobials; the *mecA* gene is carried on a mobile DNA element, the
81 staphylococcal cassette chromosome *mec* (SCC*mec*) [4].

82 The most prevalent coagulase-positive staphylococcal species in dogs, isolated both
83 from normal skin and oronasal mucosa and from skin and ear infections [5,6], was *S.*
84 *intermedius*. Recently, using a molecular identification approach, canine isolates that
85 had previously been phenotypically identified as *S. intermedius* were reclassified as *S.*
86 *pseudintermedius* [7]. Devriese et al. [8] proposed that canine strains identified by
87 traditional means should be reported as *S. pseudintermedius* unless shown by genomic
88 investigation to belong to other related species. A small proportion of *S. intermedius*
89 (old classification) strains isolated both from healthy dogs [9,10] and from dogs
90 showing skin and ear infections [6] has proven to be methicillin-resistant *mecA* positive.
91 Although *S. intermedius* (old classification) is seldom responsible of human infections,
92 transfer from dog to human is possible [11,12].

93

94 Since antimicrobials are sometimes misused in breeding kennels, the aims of this work
95 were 1) to assess the occurrence of methicillin-resistant coagulase-positive

96 staphylococci in breeding dogs; and 2) to compare the frequency of isolation of
97 resistant strains among kennels differing in the use of antimicrobials.

98

99 **2. Materials and Methods**

100 *2.1 Animals and sampling*

101 Eighty-seven breeding bitches housed in 13 kennels located in Northern Italy were
102 included in the study. The history of the kennels reported a different use/misuse of
103 antibiotics, in particular around parturition, and they were consequently divided into
104 three categories: 1) administration of amoxicillin or amoxicillin-clavulanic acid only
105 when required by pathological conditions (5 kennels, 36 bitches); 2) almost routine
106 administration of amoxicillin or amoxicillin-clavulanic acid around parturition (5
107 kennels, 29 bitches); 3) routine administration of various antimicrobial agents around
108 parturition (II and III generation cephalosporins, macrolids, adopted after amoxicillin
109 and amoxicillin-clavulanic acid had become ineffective) (3 kennels, 22 bitches).

110 Vaginal swabs were taken from the bitches 7-10 days before parturition and milk
111 samples were collected 7-10 days after parturition; the bitches belonging to kennels of
112 category II and III were under antimicrobial treatment when milk cultures were carried
113 out. A guarded sterile swab (Copan Innovation[®], Brescia, Italy) was introduced into the
114 cranial vagina after thorough disinfection of the vulva with a povidone-iodine solution,
115 and placed in the Amies transport medium provided with the swab. A drop of milk was
116 collected on a sterile swab (Copan Innovation[®], Brescia, Italy) from each of the caudal
117 mammary glands, after local disinfection. A complete post-mortem examination was
118 performed, including culture (from brain, stomach, intestine, liver, heart, lungs) and
119 sensitivity testing, on puppies that died within the first 2 weeks. All the bitches, aged
120 1.5-9 years and belonging to different breeds, were in good health at the moment of

121 sampling and no signs or symptoms of either mastitis or metritis were present during the
122 period of observation.

123

124 *2.2 Isolation of coagulase-positive Staphylococci*

125 Swabs were inoculated onto Blood Agar Base n°2 (Oxoid, Basingstoke, United
126 Kingdom) with 5% defibrinated sheep blood (DiaTech, Jesi, Italy) and streaked out to
127 obtain single colonies. After 24 hrs of incubation at 37 ± 1 °C in aerobic conditions,
128 presumptive identification of staphylococci was based on colony morphology, Gram
129 stain appearance, catalase test, haemolysis, pigment production. Coagulase-positive
130 staphylococci were identified by coagulase reaction on rabbit plasma (Istituto
131 Zooprofilattico delle Venezie, Legnaro, Italy) and clumping factor by Slidex Staph
132 (BioMérieux, Marcy l'Etoile, France). API Staph ID 32 phenotypic test (BioMérieux,
133 Marcy l'Etoile, France) and a specific PCR analysis for *S. aureus* [13] were also
134 carried out.

135

136 *2.3 Identification of S. pseudintermedius*

137 *S. pseudintermedius* identification was performed according to Bannoehr et al. [14].
138 One colony of each isolate was suspended in 1 ml Phosphate Buffered Saline (pH 7.4)
139 and DNA was extracted using DNeasy Blood & Tissue Kit (Quiagen, Hilden, Germany)
140 according to the manufacturer's instructions for Gram positive bacteria. The
141 amplification was performed in a total volume of 50 µl containing 5 µl of DNA, 1.5
142 mM of MgCl₂, 0.1 U/µl of Fast Start Taq DNA Polymerase (Roche Diagnostics,
143 Mannheim, Germany), 200 µM of each dNTPs (Applied Biosystems, Foster City, USA)
144 and 0.5 µM of primers pta_f1 and pta_r1 (Table 1) [14]. DNA amplification was carried
145 out in an Eppendorf Mastercycler Ep Gradient S (Eppendorf, Milano, Italy) with the
146 following thermal cycling conditions: initial denaturation at 95 °C for 4 min, followed

147 by 40 cycles of amplification, denaturation at 95 °C for 30 s, annealing at 55 °C for 30
148 s, extension at 72 °C for 60 s, ending with a final elongation step of 5 min at 72 °C.
149 After amplification, 10 µl of PCR products were subjected to enzymatic restriction with
150 1.5 U/µl of *Sau3AI* for 1h at 37 °C and the restriction products subsequently subjected
151 to agarose gel electrophoresis. Restriction of *S. pseudintermedius* amplicons resulted in
152 two fragment of 213 pb and 107 pb.

153

154 *2.4 Antimicrobial susceptibility*

155 Susceptibility to a panel of sixteen antimicrobial agents was determined by the disk
156 diffusion method in Mueller-Hinton agar (Sclavo Diagnostics International, Siracusa,
157 Italy) according to the guidelines of the Clinical Laboratory Standards Institute, when
158 available [15, 16].

159 Discs of penicillin G (10 IU), ampicillin (10 µg), amoxicillin-clavulanic acid (20+10
160 µg) gentamicin (10 µg), oxacillin (1 µg), cefalexin (30 µg), cefuroxime (30 µg),
161 spiramycin (100 µg), streptomycin (10 µg), tetracycline (30 µg), tilmicosin (15 µg),
162 tylosin (30 µg), enrofloxacin (5 µg), rifampin (5 µg), tiamulin (30 µg), trimethoprim-
163 sulfamethoxazole (1.25+23.75 µg) were tested. Interpretative criteria for the inhibition
164 zone diameters of tylosin, spiramycin and streptomycin were given by the
165 manufacturers.

166 Bacteria strains were stored at -80 °C and the susceptibility test was repeated after
167 species identification.

168

169 *2.5 Oxacillin resistance confirmation*

170 Coagulase-positive staphylococci strains were transferred onto a selective medium,
171 Oxacillin Resistance Screening Agar Base with selective supplement (Oxoid,

172 Basingstoke, United Kingdom) (oxacillin concentration: 2µg/ml), and incubated at
173 37°C±1°C for 24 h to confirm susceptibility to oxacillin, as a surrogate for methicillin.

174

175 *2.6 MecA gene*

176 Coagulase-positive staphylococci strains were tested for the presence of the *mecA* gene
177 by PCR, using the primers reported in Table 1 [17]. DNA was extracted from each
178 sample as previously described. The amplifications were performed in a total volume of
179 25 µl containing 5 µl of DNA, 3 mM MgCl₂, 0.05 U/µl FastStart Taq DNA Polymerase
180 (Roche Diagnostics, Mannheim, Germany), 200 µM of each dNTPs (Applied
181 Biosystems, Foster City, USA) and 0.5 µM of primer. DNA amplification was carried
182 out in an Eppendorf Mastercycler Ep Gradient S (Eppendorf, Milano, Italy) with the
183 following thermal cycling conditions: initial denaturation at 95 °C for 6 min, followed
184 by 30 cycles of amplification, denaturation at 95 °C for 15 s, annealing at 55 °C for 30
185 s, extension at 72 °C for 30 s, ending with a final elongation step of 5 min at 72 °C.
186 After amplification, 10 µl of PCR products were subjected to agarose gel
187 electrophoresis.

188

189 *2.7 Statistical analysis*

190 The frequency of isolation of coagulase-positive staphylococci, both as a whole and in
191 each of the two localisations, was compared among the three categories of breeding
192 kennels by using chi-squared analysis. The frequency of isolation of methicillin-
193 resistant coagulase-positive staphylococci strains was analyzed using the Fisher exact
194 test, considering kennels of category 1 and 2 as a unique category. A P value < 0.05
195 was considered significant.

196

197 **3. Results**

198 A total number of 76 coagulase-positive staphylococci strains were isolated from the
199 bitches (33 from vagina and 43 from milk) and 13 coagulase-positive staphylococci
200 strains were isolated from 27 dead puppies.

201 All the coagulase-positive staphylococci resulted to be *S. pseudintermedius*.

202 The frequency of *S. pseudintermedius* colonization was not significantly different
203 among the three categories of kennels, neither as a whole nor in each of the two
204 localisations. In 7 out of 13 cases of dead puppies, *S. pseudintermedius* had caused
205 septicaemia: in six cases it was also the only bacterium isolated from the milk of the
206 corresponding dams, and in one case it was isolated from the dam's vagina.

207 All the isolated *S. pseudintermedius* strains showed high percentages of resistance to
208 different antimicrobials, particularly to penicillin and ampicillin, spiramycin and
209 tetracycline (Table 2).

210 Eight strains isolated from the bitches' milk and three from the dead pups were
211 resistant to oxacillin; seven of the bitch strains and all the pup strains confirmed the
212 resistance in the selective medium, with the higher oxacillin concentration. Six out of
213 seven strains isolated from the bitches and all three strains isolated from the dead pups
214 carried the *mecA* gene. In the *mecA* negative bitch strain, either *mecA* was not present
215 or mutations in the primer region may have occurred.

216 The origin, antibiotic resistance characteristics and presence/absence of the *mecA* gene
217 in the methicillin-resistant strains are reported in Table 3. All these strains show
218 multidrug resistance. All the isolates shown in Table 3 came from two kennels
219 belonging to category 3. The isolates with numbers 6 and 7 came from two bitches,
220 while those bearing numbers 8 and 9 derived from their dead puppies. Overall, the
221 prevalence of *mecA* positive methicillin-resistant strains was 7.9% in the bitches; the
222 percentage of *mecA* positive methicillin-resistant strains on all *S. pseudintermedius*
223 isolates was 10.1%.

224 Table 4 shows the number of methicillin-resistant *mecA* positive *S. pseudintermedius*
225 strains in the three categories of kennels and in the two localizations of the bitches.
226 The frequency of isolation of methicillin-resistant *mecA* positive *S. pseudintermedius*
227 strains in the bitches was higher in kennels belonging to category 3 (χ^2 [Yates
228 corrected]=12.48; P<0.001).

229 All the staphylococci strains that resulted susceptible to oxacillin by disk diffusion test
230 confirmed their susceptibility in the selective medium and resulted *mecA* negative.

231

232 **4. Discussion**

233 Antimicrobials are sometimes misused in breeding kennels and different agents may be
234 routinely administered around parturition to prevent neonatal infections, instead of
235 adopting more appropriate measures to minimise structural predisposing factors [18].

236 By comparing the antibiotic resistance in the intestinal flora, De Graef et al. [19] found
237 higher resistance percentages in dogs kept in breeding kennels than in privately owned
238 animals; the same study described also a relation between the antimicrobials used and
239 the resistances of bacteria, thus suggesting the possibility that resistance genes may be
240 transferred among bacteria colonising group-housed dogs.

241 All the coagulase-positive staphylococci strains isolated from the bitches in our work
242 were identified as *S. pseudintermedius* by molecular analysis, in agreement with recent
243 taxonomy observations on canine isolates [1,7,8].

244 In our study, *S. pseudintermedius* showed high percentages of antimicrobial resistance:
245 also when bitches were not exposed to antimicrobial treatment before sampling, as in
246 kennels of category 1, mean resistance rates for penicillin, ampicillin and spiramycin
247 were higher than 80%, for tetracycline higher than 25% and for streptomycin higher
248 than 18%. In a recent work [20], the Authors found a widespread occurrence of
249 resistance in *S. pseudintermedius* from skin and ear infections of dogs with no recent

250 history of antimicrobial treatment. The high genetic polymorphism of the isolates
251 suggested the possible transfer of resistance genes among *S. pseudintermedius* strains
252 as well as other bacteria in the dog population and it could be worth testing this
253 hypothesis also in our experimental series.

254 The occurrence of methicillin-resistance in *S. pseudintermedius* isolated in two
255 breeding kennels, both belonging to the group characterised by excessive
256 antimicrobials use, confirms that antimicrobial overuse selects resistant strains.
257 Administration of antimicrobial drugs, specifically β -lactams and fluoroquinolones, in
258 the previous 90 days, resulted in a significant risk factor for methicillin-resistant *S.*
259 *aureus* (MRSA) infection in dogs [21].

260 Methicillin-resistant *S. pseudintermedius* (MRSP) colonization of healthy dogs living
261 in a confined environment raises a number of issues including a) possible horizontal
262 transfer from dog to dog, and particularly between females and males; b) the pattern of
263 colonization over time; c) health hazard for dogs within kennels; and d) potential health
264 hazard for breeders. A recent study by Loeffler et al. [22] showed that MRSA did not
265 transmit readily between apparently healthy dogs housed in shared kennels and that
266 MRSA carriage was only transient in a regularly cleaned and disinfected environment.
267 However, these observations should be confirmed for MRSP and, furthermore, any
268 infection developed by MRSP-colonized animals, would probably be difficult to treat.
269 In fact, MRSP isolates that are positive for the *mecA* gene are generally multiresistant
270 [23], as in our case, although not necessarily more virulent than their methicillin-
271 susceptible counterparts [24]. A longitudinal study might help assess the persistence of
272 MRSP carriage and, consequently, the effective risk that a group-housed dog
273 population may become a reservoir for resistance genes. However, if antimicrobial
274 pressure is not reduced in the concerned kennels, other resistant strains are going to be
275 selected.

276 *S. intermedius* (old classification) is not usually a human pathogen, although it is known
277 to cause invasive infection following dog-bites [25]; sporadic cases of bacteraemia in
278 patients who had undergone invasive procedures have been reported [26], one case of
279 otitis externa [27] and, recently, a case of *S. pseudintermedius* catheter-related
280 bacteraemia in a hemophilic child [28]. Transmission of *S. intermedius* (old
281 classification) from dogs to their owners can occur [11,12] and it has already been
282 described also for methicillin-resistant strains [29]. The occurrence of *S. intermedius*
283 (old classification) in the owners of dogs affected by deep pyoderma was significantly
284 higher than in the control group [12]. However a recent investigation showed that
285 MRSP nasal colonization of the owners of dogs affected by MRSP skin infection was
286 uncommon and transient [30]. Nasal carriage of MRSP was detected in one staff
287 member of a veterinary teaching hospital [31]: personnel of veterinary clinics should be
288 made aware of the risk of nosocomial transmission of MRSP.

289 Although MRSP strains are not alarming as zoonotic agents, they represent a serious
290 concern as a potential source of horizontal gene transfer to other staphylococci,
291 converting methicillin-susceptible *S. aureus* colonizing humans into MRSA through
292 transfer of the mobile SCC containing the *mecA* gene [24,32]. *S. aureus* is indeed
293 thought to have acquired resistance through horizontal gene transmission from
294 coagulase-negative *S. sciuri* [33].

295 The prevalence of MRSP found in our study is higher than the values previously
296 reported for healthy dogs (1.5% [10]; 2% [9]) and is similar to data (6.3%) reported in
297 clinical samples of diseased dogs [10,34]. However, in our work, the frequency is
298 biased in kennels where the excessive use of antimicrobials has increased the selection
299 of resistant strains.

300 Genetic characterization of our MRSP isolates would be of great epidemiological
301 interest: their belonging to the multiresistant clonal lineage widespread in several

302 European countries (including Italy [35]), would confirm the spreading of MRSP strains
303 with relatively stable clones. However, the assessment of the genetical profile of the
304 isolates was out of the scope of this research.

305

306 A previous retrospective investigation on the bacteriological status of canine milk and
307 septicaemia of neonatal puppies [36] excluded *S. intermedius* (old classification) as a
308 major cause of septicaemia in neonates because, although isolated from the milk of the
309 dams, the bacterium was never found in the organs of the septicaemic puppies. This
310 issue deserves further investigation. In our work, *S. pseudintermedius* was isolated
311 from the organs of septicaemic puppies and it was also the only bacterium isolated
312 from the milk of the corresponding dams or from the dams' vagina. Two of the milk
313 and puppy isolates were methicillin-resistant *mecA* positive. Although the isolates were
314 not typed, a link between the strains from dam and puppy is very likely.

315

316 Our results confirm that the misuse of antimicrobials may lead to serious consequences
317 because resistant strains may become a health hazard in veterinary and human medicine;
318 methicillin-resistant staphylococcal infections may become causes of morbidity and
319 mortality in companion animals but domestic animals may also represent a reservoir of
320 infection and a zoonotic source [1]. MRSP should not only be considered as a
321 nosocomial pathogen in veterinary settings [35] but also as a potentially problematic
322 commensal in particular dog populations.

323 **Acknowledgments**

324 The authors thank Roberto Perin and Anna Sturaro for technical assistance.

325

326 **References**

327

- 328 [1] Weese JS, van Duijkeren E. Methicillin-resistant *Staphylococcus aureus* and
329 *Staphylococcus pseudintermedius* in veterinary medicine. *Vet Microbiol* 2010; 140:
330 418-29.
- 331 [2] Jevons MP, Coe AW, Parker MT. Methicillin resistance in staphylococci. *Lancet*
332 1963; 1: 904-7.
- 333 [3] Boucher HW, Corey GR. Epidemiology of methicillin-resistant *Staphylococcus*
334 *aureus*. *Clin Infect Dis* 2008; 46 (Suppl. 5): 344-9.
- 335 [4] Lin AE, Davies JE. Occurrence of highly fluoroquinolone-resistant and methicillin-
336 resistant *Staphylococcus aureus* in domestic animals. *Can J Microbiol* 2007; 53: 925-
337 9.
- 338 [5] Allaker RP, Jensen L, Lloyd DH, Lamport AI. Colonization of neonatal puppies by
339 staphylococci. *Brit Vet J* 1992; 148: 523-8.
- 340 [6] Loeffler A, Linek M, Moodley A, Guardabassi L, Sung JML, Winkler M, Weiss R,
341 Lloyd DH. First report of multiresistant, *mecA*-positive *Staphylococcus intermedius* in
342 Europe: 12 cases from a veterinary dermatology referral clinic in Germany. *Vet*
343 *Dermatol* 2007; 18: 412-21.
- 344 [7] Sasaki T, Kikuchi K, Tanaka Y, Takahashi N, Kamata S, Hiramatsu K.
345 Reclassification of phenotypically identified *Staphylococcus intermedius* strains. *J*
346 *Clin Microbiol* 2007; 45: 2770–8.
- 347 [8] Devriese LA, Hermans K, Baele M, Haesebrouck F. *Staphylococcus*
348 *pseudintermedius* versus *Staphylococcus intermedius*. *Vet Microbiol* 2009; 133: 206-
349 7.
- 350 [9] Vengust M, Anderson M, Rousseau J, Weese J. Methicillin-resistant staphylococcal
351 colonization in clinically normal dogs and horses in the community. *Lett Appl*
352 *Microbiol* 2006; 43: 602-6.
- 353 [10] Griffeth GC, Morris DO, Abraham JL, Shofer FS, Rankin SC. Screening for skin
354 carriage of methicillin-resistant coagulase-positive staphylococci and *Staphylococcus*
355 *schleiferi* in dogs with healthy and inflamed skin. *Vet Dermatol* 2008; 19:142-9.
- 356 [11] Harvey RG, Marples RR, Noble WC. Nasal carriage of *Staphylococcus*
357 *intermedius* in humans in contact with dogs. *Microb Ecol* 1994; 7: 225-7.
- 358 [12] Guardabassi L, Loeber ME, Jacobson A. Transmission of multiple antimicrobial-
359 resistant *Staphylococcus intermedius* between dogs affected by deep pyoderma and
360 their owners. *Vet Microbiol* 2004; 98: 23-7.
- 361 [13] Mehrotra M, Wang G, Johnson WM. Multiplex PCR for detection of genes for
362 *Staphylococcus aureus* enterotoxins, exfoliative toxin, toxic shock syndrome toxin 1,
363 and methicillin resistance. *J Clin Microbiol* 2000; 38: 1032-5.

- 364 [14] Bannoehr J, Franco A, Iurescia M, Battisti A, Fitzgerald JR. Molecular diagnostic
365 identification of *Staphylococcus pseudintermedius*. J Clin Microbiol 2009; 47: 469-
366 71.
- 367 [15] Clinical Laboratory Standards Institute. Performance Standards for Antimicrobial
368 Disk and Dilution Susceptibility Tests for Bacteria Isolated From Animals; Approved
369 Standard- Third Edition (M31-A3), Wayne, PA, 2008.
- 370 [16] Clinical Laboratory Standards Institute. Performance Standards for Antimicrobial
371 Susceptibility Testing; Nineteenth Informational Supplement (M100-S19), Wayne,
372 PA, 2009.
- 373 [17] Louie L, Goodfellow J, Mathieu P, Glatt A, Louie M, Simor AE. Rapid detection
374 of methicillin-resistant staphylococci from blood culture bottles by using a multiplex
375 PCR assay. J Clin Microbiol 2002; 40: 2786-90.
- 376 [18] Sager M, Remmers C. Some aspects of perinatal mortality in the dog. A clinical,
377 bacteriological and pathological study [in German]. Tierärztl Prax 1990; 18: 415-9.
- 378 [19] De Graef EM, Decostere A, Devriese LA, Haesebrouck F. Antibiotic resistance
379 among fecal indicator bacteria from healthy individually owned and kennel dogs.
380 Microb Drug Resist 2004; 10: 65-9.
- 381 [20] Norström M, Sunde M, Tharaldsen H, Mørk T, Bergsjø B, Kruse H. Antimicrobial
382 resistance in *Staphylococcus pseudintermedius* in the Norwegian dog population.
383 Microb Drug Resist 2009; 15: 55-9.
- 384 [21] Faires MC, Traverse M, Tater KC, Pearl DL, Weese JS. Methicillin-resistant and -
385 susceptible *Staphylococcus aureus* infections in dogs. Emerg Infect Dis 2010; 16: 69-
386 75.
- 387 [22] Loeffler A, Pfeiffer DU, Lindsay JA, Soares-Magalhaes R, Lloyd DH. Lack of
388 transmission of methicillin-resistant *Staphylococcus aureus* (MRSA) between
389 apparently healthy dogs in a rescue kennel. Vet Microbiol 2010; 141: 178-81.
- 390 [23] Gortel K, Campbell KL, Kakoma I, Whittem T, Schaeffer DJ, Weisiger RM.
391 Methicillin resistance among staphylococci isolated from dogs. Am J Vet Res 1999;
392 60: 1526-30.
- 393 [24] Cohn LA, Middleton JR. A veterinary perspective on methicillin-resistant
394 staphylococci. J Vet Emerg Crit Care (San Antonio) 2010; 20: 31-45.
- 395 [25] Talan DA, Staats D, Staats A, Goldstein EJ, Singer K, Overturf GD.
396 *Staphylococcus intermedius* in canine gingival and canine-inflicted human wound
397 infections: laboratory characterization of a newly recognized zoonotic pathogen. J
398 Clin Microbiol 1989; 27: 78-81.
- 399 [26] Vandenesch F, Célarid M, Arpin D, Bes M, Greenland T, Etienne J. Catheter-
400 related bacteremia associated with coagulase-positive *Staphylococcus intermedius*. J
401 Clin Microbiol 1995; 33: 2508-10.

- 402 [27] Tanner MA, Everett CL, Youvan DC. Molecular phylogenetic evidence for
403 noninvasive zoonotic transmission of *Staphylococcus intermedius* from a canine pet to
404 a human. J Clin Microbiol 2000; 38: 1628–31.
- 405 [28] Chuang C-Y, Yang Y-L, Hsueh P-R, Lee P-I. Catheter-related bacteremia caused
406 by *Staphylococcus pseudintermedius* refractory to antibiotic-lock therapy in a
407 hemophilic child with dog exposure. J Clin Microbiol 2010; 48: 1497-8.
- 408 [29] van Duijkeren E, Houwers DJ, Schoormans A, Broekhuizen-Stins MJ, Ikawaty R,
409 Fluit, Wagenaar JA. Transmission of methicillin-resistant *Staphylococcus intermedius*
410 between humans and animals. Vet Microbiol 2008; 128: 213-5.
- 411 [30] Frank LA, Kania SA, Kirzeder EM, Eberlein LC, Bemis DA. Risk of colonization
412 or gene transfer to owners of dogs with methicillin-resistant *Staphylococcus*
413 *pseudintermedius*. Vet Dermatol 2009; 20: 496-501.
- 414 [31] Sasaki T, Kikuchi K, Tanaka Y, Takahashi N, Kamata S, Hiramatsu K. Methicillin-
415 resistant *Staphylococcus pseudintermedius* in a veterinary teaching hospital. J Clin
416 Microbiol 2007; 45: 1118-25.
- 417 [32] Hanssen AM, Kjeldsen G, Ericson Sollid JU. Local variants of staphylococcal
418 cassette chromosome mec in sporadic methicillin-resistant *Staphylococcus aureus* and
419 methicillin-resistant coagulase-negative staphylococci: evidence of horizontal gene
420 transfer? Antimicrob Agents Chemoter 2004; 48: 285-96.
- 421 [33] Wu S, Piscitelli C, de Lencastre H, Tomasz A. Tracking the evolutionary origin of
422 the methicillin resistance gene: cloning and sequencing of a homologue of mecA from
423 a methicillin susceptible strain of *Staphylococcus sciuri*. Microb Drug Resist 1996, 2,
424 435-41.
- 425 [34] Ruscher C, Lübke-Becker A, Wleklinski CG, Soba A, Wieler LH, Walther B.
426 Prevalence of methicillin-resistant *Staphylococcus pseudintermedius* isolated from
427 clinical samples of companion animals and equidae. Vet Microbiol 2009; 136: 197-
428 201.
- 429 [35] Perreten V, Kadlec K, Schwarz S, Grönlund Andersson U, Finn M, Greko C,
430 Moodley A, Kania SA, Frank LA, Bemis DA, Franco A, Iurescia M, Battisti A, Duim
431 B, Wagenaar JA, van Duijkeren E, Weese JS, Fitzgerald JR, Rossano A, Guardabassi
432 L. Clonal spread of methicillin-resistant *Staphylococcus pseudintermedius* in Europe
433 and North America: an international multicentre study. J Antimicrob Chemother
434 2010; 65: 1145-54.
- 435 [36] Schäfer-Somi S, Spargser J, Breitenfellner J, Aurich JE. Bacteriological status of
436 canine milk and septicaemia in neonatal puppies--a retrospective study. J Vet Med B
437 Infect Dis Vet Public Health 2003; 50: 343-6.
- 438

439 Table 1. Primers used to identify *Staphylococcus pseudintermedius* and to detect the presence of the *mecA* gene

440

441

Primers	Sequence 5'-3'	Product size (bp)	Reference
Pta_f1	AAA GAC AAA CTT TCA GGT AA	320	[14]
Pta_r1	GCA TAA ACA AGC ATT GTA CCG		
<i>mecA</i> _F	AAA ATC GAT GGT AAA GGT TGG C	533	[16]
<i>mecA</i> _R	AGT TCT GCA GTA CCG GAT TTG C		

442

443 Table 2. Percentages of resistance to different antimicrobials of *Staphylococcus pseudintermedius* strains isolated in two localisations from bitches
 444 housed in three categories of kennels

Kennel category	1		2		3	
Origin^a	M	V	M	V	M	V
N° of isolates	21	13	9	12	13	8
Penicillin	85.7	92.3	88.9	100	100	100
Ampicillin	80.9	92.3	88.9	100	100	100
Amoxicillin-clavulanic acid	0	0	0	0	53.8	12.5
Oxacillin	0	0	0	0	61.5	0
Cefalexin	4.8	0	0	0	38.5	0
Cefuroxime	4.8	0	0	0	38.5	0
Spiramycin	90.5	69.2	88.5	90.0	100	100
Rifampin	4.8	0	0	0	0	0
Tilmicosin	0	7.7	0	10	84.6	12.5
Tylosin	0	15.4	22.2	30.0	100	37.5
Tetracycline	23.8	30.8	44.4	60.0	84.6	62.5
Streptomycin	14.3	23.1	55.6	30.0	92.3	37.5
Gentamycin	0	0	0	0	38.5	0
Enrofloxacin	0	0	0	0	53.8	0
Trimethoprim-sulfamethoxazole	9.5	15.4	11.1	20.0	84.6	12.5
Tiamulin	4.8	0	11.1	0	0	0

445 ^aM, milk; V, vagina.

448 Table 3. Antibigrams of methicillin-resistant *Staphylococcus pseudintermedius* isolates. Dams and corresponding puppies are linked with brackets.

Strain	1	2	3	4	5	6	7	8	9	10
Origin^a	M	M	M	M	M	M	M	P	P	P
Kennel category	3	3	3	3	3	3	3	3	3	3
Penicillin	R	R	R	R	R	R	R	R	R	R
Ampicillin	R	R	R	R	R	R	R	R	R	R
Amoxicillin-clavulanic acid	R	R	R	R	R	R	R	R	R	R
Oxacillin	R	R	R	R	R	R	R	R	R	R
Cefalexin	R	I	R	S	R	R	R	R	R	R
Cefuroxime	R	R	R	S	R	R	R	R	R	R
Spiramycin	R	R	R	R	R	R	R	R	R	R
Rifampin	S	S	S	S	S	S	S	S	S	S
Tilmicosin	R	R	R	R	R	R	R	R	R	R
Tylosin	R	R	R	R	R	R	R	R	R	R
Tetracycline	R	R	S	I	R	R	R	R	R	R
Streptomycin	R	R	R	R	R	R	R	R	R	R
Gentamycin	R	I	R	I	R	I	R	R	R	R
Enrofloxacin	R	R	R	R	R	R	R	R	R	R
Trimethoprim-sulfamethoxazole	R	R	R	R	R	R	R	R	R	R
Tiamulin	S	S	S	S	S	S	S	S	S	S
<i>mecA</i>	+	+	+	+	-	+	+	+	+	+

449 ^aM, milk; P, dead pup. R, resistant; S, susceptible; I, intermediate

450

451 Table 4. *Staphylococcus pseudintermedius* colonisation of the vagina and milk of the bitches belonging to the three categories of kennels (1= low,
 452 correct use of antimicrobials ; 2= moderate; 3= excessive); occurrence of methicillin-resistant *S. pseudintermedius* (MRSP) strains.

Kennel category	1	2	3
N of bitches	36	29	22
Percentage and (N) of bitches colonised by <i>S. pseudintermedius</i> in vagina and/or milk	66.7 (24)	65.5 (19)	77.3 (17)
Percentage and (N) of vaginal isolates	36.1 (13)	41.4 (12)	36.4 (8)
Percentage and (N) of milk isolates	52.8 (19)	37.9 (11)	59.1 (13)
Total N of isolates	32	23	21
Percentage and (N) of MRSP on vaginal isolates	0 (0/13)	0 (0/12)	0 (0/8)
Percentage and (N) of MRSP on milk isolates	0 (0/19)	0 (0/11)	46.1 (6/13)

453

454

