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Short Communication

Anatomical patterns of colonization of pets with staphylococcal species in homes of people with methicillin-resistant *Staphylococcus aureus* (MRSA) skin or soft tissue infection (SSTI)

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ABSTRACT

Methicillin-resistant strains of *Staphylococcus aureus* (MRSA), *Staphylococcus pseudintermedius* (MRSP), and other pathogenic staphylococci can cause infections in companion animals and humans. Identification of colonized animals is fundamental to research and practice needs, but harmonized methods have not yet been established. To establish the optimal anatomic site for the recovery of methicillin-resistant coagulase positive staphylococci (CPS), survey data and swabs were collected from 196 pets (dogs, cats, reptiles, birds, fish and pocket pets) that lived in households with an MRSA-infected person. Using broth-enrichment culture and PCR for speciation, *S. aureus* was identified in 27 of 179 (15%) pets sampled at baseline and 19 of 125 (15%) pets sampled at a three-month follow-up home visit. *S. pseudintermedius* was isolated from 33 of 179 (18%) pets sampled at baseline and 21 of 125 (17%) of pets sampled at follow-up. The baseline MRSA and MRSP prevalence was 8% and 1% respectively from 145 mammalian pets. The follow-up MRSA and MRSP prevalence was 7% and <1% respectively from 95 mammalian pets. The mouth was the most sensitive single site sampled for isolation of *S. aureus* and *S. pseudintermedius* in mammals. In a subset of pets, from which all available isolates were identified, dual carriage of *S. aureus* and *S. pseudintermedius* was 22% at baseline and 11% at follow-up. These results identify the mouth as the most sensitive site to screen for pathogenic staphylococci and suggest that it should be included in sampling protocols.

1. Introduction

Staphylococcus aureus and *Staphylococcus pseudintermedius* (formerly *S. intermedius*) are receiving attention in both human and veterinary medicine because of increased reports of methicillin resistance. Methicillin resistant *S. aureus* (MRSA) infections have been shown to occur in

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animals, and pets are increasingly considered as potential MRSA reservoirs in cases of refractory or recurrent human infections (Loeffler and Lloyd, 2010). Furthermore, methicillin-resistant *S. pseudintermedius* (MRSP) colonization has been reported occasionally in humans (Guardabassi et al., 2004; Frank and Loeffler, 2012). These observations underscore the need for a one health approach to monitor pathogenic staphylococci in both research and clinical settings.

Despite the need for standardized methods to screen companion animals for staphylococcal carriage, particularly animals with known pathogen exposure such as those living with MRSA-infected owners, lack of harmonization in sampling and culture methodologies has limited comparability of the studies published to date. Several studies have considered anatomic site patterns of *S. pseudintermedius* carriage in dogs (Harvey and Noble, 1998; Hartmann et al., 2005; Griffeth et al., 2008; Rubin and Chirino-Trejo, 2011; Paul et al., 2012) and cats (Abraham et al., 2007). However, fewer studies that detail canine and especially feline anatomic carriage site patterns of *S. aureus* are available (Abraham et al., 2007; Griffeth et al., 2008; Fazakerley et al., 2009; Davis et al., 2014). The primary aim of this study was to systematically test the sensitivity of different anatomic sites for the recovery of *S. aureus* and MRSA among companion animals living in the home of a person recently treated for MRSA skin or soft tissue infection (SSTI). The secondary aim was to evaluate anatomic site sensitivity for recovery of *S. pseudintermedius* and other coagulase-positive staphylococci (CPS) among this community population of companion animals not associated with a veterinary healthcare setting. We also explored whether randomization of all humans residing in the household to a decolonization protocol between home visits impacted the prevalence and sensitivity of staphylococcal recovery from pets.

2. Materials and methods

2.1. Household recruitment and questionnaire administration

Households were recruited as part of a randomized-controlled trial (RCT) that targeted human outpatients treated at one of five participating institutions in the United States: two urban adult acute care hospitals, an adult community hospital, an urban children's hospital, and a rural adult and pediatric hospital. Inclusion in the RCT was based on a laboratory-confirmed MRSA skin or soft tissue infection (SSTI) in a human household member. Any household (with or without pets) enrolled in the RCT between January and December of 2012 was invited to participate in the nested study of the household environment and resident animals described here. Participating households were visited twice, approximately three months apart, and as part of the RCT protocol all human household members were randomized to a one-week decolonization treatment, which consisted of twice-daily nasal mupirocin and a chlorhexidine body wash and occurred between visits. Verbal questionnaires were conducted at each visit using an iFormBuilder (iFormBuilder, Herndon, VA) application for iPad (Apple, Cupertino, CA) and data regarding pet-related characteristics were collected.

2.2. Companion animal sampling

At each household visit, all pets were sampled under the supervision of a veterinarian using dry culture swabs with transport media (BBL™ Culture Swabs). Four swabs were collected from each pet from the nares, mouth, inguinal region, and perineum. The swab tip was inserted into the nares, or the nasal planum was swabbed when necessitated by poor patient tolerance or small size of the nares. For the mouth, the tongue, gingiva, or hard palate was swabbed. For inguinal and perineal samples, the swab was rubbed gently against the skin of the appropriate region.

2.3. Bacterial culture

Culture swabs were transported to the laboratory and culture-based laboratory methods consisting of two parallel enrichment arms (optimized for methicillin-susceptible (MS) or methicillin-resistant (MR) isolates) were used for recovery of CPS as previously described (Davis et al., 2012a). Swabs were enriched in a Mueller-Hinton broth + 6.5% NaCl and then (for MR only) a Tryptic Soy Broth + 2.5% NaCl + 3.5 mg/L cefoxitin + 10 mg/L aztreonam. Broths were incubated at 37 °C for 16–20 h and then a 10 μl aliquot was subcultured to BBL™ Columbia CNA agar with 5% sheep blood; plates were incubated at 37 °C for 16–20 h. Presumptive staphylococcal colonies were identified on CNA and all phenotypically unique colonies were subcultured to Baird-Parker (BP) agar. All presumptive CPS (based on BP phenotype and additional tube coagulase testing for MS isolates that did not demonstrate lecithinase activity on BP) were archived to Microbank™ tubes (Pro-Lab Diagnostics, Canada) and held at −80 °C. *S. aureus* ATCC43300, *S. pseudintermedius* ATCC49444, and *S. schleiferi* VHUP1939-05 were used as positive controls for culture and PCR.

2.4. PCR speciation of isolates

A single isolate per visit from each animal was selected by one member of the study team (M.F.D.) for speciation by PCR based on blood agar phenotype. Specifically, hemolytic, gold colonies (presumptive *S. aureus*) from the methicillin-resistant-selective culture arm were chosen over non-hemolytic, non-gold colonies not selected for resistance. To identify *S. aureus*, *S. pseudintermedius*, or *S. schleiferi*, a multiplex PCR assay that amplifies species-specific segments of the nuclease gene (*nuc*) was performed as previously described (Sasaki et al., 2010). Methicillin-resistant isolates (MRSA, MRSP) were determined by presence of a universal *mecA/C* sequence, with ATCC43300 and LGA251 used as *mecA* and *mecC* positive controls respectively (Garcia-Álvarez et al., 2011).

2.5. Statistical analysis

Descriptive and statistical analyses were performed using Stata statistical software (version 12.0, Stata Corp, College Station, TX). Survey-weighted logistic regression, controlling for correlation of pets within households, was used to assess risk factors for anatomic site-specific positivity.

2.6. Subset analysis

A subset of 25 households (the first 20 homes enrolled through the four urban-based hospitals, and the first five homes enrolled through the rural hospital) was selected for more detailed analysis to evaluate any bias introduced by isolate selection. All isolates identified from pets in these households were speciated by PCR. Population-averaged, longitudinal analysis was conducted using generalized estimating equation models (XTGEE) in Stata 13.1, accounting for correlation of isolates within pet.

3. Results

3.1. Enrollment

One hundred and seventy-nine (97% of 184 enrolled) pets were sampled at the baseline visit, and 125 at follow-up (96% of 130 enrolled; 108 continuing pets, 17 new pets). Supplemental Table 1 demonstrates that dogs and cats were the most prevalent species, followed by reptiles (primarily aquatic turtles). Thirty percent of owners reported that their pets had contact with a veterinary healthcare setting and five percent reported pet use of antimicrobial drugs in the prior year.

Supplementary Table 1 related to this article can be found, in the online version, at http://dx.doi.org/10.1016/j.vetmic.2015.01.003.

3.2. CPS and staphylococcal species prevalence

The prevalence of CPS at baseline was 74% (132/179) of sampled pets (Table 1a). Based on PCR of a single isolate from each positive pet, the prevalence of *S. aureus* and *S. pseudintermedius* was 15% and 18% respectively. Supplemental Table 2 displays results from non-mammalian pets, which were significantly less likely to carry CPS than mammals (OR = 0.11; 95% CI: 0.05, 0.26; $p < 0.001$). Among 145 mammalian pets at baseline, the prevalence of MRSA carriage was 8%, MSSA was 9%, MRSP was 1% and MSSP was 19%. *S. schleiferi* was isolated from only one dog (1%) (mouth). The majority of isolates from cats (34/47) and pocket pets (8/8) were CPS species other than *S. aureus*, *S. pseudintermedius* or *S. schleiferi* based on the results of the *nuc* PCR. No further characterization was performed.

Supplementary Table 2 related to this article can be found, in the online version, at http://dx.doi.org/10.1016/j.vetmic.2015.01.003.

Follow-up visits occurred approximately three months after the baseline visit (mean: 93.5 days; SD: 17.3); during the interim time period, 23 of 44 continuing homes (52%) were randomized to a household-wide human decolonization protocol. At the follow-up visit, 63% of 125 sampled pets were positive for CPS (Table 1b). Among 95 mammalian pets at follow-up, the prevalence of MRSA carriage was 7%, MSSA was 13%, MRSP was <1% and MSSP was 20%; no pets were positive for *S. schleiferi*. Among 82 mammalian pets sampled at both baseline and follow-up visits, pets MRSA positive at baseline were 11 times more likely to remain MRSA positive at three months (95% CI: 1.6, 67.3; $p = 0.02$). Randomization of humans in households to decolonization treatment was not associated with differences in companion animal MRSA, *S. aureus*, or *S. pseudintermedius* prevalence.

3.3. Anatomical site analyses

The sensitivity at each sampled anatomic site was determined only from mammalian pets. Sensitivities for the single most sensitive site and the most sensitive combination of two sites for the isolation of CPS are shown in Table 2. The mouth was the single most sensitive site for the isolation of *S. aureus* among 6/6 groups considered. The most sensitive single site for the isolation of *S. pseudintermedius* was the mouth in 4/6 groups, and the perineum in 3/6 groups considered. The most sensitive combination of sites varied by staphylococcal species and time point. Dogs were nearly three times more likely than cats to have CPS isolated from the nares (OR = 2.5; 95% CI: 1.2, 4.9; $p = 0.011$) and perineum (OR = 2.9; 95% CI: 1.4, 6.2; $p = 0.005$). Neither use of antimicrobials by companion animals nor randomization of people in households to decolonization treatment between visits was associated with significant changes in anatomic site sensitivity.

Table 1a
Prevalence of staphylococcal species among sampled pets at baseline.

Pet species, *N*	Prevalence, *N* (%)			
	CPS[a]	*S. aureus*[b]	*S. pseudintermedius*[b]	Other staph[b,c]
All pets[d], 179	132 (74%)	27 (15%)	33 (18%)	7 (40%)
Dogs[e], 71	65 (92%)	14 (20%)	29 (41%)	21 (30%)
Cats, 63	47 (75%)	11 (17%)	2 (3%)	34 (54%)
Pocket pets, 11	8 (73%)	0 (0%)	0 (0%)	8 (73%)

[a] Coagulase-positive staphylococci.
[b] Based on molecular identification of a single screening isolate for each pet-visit.
[c] PCR negative for *S. aureus*, *S. pseudintermedius*, and *S. schleiferi*.
[d] Includes pets of all species sampled (dogs, cats, pocket pets, reptiles, fish tanks, and birds). Prevalence data for reptiles, fish tanks, and birds is available in Supplementary Table 1.
[e] 1 dog was positive for *S. schleiferi*.

Table 1b
Prevalence of staphylococcal species among sampled pets follow-up.

Pet species, *N*	Prevalence, *N* (%)			
	CPS[a]	*S. aureus*[b]	S. *pseudintermedius*[b]	Other staph[b,c]
All pets[d], 125	79 (63%)	19 (15%)	21 (17%)	39 (31%)
Dogs, 38	34 (89%)	9 (34%)	20 (53%)	5 (13%)
Cats, 48	33 (69%)	10 (21%)	1 (2%)	22 (77%)
Pocket pets, 9	7 (78%)	0 (0%)	0 (0%)	7 (78%)

[a] Coagulase-positive staphylococci.
[b] Based on molecular identification of a single screening isolate for each pet-visit.
[c] PCR negative for *S. aureus*, *S. pseudintermedius*, and *S. schleiferi*.
[d] Includes pets of all species sampled (dogs, cats, pocket pets, reptiles, fish tanks, and birds). Prevalence data for reptiles, fish tanks, and birds is available in Supplementary Table 1.

Table 2
Anatomic site sensitivity[a] by pet species and staphylococcal species.

	CPS[b]		*S. aureus*[c]		*S. pseudintermedius*[c]		Other staph[c,d]	
	Baseline	Follow-up	Baseline	Follow-up	Baseline	Follow-up	Baseline	Follow-up
All mammals								
Positive pets/ Total pets	120/145	74/95	25/145	19/95	31/145	21/95	63/145	34/95
Most sensitive single site	Mouth (78%)	Mouth (74%)	Mouth (96%)	Mouth (79%)	Mouth (81%)	Mouth (86%)	Mouth (78%)	Mouth (78%)
Most sensitive pair of sites	Mouth + Nares (92%)	Mouth + Perineum (92%)	Mouth + Perineum (100%)	Mouth + Nares (89%)	Mouth + Perineum (100%)	Mouth + Perineum (100%)	Mouth + Nares (87%)	Mouth + Nares (87%)
Dogs								
Positive pets/ Total pets	65/71	34/38	14/71	9/38	29/71	20/38	21/71	5/38
Most sensitive single site	Mouth (85%)	Mouth (85%)	Mouth (100%)	Mouth (89%)	Perineum (90%)	Mouth (85%)	Mouth (76%)	Mouth (80%)
Most sensitive pair of sites	Mouth + Nares (97%)	Mouth + Perineum (97%)	Perineum[e] (86%)	Mouth + Perineum (100%)	Mouth + Perineum (100%)	Mouth + Perineum (100%)	Mouth + Nares (100%)	Mouth + Nares (100%)
Cats								
Positive pets/ Total pets	47/63	33/48	11/63	10/48	2/63	1/48	34/63	22/48
Most sensitive single site	Mouth (70%)	Mouth (67%)	Mouth (91%)	Mouth (70%)	Perineum (100%)	Nares/ Mouth/ Perineum[f]	Mouth (65%)	Mouth/ Inguinal (64%)
Most sensitive pair of sites	Mouth + Inguinal (85%)	Mouth + Inguinal (89%)	Mouth + Nares (100%)	Mouth + Nares (90%)	Nares/Mouth[g] (50%)	n/a[h]	Mouth + Inguinum (85%)	Mouth + Inguinum/ Perineum (91%)

[a] The sensitivity of each anatomic site was calculated by dividing the number of animals positive at a specific anatomic site by the number of animals positive at any site.
[b] Coagulase-positive *Staphylococcus*.
[c] CPS carriage based on pet-level assignment using molecular identification of a single screening isolate per pet-visit.
[d] Screening isolate PCR negative for *S. aureus*, *S. pseudintermedius*, and S. *schleiferi*.
[e] 100% sensitivity was achieved with the mouth alone. The perineum was the second most sensitive single site.
[f] For the one cat that was positive for *S. pseudintermedius* at follow-up, isolates were obtained from the nares, mouth, and perineum.
[g] 100% sensitivity was achieved with the perineum alone. The mouth and nares were both the second most sensitive site.
[h] 100% sensitivity for all combinations of sites.

3.4. Subset analysis

Characteristics of the subset of 25 households (the first 20 homes enrolled through the four urban-based hospitals, and the first five homes enrolled through the rural hospital) are displayed in Supplemental Table 3. Among 32 mammalian pets at baseline, the prevalence of MRSA carriage was 9%, MSSA was 28%, MRSP was 3% and MSSP was 41%. Among 19 mammalian pets at follow-up, the prevalence of MRSA carriage was 0%, MSSA was 26%, MRSP was 0% and MSSP was 42%. No *S. schleiferi* isolates were identified from animals in the subset. Table 3 provides

Table 3
Anatomical site prevalence in the subset of sampled pets with complete testing.

	S. aureus		*S. pseudintermedius*	
	Baseline	Follow-up	Baseline	Follow-up
All mammals, n = 32 at baseline, 19 at follow-up				
Nares, *n* (%)[a]	4 (13%)	**3 (16%)**	5 (16%)	3 (16%)
Mouth, *n* (%)	**10 (31%)**	2 (11%)	**8 (25%)**	**7 (37%)**
Inguinum, *n* (%)	2 (6%)	1 (5%)	7 (22%)	3 (16%)
Perineum, *n* (%)	2 (6%)	1 (5%)	**8 (25%)**	4 (21%)
Dogs, n = 14 at baseline, 7 at follow-up[b]				
Nares, *n* (%)	2 (14%)	1 (14%)	5 (36%)	3 (43%)
Mouth, *n* (%)	**7 (50%)**	**2 (29%)**	**7 (50%)**	**5 (71%)**
Inguinum, *n* (%)	1 (7%)	1 (14%)	**7 (50%)**	3 (43%)
Perineum, *n* (%)	1 (7%)	0 (0%)	6 (43%)	3 (43%)
Cats, n = 14 at baseline, 9 at follow-up				
Nares, *n* (%)	2 (14%)	**2 (22%)**	0 (0%)	0 (0%)
Mouth, *n* (%)	**3 (21%)**	0 (0%)	1 (7%)	**2 (22%)**
Inguinum, *n* (%)	1 (7%)	0 (0%)	0 (0%)	0 (0%)
Perineum, *n* (%)	1 (7%)	1 (11%)	**2 (14%)**	1 (11%)

The bold highlights the anatomic site with the highest prevalence in each group.
[a] *n* = 31 for nares at baseline due to one rodent that had a combined nares/mouth sample. This sample is counted only for the mouth.
[b] *S. aureus* and *S. pseudintermedius* categories are non-exclusive; carriage of *S. aureus* and *S. pseudintermedius* at the same anatomical site was identified in one dog at the nares at the follow-up visit, in two dogs at the mouth at the baseline visit, and in one dog at the perineum at the baseline visit.

details of staphylococcal species prevalence by anatomical site among mammalian pets at each visit, and demonstrates that the mouth was most frequently the site of highest prevalence for *S. aureus* and *S. pseudintermedius*. Prevalence of carriage of both *S. aureus* and *S. pseudintermedius* by the same pet was 22% at baseline and 11% at follow-up, with MSSA-MSSP representing the most common dual carriage combination. In one dog, MRSA and MRSP isolates were identified from the perineal sample at baseline. Dogs and cats were 2.9 times more likely to have *S. pseudintermedius* isolated from the mouth than the nares (95% CI: 1.2, 7.4; $p = 0.02$).

Supplementary Table 3 related to this article can be found, in the online version, at http://dx.doi.org/10.1016/j.vetmic.2015.01.003.

4. Discussion

This work identifies the mouth as the most sensitive anatomic site to sample for the detection of MRSA and other CPS among companion animals recently exposed to MRSA-infected owners, a pet population that may be considered as a potential reservoir in cases of refractory human disease. These results suggest that sampling protocols for MRSA and other CPS should always include the mouth. This is in contrast to the predominantly nares-based sampling strategies reported in the literature (Bender et al., 2011; Faires et al., 2009; Ferreira et al., 2011). For the isolation of *S. pseudintermedius*, the perineum was an important secondary site, especially among dogs. It is notable that among all mammals as a group and dogs as a species, the combination of mouth + perineum achieved 100% sensitivity for the detection of *S. pseudintermedius* at both visits.

The inguinal site was not an informative sampling site for CPS, either *S. aureus*, or *S. pseudintermedius*, as any animal that was positive at the inguinal site was also positive at one or more other sites. Among cats, the mouth + inguinal site was the most sensitive combination for the detection of CPS and other staphylococcal species (not *S. aureus*, *S. pseudintermedius*, or *S. schleiferi*), suggesting that the inguinal site is sensitive for the detection of these other CPS species, which were frequently noted among cats. Further work is needed to determine which coagulase-positive *Staphylococcus spp.* this category represents.

Pets were sampled at two time points approximately three months apart. The prevalence of MRSA at both visits was within the range observed in dogs (2.6–14.9%) and cats (0–9%) in similar studies that sampled animals in the homes of an MRSA-positive human (Faires et al., 2009; Bender et al., 2011; Ferreira et al., 2011; Morris et al., 2012). There were slight differences between the most sensitive sites and most sensitive combination of two sites between the baseline and follow-up populations in Table 2, which may be the result of minor changes in the sampling population over time as pets left or joined the household. Randomization of humans in the house to decolonization treatment between visits was not associated with changes in prevalence or anatomic site carriage in pets at the follow-up visit. While this was expected for *S. pseudintermedius*, which is a host specialist for canidae (Bannoehr and Guardabassi, 2012), this finding was surprising for *S. aureus* and MRSA, given that pets have been demonstrated to carry human epidemic strains (Bender et al., 2011; Ferreira et al., 2011; Harrison et al., 2014) and that delays between MRSA diagnosis of an owner and sampling of a pet previously have been shown to be associated with reductions in pet carriage (Morris et al., 2012). This could be related to poor participant compliance with the protocol or could be due to environmental contamination of the household, which may have perpetuated exposure (Davis et al., 2012b).

Carriage of multiple staphylococcal species by an animal may allow for increased opportunities for horizontal gene transfer (Bloemendaal et al., 2010). Dual carriage

of target CPS in the subset analysis was slightly higher (22% at baseline, 11% at follow-up) than in previous reports, and one dog was identified that carried MRSA and MRSP from the same perineal sample. Gomez-Sanz et al. found dual carriage (MSSA and MRSP) in 2% (1/54) of dogs (Gomez-Sanz et al., 2012). *S. aureus* and *S. pseudintermedius* co-colonization was found in 6% (3/48) of cats with skin disease and 8% (4/50) of healthy cats (Abraham et al., 2007). Similarly, Griffeth et al. found co-carriage (*S. aureus* and *S. pseudintermedius*; *S. schleiferi* and *S. pseudintermedius*) in 3% (2/59) of dogs with skin disease and 4% (2/50) of healthy dogs (Griffeth et al., 2008). Carriage profiles in our study may have been influenced by household MRSA exposure, low veterinary contact, or an unidentified factor.

The population of pets considered in this study had a known MRSA exposure, and results may not be generalizable to all pets. Another limitation of this study is that our laboratory culture methods were optimized for detection of *S. aureus*; however, any isolate that was negative for lecithinase activity on Baird Parker agar was then tube coagulase tested, so it is unlikely that CPS were missed. Further, our broth enrichment and blood agar identification protocol were similar to those used by prior studies for evaluation of pet staphylococci, including *S. pseudintermedius* and *S. schleiferi* (Hanselman et al., 2009; Paul et al., 2012). Prevalence by staphylococcal species was based on a single screening isolate; therefore, dual carriage was not captured except in the subset, and true positivity for *S. aureus*, *S. pseudintermedius*, or *S. schleiferi* may have been missed if the screening isolate was PCR negative for these species. Results of the subset analysis suggested that screening was accurate for MRSA carriage, the bacterial species for which the screening protocol was designed, but underestimated MSSA and MSSP prevalence. Results reported here represent two cross-sectional sampling events, and cannot differentiate between contamination, intermittent and persistent carriage. However, pets MRSA-positive at baseline were more likely than MRSA-negative pets to be MRSA-positive three months later, which may suggest persistence of either carriage or exposure. More frequent sampling and genetic testing of isolates may be necessary to determine a pet's carrier status.

As veterinarians are increasingly presented with pets of MRSA-diagnosed individuals to determine carriage status, correct identification of positive pets is critical for a one health approach to patient management. Further, accurate characterization of companion animal staphylococcal carriage profiles is increasingly important in the research setting. Most prior studies relied on testing of the nares or the nares with skin or perineum for detection of MRSA (Faires et al., 2009; Hanselman et al., 2009; Bender et al., 2011; Ferreira et al., 2011; Gomez-Sanz et al., 2012; Walther et al., 2012). Our results strongly suggest that the mouth should be included in sampling protocols to detect *S. aureus* or *S. pseudintermedius*, particularly in pets exposed to MRSA-diagnosed people. If possible, the perineum also should be sampled. These results inform the development of harmonized sampling protocols that will increase comparability among studies and assist physicians and veterinarians to develop household-wide treatment plans that target recurrent infections in people and pets.

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