

## The prevalence of carriage of meticillin-resistant staphylococci by veterinary dermatology practice staff and their respective pets

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### Conflict of Interest

No conflicts of interest have been declared.

### Abstract

**It has been shown that people and pets can harbour identical strains of meticillin-resistant (MR) staphylococci when they share an environment. Veterinary dermatology practitioners are a professional group with a high incidence of exposure to animals infected by *Staphylococcus* spp. The objective of this study was to assess the prevalence of carriage of MR *Staphylococcus aureus* (MRSA), MR *S. pseudintermedius* (MRSP) and MR *S. schleiferi* (MRSS) by veterinary dermatology practice staff and their personal pets. A swab technique and selective media were used to screen 171 veterinary dermatology practice staff and their respective pets (258 dogs and 160 cats). Samples were shipped by over-night carrier. Human subjects completed a 22-question survey of demographic and epidemiologic data relevant to staphylococcal transmission. The 171 human-source samples yielded six MRSA (3.5%), nine MRSP (5.3%) and four MRSS (2.3%) isolates, while 418 animal-source samples yielded eight MRSA (1.9%) 21 MRSP (5%), and two MRSS (0.5%) isolates. Concordant strains (genetically identical by pulsed-field gel electrophoresis) were isolated from human subjects and their respective pets in four of 171 (2.9%) households: MRSA from one person/two pets and MRSP from three people/three pets. In seven additional households (4.1%), concordant strains were isolated from only the pets: MRSA in two households and MRSP in five households.**

**There were no demographic or epidemiologic factors statistically associated with either human or animal carriage of MR staphylococci, or with concordant carriage by person-pet or pet-pet pairs. Lack of statistical associations may reflect an underpowered study.**

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### Introduction

Bacteria of the genus *Staphylococcus* are residents of the healthy skin and mucous membranes of humans and animals. Under favourable conditions, some *Staphylococcus* spp. may also become opportunistic pathogens that cause serious skin and soft tissue infections (SSTI). The primary species causing both colonization and SSTI of human beings is *Staphylococcus aureus*,<sup>1</sup> while in dogs, *S. intermedius* (now known as *S. pseudintermedius*)<sup>2,3</sup> and *S. schleiferi* dominate.<sup>4</sup> *Staphylococcus intermedius* and *S. aureus* are commonly isolated both from healthy cats and those with inflammatory skin diseases, while isolation of *S. schleiferi* remains rare.<sup>5</sup>

Over the past decade, the prevalence of staphylococcal resistance to the semi-synthetic penicillinase-resistant penicillins (a class which includes meticillin and oxacillin) has escalated rapidly among SSTI isolates of both human and animal origin.<sup>6,7</sup> However, current protocols for the treatment and prevention of recurrent meticillin-resistant (MR) *S. aureus* (MRSA) infections in individuals, whether human or animal, often do not consider a potential role for cross-colonization between people and their pets. Yet it is known that a person who lives in close contact with a MRSA-infected patient may be colonized by that MRSA strain, and then serve as a source of secondary transmission to other people.<sup>8,9</sup> Colonization may persist for months to years in some individuals.<sup>10</sup>

The current veterinary literature<sup>11–17</sup> suggests that pets are capable of being infected or colonized by strains of MRSA that are known to circulate commonly in the community or within human healthcare facilities, and which cause SSTI in human. In published studies, MRSA strains isolated from pets, and veterinary personnel have often been indistinguishable, suggesting some mode of cross-transmission, although directionality of transmission is entirely speculative.<sup>11,12,17</sup>

Recent evidence also suggests that human colonization by *S. intermedius*/*S. pseudintermedius* occurs in dog owners and veterinarians.<sup>18–20</sup> While, the zoonotic potential of MR *S. pseudintermedius* (MRSP) is not completely

understood, it is not generally considered to be a human pathogen. Historical evidence has suggested that *S. intermedius* strains isolated from humans may be identical to those that infect their pets.<sup>19</sup> Additionally, strains of *S. intermedius* resistant to multiple antibiotic classes have been isolated from owners of dogs that presented with deep pyoderma.<sup>20</sup>

The potential for cross-transmission of *S. schleiferi* between humans and animals has not been systematically evaluated. *Staphylococcus schleiferi* subsp. *coagulans* is thought to be the primary subspecies that causes infections in dogs,<sup>21</sup> while it is the coagulase-negative variant, *S. schleiferi* subsp. *schleiferi*, that has been shown to be pathogenic in people. The latter is thought to be part of the normal axillary flora of humans,<sup>22</sup> and it has been shown to cause post-surgical SSTI.<sup>23–26</sup> By contrast, only two reports of human infection by *S. schleiferi* subsp. *coagulans* have been published.<sup>27,28</sup> One of these studies suggested that the patient's pet dog could have been the source, although the dog was not screened at that time by bacterial culture, despite having active otitis externa.<sup>28</sup>

In light of these past reports, we hypothesized that dermatologists and their technical staff could be a veterinary professional population at increased risk for cross-transmission of MR staphylococci, including MRSA, MRSP and MR *S. schleiferi* (MRSS). This hypothesis was based on the frequent contact with purulent exudates that dermatology practitioners experience on a daily basis, the nature of a dermatology referral patient population (one which has typically received numerous antimicrobial regimens for staphylococcal infections prior to referral), and the increased frequency with which veterinary dermatologists now diagnose MR staphylococcal infections in pets. As most veterinary personnel live with pets, it was hypothesized that a reciprocal reservoir could be established in the homes of these people through cross-colonization with their personal pets.

The objective of this study was to test the primary hypothesis that people and pets that live in close contact share strains of methicillin-resistant *Staphylococcus* spp. that are commonly associated with human and animal SSTI.

## Materials and methods

### Regulatory approvals

Approval for human specimen acquisition and processing and administration of the survey questionnaire, was granted by the University of Pennsylvania's Institutional Review Board (IRB). Approval for pet sampling was granted by the Institutional Animal Care and Use Committee.

### Subject recruitment

Practicing veterinary dermatologists, residents-in-training and their respective technical staff were recruited for participation through the electronic mail listservs administered by the American College of Veterinary Dermatology (ACVD). For inclusion, subjects were required to have practised dermatology, with direct patient contact, at least 2 days/week (on average) during the 4 weeks immediately preceding enrolment. Only residents of the USA and Canada were eligible. Those that agreed to participate were sent all study instruments, including sampling and shipping materials, explicit instructions for human and animal sampling techniques, and the study questionnaire.

Human subjects were instructed to sample their own nares with cotton-tipped swabs. The swab was to be passed along the medial septum to a depth of 2.5 cm, held in place for 5–10 s and rotated, then withdrawn slowly. A single swab was used to sample both nares. Pets were sampled at four body sites that have been established as primary colonization sites in dogs and cats: anal mucosa, groin, distal nares and oral mucosa.<sup>4,5</sup> The oral cavity was swabbed first, followed by each nare, then the groin and finally the anus. If evidence of active staphylococcal infection was present in the pet, participants were instructed to sample a representative site with an additional swab. Swabs were shipped by over-night carrier to the investigators' laboratory.

To preserve anonymity of human subjects, data were grouped by geographical zones as defined by the US Centers for Disease Control and Prevention (CDC; Figure 1) and blinded to the investigators. Canadian provinces contiguous with Northern US regions were included in those groups (not shown). As a large number of potential subjects resided in California, residents of this state were asked to self-identify. Residents of all other states and provinces were asked to identify only according to their region. Upon receipt of swabs by the investigators' laboratory, human and animal paired samples were coded, and data were stored in a secure database.

### Specimen processing

Each swab tip was submerged in mannitol salt broth (MSB) with 4 µg/mL oxacillin (Northeast Laboratory, Waterville, ME, USA) and incubated for a minimum of 18 h at 35 °C to select for growth of MR staphylococci. One microlitre of MSB was subcultured to mannitol salt agar with 4 µg/mL oxacillin and incubated for a minimum of 18 h at 35 °C. Each colony that showed a unique morphology was subcultured onto blood agar and incubated at 35 °C overnight for further laboratory analyses. Catalase positive, gram-positive cocci were presumptively identified as *Staphylococcus* spp. and were tested for the production of coagulase by a tube test.

Bacterial identification and antimicrobial susceptibility testing was performed by an automated system (MicroScan Walkaway 40; Dade Behring, Irvine, CA, USA). Isolates resistant to oxacillin as defined by the Clinical Laboratory Standards Institute guidelines,<sup>29</sup> and identified as *S. aureus*, *S. pseudintermedius*, or *S. schleiferi*, were cryopreserved (Microbank; Pro-Lab Diagnostics, Austin, TX, USA) for subsequent testing. Oxacillin resistance was confirmed by a rapid slide latex agglutination test for PBP2a (Oxoid; Remel Inc., Lenexa, KS, USA).<sup>30,31</sup>

### Molecular testing

#### Pulsed-field gel electrophoresis

Pulsed-field gel electrophoresis (PFGE) was performed on all isolates as described previously, following *Sma*I restriction enzyme digestion of bacterial DNA.<sup>16</sup> BioNumerics software version 5.0 (Applied



**Figure 1.** Geographical regions of the United States used for data analysis (Canadian provinces not shown). Due to a large number of participants from California (indicated by \*), data from this state was analysed separately, as a region distinct from the rest of the Western States.

Maths, Kortrijk, Belgium) was used to identify percent similarities and a dendrogram was created derived from the unweighted pair group method using arithmetic averages (UPGMA) based on Dice coefficients of similarity. A similarity coefficient of 80% was selected to define pulsed-field profile (PFP) clusters as previously described.<sup>32</sup> This technique was used for three purposes: to confirm clonality when the same MR staphylococcal species was isolated from both the human subject and a pet; to make clonal inferences about all isolates collected during the study (i.e. comparisons by region of origin) and to identify MRSA isolates by the USA strain type nomenclature system.<sup>33</sup> For MRSP and MRSS, PFGE typing facilitated confirmation of correct biochemical identification.

### Survey instrument

Each subject completed a survey questionnaire designed to capture data regarding human risk factors for MRSA colonization, of the subject or anyone that resided in the subject's home, within the 12 months prior to sampling. The survey also captured data regarding pet-related factors, such as living conditions (indoor/outdoor/mixed), presence of other pets in the household, and the nature of person and pet contact. Animal health questions documented comorbid conditions such as diabetes mellitus, renal insufficiency, hepatic insufficiency, neoplasia, retroviral infection (cats), corticosteroid use and other immunosuppressive therapies within the preceding 30 days. All antimicrobial therapy of human and animal subjects within the 90 days preceding study enrolment was also documented, including the antibiotic class as well as the specific antimicrobial agent.

The nature of human and animal contact was defined as either 'close' or 'casual'. This definition was extrapolated from the medical literature on interpersonal MRSA transmission within households.<sup>8</sup> Subjects were asked several questions about person and pet interaction, and points were assigned as follows: (i) Human subject is the primary care-provider for the pet (feeding, grooming, bathing, medicating, exercising): yes = 1 point, no = 0; (ii) The pet sleeps in/on the human subject's bed: yes = 2 points, no = 0; (iii) Human subject allows the pet to lick the face or hands: daily = 4 points, weekly = 2 points, monthly = 1 point, no = 0 and (iv) The pet is housed: exclusively indoors = 2 points, indoor/outdoor = 1 point, exclusively outdoors = 0 points. The maximum point total was 9. The contact score was dichotomized for statistical analysis, and 'close' contact was defined as a score of 6 or greater, while 'casual' contact was defined as a score <6.

### Sample size and power

A participation rate of 50% was predicted for the 199 ACVD college members and their 49 residents (124 persons), plus an average of 1.5 technicians per participating veterinarian, for a total of 310 person-households. An average of two pets per household (620 pets) was anticipated, with a 2:1 ratio of dogs:cats. It was expected that the prevalence of human colonization by MRSA would approximate 6%<sup>32</sup> and that the prevalence of pet colonization by MRSP and MRSS would approximate 4% and 1.5% respectively.<sup>4,5</sup> Independence of pet observations was assumed, as was a 15% (minimum) rate of person to pet cross-transmission for all three staphylococcal species,<sup>8</sup> to yield a total of six concordant (case) households. Power

was calculated assuming that the prevalence of the exposure (i.e. 'close' contact) would be  $\times 7.5$  higher in these concordant households than would 'casual' contact.<sup>8</sup> Given all assumptions, 99% power was attainable to detect an odds ratio of 2.0 for the risk factor of 'close' contact. Statistical evaluation of other potential risk factors was considered to be exploratory, as adequate statistical power was not anticipated.

### Statistical analysis

Cell count tables and allied tests were used in the cross-tabulation of categorical variables of major interest. Pearson's chi-squared test was used to detect significant associations of the covariates where all cell counts exceeded five, but for tables with smaller counts Fisher's exact test was used. To quantitatively associate dichotomous outcomes with categorical or continuous predictors (risk factors) logistic regression was used. Here, the measure of the strength of association of the risk factor with the outcome was expressed in terms of the odds ratio. Again, where smaller numbers of observations were involved, and the risk factor was categorical, *P*-values were checked using the Fisher's exact test. For continuous covariates the linearity of the outcome-risk factor relationship was confirmed following the methods suggested by Hosmer and Lemeshow.<sup>34</sup> Finally, for situations where the outcome was continuous and the predictor categorical, the Kruskal-Wallis test were used. All statistics were conducted with the aid of Stata 10.1 (Stata Corp, College Station, TX, USA), and a *P*-value of 0.05 was set to locate significant associations.

### Results

Swab samples were submitted by 171 people and 418 pets. Participants were distributed evenly in number across geographical regions. There were enough participants from California to consider it as a separate region for analysis. The number of pets sampled per person ranged from one to ten (median = 2, mode = 2). Of the 418 pets, 258 were dogs and 160 were cats (ratio = 1.6:1).

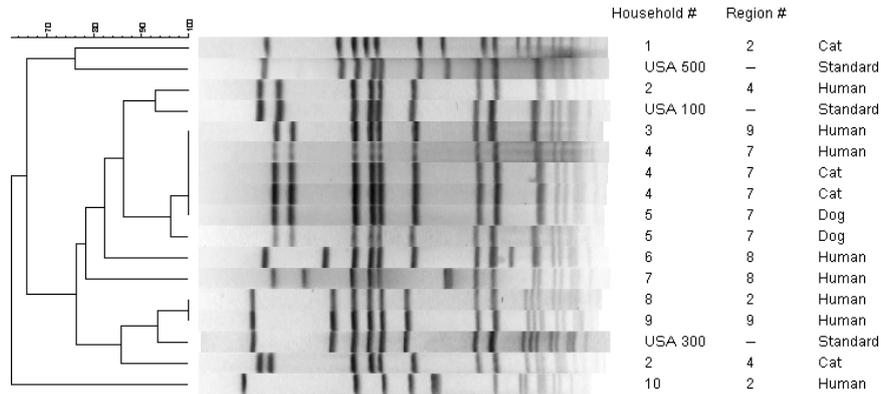
There was complete concordance between oxacillin minimal inhibitory concentration (MIC) and penicillin binding protein (PBP) latex agglutination test results. MRSA was isolated from six of 171 human samples (3.5%): nine MRSP (5.3%) and four MRSS isolates (2.3%) were also isolated from humans. MRSA was isolated from eight of 418 pet samples (1.9%): 21 MRSP (5.0%) and two MRSS isolates (0.5%) were also isolated from pets. Of these, six MRSA isolates and five MRSP isolates were obtained from cats (Table 1). There was no statistical difference in the overall frequency of MR staphylococcal isolation from cats versus dogs. Although the majority of pet MRSA isolates were from cats, data were too sparse for meaningful statistical analyses using the individual bacterial

**Table 1.** Total numbers of study subjects, meticillin-resistant staphylococcal isolates obtained and concordant households. A concordant household is defined as one from which two (or more) study subjects contributed clonal staphylococcal isolates. Clonality is defined as  $\geq 80\%$  similarity based upon pulsed-field gel electrophoresis profiles.

	People	All Pets	Dogs	Cats	Concordant person-pet households	Concordant pet-pet households
Total	171	418	258	160	4 (2.3)	7 (4.1)
MRSA	6 (3.5)	8 (1.9)	2 (0.8)	6 (3.75)	1 (0.5)	2 (1.2)
MRSP	9 (5.3)	21 (5.0)	16 (6.2)	5 (3.1)	3 (1.75)	5 (2.9)
MRSS	4 (2.3)	2 (0.5)	2 (0.8)	0	0	0

Values are given as *n* (%).

MRSA, meticillin-resistant *Staphylococcus aureus*; MRSP, meticillin-resistant *Staphylococcus pseudintermedius*; MRSS, meticillin-resistant *Staphylococcus schleiferi*.



**Figure 2.** Dendrogram of 14 meticillin-resistant *Staphylococcus aureus* isolates. Strains USA 100, USA 300 and USA 500 are included as standard references. Strains are numbered according to the household and region (see Figure 1) of origin. Two major clonal groups are represented (>80% similarity) and which cluster with strains USA 100 and USA 300. Two individual and unrelated isolates are also represented.

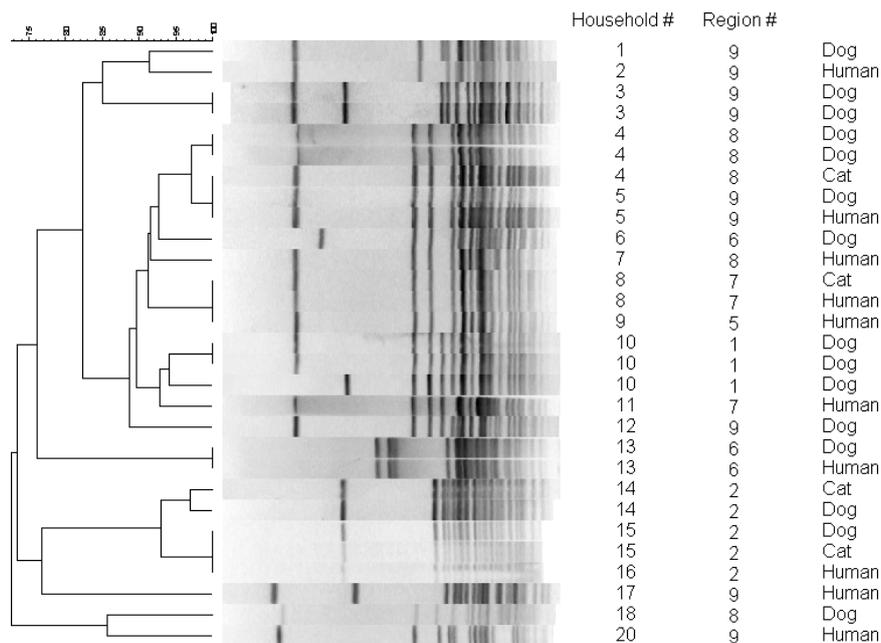
species as dependent variables. Of the six MRSS strains isolated in this study, four were coagulase-positive (*S. schleiferi* subsp. *coagulans*) and two were coagulase-negative (*S. schleiferi* subsp. *schleiferi*). Of the latter, one was isolated from a dog and the other from a person.

Concordant strains (genetically identical *Sma*I PFGE profiles) were isolated from four people and their respective pets (2.3% of households): MRSA from one person and their two cats, and MRSP in three people and their respective pets (two dogs and one cat). In one household, MRSA was isolated from a person and a cat, but PFGE showed that the isolates were different (Table 1). Within seven households (4.1%), concordant strains were isolated from only the pets (Table 1). In one household, concordant MRSA strains were isolated from two dogs. In five households, concordant MRSP strains were isolated from the following: two households with two positive pets each (all dogs), and three households with three positive pets each (one household with all dogs, one

household with two dogs and one cat, and one household with one dog and two cats) (Table 1).

The contact scores for person and pet pairs ranged from 2 to 9, and were normally distributed (mean = 5.4, SD of the mean = 2.1). There were no significant differences in pet and person contact scores across geographical regions, or within concordant households. As a group, cats had a significantly lower mean contact score with their owners than did dogs [OR, 0.86 (95% CI, 0.78–0.95);  $P = 0.003$ ].

Of the 14 MRSA strains typed by PFGE in this study, nine were identified as USA 100 (from five people and four pets), three were identified as USA 300 (from two people and one pet), and two isolates could not be assigned to USA clonal group of interest (Figure 2). MRSP isolates segregated into two major clusters, within which several clonal pairs and groups were evident (Figure 3). One MRSP isolate was not susceptible to *Sma*I digestion, and is not represented on the dendrogram.



**Figure 3.** Dendrogram of 29 meticillin-resistant *Staphylococcus pseudintermedius* isolates. Strains are numbered according to the household and region (see Figure 1) of origin. Two major clusters are represented, within which are several clonal pairs or larger groups (>80% similarity).

There were no demographic or epidemiologic factors statistically associated with either human or animal carriage of MR *Staphylococcus*.

## Discussion

Prior studies of MRSA prevalence associated with small animal healthcare have focused either on veterinary practitioners alone,<sup>35</sup> veterinary practitioners and their patients,<sup>11,12,15,17</sup> or the owners of pets diagnosed with MRSA infection.<sup>11</sup> The study reported here is the first to have attempted to quantify the prevalence of MR staphylococcal carriage by veterinary staff in conjunction with their personal pets, and to focus on all three major species of pathogenic staphylococci common to veterinary practice.

The prevalence rates of MRSA carriage by pets (1.9%) and veterinary personnel (3.5%) documented by this study approximate previous reports from veterinary sources.<sup>4,5,35</sup> The prevalence of MRSP carriage by dogs (6.2%) and cats (3.1%) was double that reported for populations of client-owned animals documented previously.<sup>4,5</sup> Although the prevalence of MRSP nasal carriage by the general pet-owning population of the US is unknown, the rate observed in the human subjects of the present study (5.3%), along with identification of three concordant person-pet pairs, suggest animal to human cross-transmission. As these study participants reported neither current infection of the pet, nor antimicrobial treatment of the pet within 90 days preceding enrolment, human acquisition of MRSP in the professional environment with cross-transmission to the household pet could also be speculated. Additionally, this study documented a higher prevalence of MRSS carriage by people than by pets, and all but one human isolate was identified as *S. schleiferi* subsp. *coagulans*, a subspecies rarely isolated from people. Although there were no concordant MRSS pairs, these results suggest that colonization by MRSS may be an occupational risk for veterinary practitioners.

In recent years MRSA, MRSP and MRSS have emerged as clinically important pathogens that cause treatment-resistant infections of dogs and cats.<sup>36,37</sup> As observed in MRSA strains, meticillin resistance in *S. intermedius* and *S. schleiferi* strains is known to be mediated by penicillin-binding protein 2a, which is encoded by a *mecA* gene.<sup>31</sup> Human MRSP carriage is assumed to be related to pet ownership,<sup>19,20</sup> but in veterinary practitioners, the original source could be either a personal pet or an animal patient. For example, a targeted veterinary hospital prevalence study conducted over a 3-month period showed that while 29.8% of canine patients were positive for MRSP, only one of twenty hospital staff members was positive.<sup>38</sup>

Human beings are the primary reservoir for *S. aureus* carriage, and in the United States, about one-third of all persons sampled by nasal swab on a single day will yield a positive culture.<sup>39</sup> By comparison, the prevalence of nasal colonization by MRSA in the US population, for the period of 2001–2004, remained much lower at 1.5%.<sup>40</sup> Despite this seemingly low prevalence of subclinical MRSA carriage, the proportion of *S. aureus* infection iso-

lates that are MR has been reported to be as high as 72% amongst local community-onset cases.<sup>39</sup> MRSA has also become the most prevalent nosocomial pathogen in North America.<sup>6</sup> Although the prevalence of MRSA isolated from human subjects in this study (3.5%) exceeded the estimate for the general population of the United States, direct comparison is not valid due to differences in the demographic characteristics of the populations sampled, the time-frame of sampling, and the small sample size of the current study. As dogs are not preferentially colonized by *S. aureus*, it is widely assumed that infection or colonization of dogs by MRSA is the result of transfer from humans.<sup>4</sup> The case for cats is less clear, as they appear to be natural hosts of *S. aureus*.<sup>5</sup> The prevalence of MRSA carriage documented for cats by this study (3.75%) approximates that reported for client-owned pet cats in a limited regional study reported previously.<sup>5</sup>

It has been widely documented that asymptomatic carriers can transmit MRSA to susceptible individuals, both within households<sup>8,9</sup> and within the community.<sup>41,42</sup> Studies of the prevalence of MRSA cross-colonization between people have estimated rates that ranged 14.5–70%.<sup>8,9</sup> Close contacts of MRSA patients, defined as a spouse, parent, child, or caregiver, were at a 7.5-fold greater risk of nasal carriage versus casual contacts (other individuals such as roommates, siblings and friends).<sup>8</sup> Although the relationships between people and their pets vary widely, there is no validated system for quantifying these relationships. Yet, it is obvious that a large proportion of pet owners have a relationship to their pets that would qualify as 'close contact'. In order to examine this relationship as a potential risk factor for cross-colonization by MR staphylococci, a quantitative definition of 'close' versus 'casual' contact was developed and used as the primary independent variable by which the study was powered. Likely due to the low rate of isolation of MR staphylococci from human subjects, no statistical associations with the contact score could be detected.

Data were also collected from subjects with regard to several risk factors for community-based acquisition of MRSA (participation in team sports, utilization of a gym/health club, residence in group housing) versus nosocomial acquisition (recent surgery, hospitalization, emergency room visits, repeated visits to outpatient treatment facilities, employment in human health care), in an attempt to correlate these risk factors with the strain types isolated from individual households. In order to determine clonal groups of MRSA isolates and classify them using the USA strain typing nomenclature from the CDC, PFGE was utilized. USA 100 has long been the predominant clonal group of MRSA that cause nosocomial infections in the United States,<sup>39</sup> whereas USA 300 has been associated with community-onset infections since the mid-1990s.<sup>43</sup> USA 500 strains are most commonly isolated from horses and the people who work with them.<sup>44</sup> Although several subjects reported regular contact with horses, no USA 500 strains were isolated. The majority of isolates (9 of 14) were strain USA 100, although no positive households reported nosocomial risk

factors. However, this strain has recently migrated from hospitals into the community,<sup>6,45,46</sup> and is now responsible for nasal colonization within the general human population in the United States.<sup>40</sup> It has also been reported previously from veterinary surveys and appears to be the predominant strain causing infection of small animal patients and colonization of small animal practitioners.<sup>11,16,17,35</sup>

Several technical and epidemiologic limitations of this study should be considered when evaluating the results. The automated system used for identification of *Staphylococcus* spp. in this study utilizes biochemical algorithms for species differentiation, and has been validated by the manufacturer. As this system will (rarely) misidentify MRSA as MRSS (and vice-versa) PFGE was used to compare pulsed-field profiles of all study isolates to type strains of MRSA and MRSS obtained from the American Type Culture Collection. This allowed confirmation of proper staphylococcal species identification. It is not possible for automated biochemical systems to differentiate between *S. intermedius* and *S. pseudintermedius*. For this purpose, a genotyping method which utilizes PCR to amplify the *sodA* and *hsp60* genes, which are particular to *S. pseudintermedius*, is necessary.<sup>3</sup> However, Devriese *et al.*<sup>47</sup> have recommended that all canine-source strains identified as *S. intermedius* by traditional means be reported as *S. pseudintermedius*. The latter approach was taken in the present study, where all human and feline-source strains clonally related to canine-source MRSP strains (as estimated by PFGE) were also assumed to be MRSP.

The prevalence of MR staphylococcal carriage by both human and animal subjects may have been underestimated. In human subjects, only the nares were screened but it is known that the throat is also an important colonization site for *S. aureus*. In a study that evaluated colonization of patients with active MRSA infection, the throat was the only positive site in 17% of patients and 30% of their interpersonal contacts.<sup>48</sup> Secondly, media containing oxacillin were used for selection of methicillin-resistant *Staphylococcus* spp. strains from human and animal-source specimens. While such media may be ideal for selection of MRSP and MRSS,<sup>31</sup> oxacillin has lower sensitivity for selection of MRSA from human-source specimens.<sup>49</sup> Therefore, use of a single type of selective media may have resulted in underestimation of MRSA prevalence. Finally, pets were sampled at four potential carriage sites with the same swab, in order to conserve resources. It is unknown what effect this might have had on isolation rates versus sampling each site individually.

This study was likely underpowered to detect association between the isolation of MR staphylococci and the risk factors proposed. This was a known limitation at the outset, as the study populations were not clinical patients with confirmed infections, and carriage of MR staphylococci is still a relatively rare event in both humans and animals. Additionally, the methodology utilized does not allow deduction of the original source of MR organisms within the household, as cross-sectional surveys cannot comment on cause-effect relationships. Therefore, the information reported should

be regarded as pilot data. However, the results of this study do suggest that concordant person-pet carriage of MR staphylococci is uncommon within the population surveyed, which is a favourable conclusion for veterinary dermatology practitioners. Longitudinal, population-based cohort studies are recommended to more completely characterize the frequency and directionality of MR staphylococcal transmission, and the risk associated with contact between veterinary practitioners, their patients in the professional environment and their personal pets in the home.

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**Résumé** Il a été montré que homme et animal issus du même environnement peuvent être porteurs des mêmes souches de staphylocoques méthicilline-résistant (MR). Les dermatologues vétérinaires sont des professionnels fortement exposés aux animaux infectés par *Staphylococcus* spp. L'objectif de cette étude était de déterminer la prévalence du portage de *Staphylococcus aureus* MR (MRSA), *S. pseudintermedius* MR (MRSP) et *S. schleiferi* MR (MRSS) par le personnel des cliniques de dermatologie vétérinaire et leurs propres animaux de compagnie. Un écouvillon et un milieu de culture sélectif ont été utilisés sur 171 membres d'équipes de dermatologie vétérinaire et leurs animaux respectifs (258 chiens et 160 chats). Les prélèvements ont été acheminés par porteur pendant la nuit. Chaque personne a répondu à 22 questions portant sur des données démographiques et épidémiologiques de la transmission staphylococcique. Les 171 échantillons prélevés sur les propriétaires ont donné six MRSA (3.5%), neuf MRSP (5.3%) et quatre MRSS (2.3%) alors que les 418 échantillons prélevés sur les animaux ont donné huit MRSA (1.9%), 21 MRSP (5%) et deux isolats de MRSS (0.5%). Des souches concordantes (génétiquement identiques par électrophorèse pulsée sur gel) ont été isolées des sujets humains et leurs animaux respectifs dans 4 cas sur 171 (2.9%) : MRSA sur 1 personne/2 animaux et MRSP sur 3 personnes/3 animaux. Dans 7 autres habitats (4.1%), des souches concordantes ont été isolées à partir des animaux seulement : MRSA dans 2 habitats et MRSP dans 5 autres. Il n'y avait statistiquement pas de facteurs démographique ou épidémiologique en relation avec le portage humain ou animal de staphylocoques MR ou avec le portage concordant par un propriétaire et son animal ou par deux animaux. Le manque d'associations statistiques pourrait être dû à une étude trop restreinte.

**Resumen** Se ha demostrado que los humanos y sus mascotas pueden ser portadores de cepas idénticas de estafilococos resistentes a meticilina (MR) cuando comparten el mismo ambiente. Los veterinarios dermatólogos son un grupo profesional con una elevada exposición a animales infectados con *Staphylococcus* spp. El objetivo de este estudio fue evaluar la prevalencia de portadores de MR *Staphylococcus aureus* (MRSA), MR *S. pseudintermedius* (MRSP) y MR *S. schleiferi* (MRSS) entre empleados de clínicas de dermatología veterinaria y sus mascotas personales. Se utilizó una técnica de muestreo con hisopo y un medio selectivo para evaluar 171 empleados y sus mascotas (258 perros y 160 gatos). Las muestras fueron enviadas por mensajero para entrega al día siguiente. Las personas completaron un cuestionario de 22 preguntas con datos epidemiológicos y demográficos de relevancia en la transmisión de estafilococos. Las muestras de las 171 personas dieron un total de 6 aislados de MRSA (3,5%), nueve de MRSP (5,3%) y cuatro de MRSS (2,3%), mientras que los 418 animales presentaron un total de 8 aislados de MRSA (1,9%), 21 de MRSP (5%) y dos de MRSS (0,5%). Cepas concordantes (con igualdad genética mediante electroforesis en gel de campo pulsante) fueron aisladas de las personas y sus mascotas en cuatro de los 171 hogares (2,9%): MRSA de una persona /2 mascotas y MRSP de 3 personas/3 mascotas. En otros siete hogares (4,1%), cepas concordantes solo se aislaron de las mascotas: MRSA en dos hogares y MRSP en cinco hogares. No hubo factores demográficos ni epidemiológicos estadísticamente asociados con portadores humanos o animales de estafilococos MR, o con portadores concordantes entre personas-mascotas o mascotas-pelo de mascotas. La falta de asociación estadística puede reflejar un estudio de bajo potencial.

**Zusammenfassung** Es konnte gezeigt werden, dass Menschen und Haustiere, die in derselben Umgebung leben, identische Methicillin-resistente (MR) Staphylokokken Stämme beherbergen können. Veterinärdermatologen gehören in eine Berufsgruppe, die mit großer Häufigkeit mit Tieren konfrontiert ist, die eine *Staphylokokken* spp. Infektion haben. Das Ziel dieser Studie war es, die Prävalenz der MR *Staphylokokkus aureus* (MRSA), MR *S. pseudintermedius* (MRSP) und MR *S. schleiferi* (MRSS) TrägerInnen unter veterinärmedizinischem Personal und unter ihren persönlichen Haustieren zu ermitteln. Eine Tupfermethode und selektive Medien wurden für ein Screening von 171 MitarbeiterInnen in veterinärdermatologischen Praxen und ihrer jeweiligen Haustiere (258 Hunde und 160 Katzen) eingesetzt. Die Proben wurden über Nacht verschickt. Die menschlichen Probanden füllten einen Fragenkatalog mit 22 Fragen bezüglich demographischer und epidemiologischer Daten aus, die relevant waren für eine Staphylokokkenübertragung. Die 171 Proben, die von Menschen genommen wurden, erbrachten sechs MRSA (3,5%), neun MRSP (5,3%) und vier MRSS (2,3%) Isolate, während die 418 von Tieren genommenen Proben acht MRSA (1,9%), 21 MRSP (5%) und zwei MRSS (0,5%) Isolate ergaben. Übereinstimmende Stämme (genetisch identisch mittels Pulsfeldelektrophorese) wurden von Menschen und ihren jeweiligen Haustieren in vier von 171 (2,9%) Haushalten isoliert: MRSA von einer Person/zwei Haustieren und MRSP von 3 Menschen/3 Haustieren. In sieben weiteren Haushalten (4,1%) wurden übereinstimmende Stämme nur von den Haustieren isoliert: MRSA in zwei Haushalten und MRSP in fünf Haushalten. Statistisch konnten demographische oder epidemiologische Faktoren weder mit den menschlichen oder tierischen Trägern von MR Staphylokokken noch mit den Trägern von übereinstimmenden Stämmen zwischen Personen-Haustier oder Haustier-Haustier-Paaren in Verbindung gebracht werden. Ein Mangel an statistischen Zusammenhängen könnte eine „underpowered study“ bedeuten.

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