Environmental Methicillin-Resistant *Staphylococcus aureus* in a Veterinary Teaching Hospital During a Nonoutbreak Period

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Abstract

Concurrent to reports of zoonotic and nosocomial transmission of methicillin-resistant *Staphylococcus aureus* (MRSA) in veterinary settings, recent evidence indicates that the environment in veterinary hospitals may be a potential source of MRSA. The present report is a cross-sectional study to determine the prevalence of MRSA on specific human and animal contact surfaces at a large veterinary hospital during a nonoutbreak period. A total of 156 samples were collected using Swiffers® or premoistened swabs from the small animal, equine, and food animal sections. MRSA was isolated and identified by pre-enrichment culture and standard microbiology procedures, including growth on Mueller-Hinton agar supplemented with NaCl and oxacillin, and by detection of the *mecA* gene. Staphylococcal chromosome cassette *mec* (SCC*mec*) typing and pulsed-field gel electrophoresis profile were also determined. MRSA was detected in 12% (19/157) of the hospital environments sampled. The prevalence of MRSA in the small animal, equine, and food animal areas were 16%, 4%, and 0%, respectively. Sixteen of the MRSA isolates from the small animal section were classified as USA100, SCC*mec* type II, two of which had pulsed-field gel electrophoresis pattern that does not conform to any known type. The one isolate obtained from the equine section was classified as USA500, SCC*mec* type IV. The molecular epidemiological analysis revealed a very diverse population of MRSA isolates circulating in the hospital; however, in some instances, multiple locations/surfaces, not directly associated, had the same MRSA clone. No significant difference was observed between animal and human contact surfaces in regard to prevalence and type of isolates. Surfaces touched by multiple people (doors) and patients (carts) were frequently contaminated with MRSA. The results from this study indicate that MRSA is present in the environment even during nonoutbreak periods. This study also identified specific surfaces in a veterinary environment that need to be targeted when designing and executing infection control programs.

Key Words: environment—MRSA—nosocomial—veterinary hospital.

Introduction

IN RECENT YEARS, methicillin-resistant *Staphylococcus aureus* (MRSA) infections have become a growing concern in veterinary medicine. Several reports have shown that MRSA can also spread in veterinary hospital settings from humans to animals (reverse zoonosis) and from animals to humans (zoonosis), and has the ability to survive in the environment (Seguin et al. 1999, Van Duijkeren et al. 2004, Weese et al. 2004, 2005, 2006, Baptiste et al. 2005, O'Mahony et al. 2005, Leonard

et al. 2006). Not only is this a concern from the point of view of nosocomial transmission in veterinary hospitals and the negative effect on animal health, the presence of MRSA in veterinary settings is also a growing occupational health issue for the veterinary community, where staff and veterinarians could be routinely exposed to this pathogen (Benedict et al. 2008).

Concurrent to reports of zoonotic and nosocomial transmission of MRSA in veterinary settings, there is new evidence to support MRSA survival in the veterinary hospital

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environment, as has been observed in human hospitals (Weese et al. 2004, Loeffler et al. 2005, Heller et al. 2009). Weese et al. (2004) have indicated that the environment may be a source of MRSA infection for animals and humans, especially if the environment is not disinfected thoroughly after MRSA-positive animals have been admitted. Nevertheless, MRSA environmental contamination in veterinary hospitals is not well understood, especially during nonoutbreak periods.

An internal retrospective study from 2004 to 2006 at The Ohio State University Veterinary Medical Center (OSU-VMC) determined that MRSA was already prevalent in clinical cases in dogs, horses, cats, and other animal species admitted to the hospital. From 109 *S. aureus* isolates identified by the clinical microbiology laboratory from a variety of host species at the OSU-VMC, 53 (48.6%) were classified as MRSA (Hoet, A.E., unpublished data). These data clearly showed that MRSA-positive animals were visiting the hospital regularly and possibly contaminating the environment.

As contaminated environments at veterinary teaching hospitals may serve as a potential source of this important pathogen to humans as well as animals, a cross-sectional study was performed to determine the prevalence of MRSA on specific human and animal contact surfaces of the small animal, equine, and food animal sections of the veterinary teaching hospital. The specific aims of the study were to document the extent of MRSA contamination of the environment in a large veterinary hospital, and to identify the most commonly contaminated surfaces, or hot spots, which may be targeted for specific disinfection and cleaning, as well as for monitoring the presence and spread of this emerging veterinary nosocomial pathogen.

Materials and Methods

Locations and surfaces sampled

This cross-sectional study was conducted at the OSU-VMC from March to May 2007. An initial sampling of 57 surfaces from the environment in the small animal section was completed and followed a month and a half later by a second sampling (see Table 2), in which a total of 100 surfaces were sampled from the environment across the small animal ($n = 53$), equine ($n = 23$), and food animal ($n = 24$) sections of the OSU-VMC. Within each section, specific environments such as the ICU, surgery suites, examination rooms, dermatology area, animal wards, and animal pens were targeted for surveillance. These areas were selected, as the presence of MRSA in these environments could represent a major risk for ICU or surgery patients, as well as susceptible dermatology patients. Sampling was performed during a period when, up to 1 week before collection, there had been no identified MRSA outbreaks or hospitalization of clinical MRSA cases.

The environmental sampling locations within each section were categorized as human and animal contact surfaces as described in Table 1. These surfaces were selected based on the following criteria: the animal contact surfaces were directly contacted by multiple animals (e.g., gurneys, examination tables, and restraining equipment), and the human contact surfaces were directly contacted by multiple people and were out of direct reach of animals (e.g., light switches, computer keyboards, and doors). Other general surfaces of interest such as air vents and vacuum equipment were also sampled.

Sampling techniques and processing

Swiffer® (Proctor and Gamble) or swab sampling techniques were used on each surface depending on their size and type of surface. For example, keyboards and light switches were sampled with swabs due to their small surface area, whereas cages and gurneys were sampled with a Swiffer due to the large surface to be sampled. Table 1 summarizes which method was used to sample each human and animal contact surface. In a few cases, multiple surfaces in the same area were sampled together as a pool, such as computer keyboards/mice, light switches, microscopes knobs, drawer handles, countertops, muzzles, and cages (see Table 1). The doors were sampled by using a swiffer on the handles and their surrounding areas up to a foot in either direction from the handle in both sides of the door.

All samples were systematically collected by the surveillance team in the preselected areas by swabbing sterile cotton-tip culture swabs (premoistened in sterile tryptone soy broth) or using electrostatic commercial cloths (Swiffer) to cover the entire surface. After collection the swabs were placed in tryptone soy broth and incubated aerobically at 35°C for 24 h as described previously (Weese et al. 2004). When sampling with a Swiffer cloth, only one side of the cloth was used to sample the surface, which then was folded and placed in a sterile bag. Gloves were used at all time when collecting samples and they were changed between samples. Soon after collection, sterile buffered peptone water was added to each bag using aseptic techniques at the Diagnostic and Research Laboratory for Infectious Diseases, at the OSU College of Veterinary Medicine. All bags were then incubated at 35°C for 24 h. For quality assurance, negative controls for both the swab and electrostatic cloth were included in every sampling.

Isolation and identification

After incubation in the pre-enrichment media, the samples were streaked onto mannitol salt agar plates containing Oxacillin (2 µg/mL), which were incubated at 35°C. Plates were examined at 24 h; if negative, they were incubated for additional 24 h. Three colonies with typical mannitol reaction were selected to be plated on Tryptic Soy Agar with 5% Sheep Blood plates to be further characterized. *S. aureus* was identified by standard colony morphology, size, pigmentation, and hemolysis pattern, as well as mannitol fermentation, gram stain reaction, catalase reaction, tube coagulase reaction, anillin reaction, Polimixin B susceptibility, acetoin production (Voges-Proskauer test), and latex agglutination reaction (Sure-View® Color Staph ID; Biokit USA, inc.). Phenotypic identification of MRSA was confirmed by growth on Oxacillin Screen Agar® plates contains 6 µg/mL of Oxacillin supplemented with NaCl (BD BBLTM, Becton Dickinson and Company) following Clinical and Laboratory Standards Institute protocols (CLSI 2008).

Antimicrobial susceptibility testing (phenotyping)

Antimicrobial susceptibility patterns for all MRSA isolates detected were determined by the Kirby-Bauer disc diffusion method, as described by the CLSI (2008). The antimicrobial susceptibility panel included 16 antibiotics: amikacin, ampicillin, amoxicillin with clavulanate, cefovecin, cefpodoxime,

cephalothin, chloramphenicol, ciprofloxacin, clindamycin, doxycycline, enrofloxacin, erythromycin, gentamicin, oxacillin, tetracycline, and trimethoprim with sulfa. Vancomycin resistance was screened using Vancomycin Screen Agar plates (6 mg/L) (BD Diagnostic System). The following quality control strains were used during the phenotyping: *Enterococcus faecalis* (ATCC® 23212), *Escherichia coli* (ATCC 25922), *Pseudomonas aeruginosa* (ATCC 27853), *S. aureus* (ATCC 29213), *S. aureus* (ATCC 25923), and *S. aureus* (ATCC 43300). Multi-drug resistance was defined as resistance to three or more classes of antimicrobial agents. Inducible clindamycin resistance was determined by placing the erythromycin disk 12 mm from the edge of a clindamycin disk (Fiebelkorn et al. 2003).

S. aureus confirmation, *mecA* confirmation, *Staphylococcal chromosome cassette mec* typing, and pulsed-field gel electrophoresis

A random subset of isolates were submitted to the Animal Disease Diagnostic Laboratory of the Ohio Department of Agriculture for microbiological and genetic (16S rRNA sequencing) confirmation. All MRSA isolates were screened to confirm the presence of the *mecA* gene using a multiplex polymerase chain reaction approach, modified from the protocol by Oliveira and Lencastre (2002), which simultaneously allows for the rapid assignment of *Staphylococcal* chromosome cassette *mec* (SCC*mec*) types to MRSA strains. All isolates were then characterized further by pulsed-field gel electrophoresis (PFGE). The macrorestriction of genomic DNA of all MRSA isolates was performed as described by Mulvey et al. (2001). A dendrogram showing the level of clonal relatedness was created and analyzed with commercial software (Bionumerics; Applied Maths, Inc.) and with visual confirmation. Percent similarities were identified on a dendrogram derived from the unweighted pair group method using arithmetic averages and based on Dice coefficients. Band position tolerance and optimization were set at 1.5%. A similarity coefficient of 80% was selected to define the pulsed-field type (PFT) clusters after including the phenotyping and SCC*mec* typing associated with each of the isolates.

Data analysis

The data were analyzed separately according to human and animal contact surfaces, and separated by veterinary hospital section. A chi-squared test was conducted to compare the relationship between human and animal contact surfaces. Statistical significance was determined at the cut-off value of 0.05 ($p \leq 0.05$).

Results

Environmental MRSA detection

A total 157 samples were collected from the environment in three different sections of the veterinary teaching hospital (Table 1). In the small animal section, 110 samples were collected in two separate days: 57 on the first sampling and 53 on the second sampling 1.5 months later. The second sampling of the small animal section was performed to confirm the results obtained in the first sampling of such section. Samples were collected from the same surfaces during the second sampling, with the exception of the air vents and vacuum equipment

which were sampled together as a pool during the second sampling instead of individual samples as in the first sampling.

On average, 49.7% (78/157), 47.8% (75/157), and 2.5% (4/157) of the total sample collected came from human and animal contact surfaces as well as from general contact surfaces, respectively. MRSA was detected in 12.1% (19/157) of the human and animal contact surfaces. No MRSA was recovered from air vents or the vacuum equipment on either date. The highest detection rate of MRSA in the environment was found in the small animal section of the hospital, with an average of 16.4% (18/110), whereas only one MRSA isolate was recovered from the equine section and no isolates were detected from the food animal section of the hospital (Table 2).

There was no statistically significant difference between MRSA contamination on animal contact surfaces (14.7%, 11/75) and human contact surfaces (10.3%, 8/78) ($p > 0.4$). All 11 MRSA isolates detected from animal contact surfaces were from the small animal section, where the positive surfaces were carts/gurneys (3), cages (3), examination tables (1), examination floors (1), muzzles (1), water bowls (1), and general equipment (1). Seven of the MRSA isolates detected in human contact surfaces were from the small animal section from doors (5), one computer keyboard/mouse (1), and bathroom faucets (1). The only isolate detected in the equine section was also obtained from a door.

Phenotyping

All the MRSA isolates obtained from the small animal section had the same antimicrobial resistance pattern. These isolates showed resistance to all beta-lactamic drugs tested (ampicillin, amoxicillin with clavulanate, cefovecin, cefpodoxime, cephalothin, and oxacillin) as expected. They were also resistant to Erythromycin, as well as quinolones (ciprofloxacin and enrofloxacin). Interestingly, all 19 MRSA isolates showed inducible clindamycin resistance. The MRSA isolates from this section were 100% susceptible to the following classes of antimicrobial drugs: gentamicin, tetracyclines, chloramphenicol, trimethoprim/sulfa, and vancomycin; they showed intermediate resistance to amikacin. In contrast, the sole isolate from the equine section showed a broad multidrug resistance profile, with resistance to all beta-lactams, erythromycin, gentamicin, and trimethoprim/sulfa, and susceptibility to quinolones, amikacin, chloramphenicol, clindamycin, vancomycin, and doxycycline. Interestingly, this last isolate was the only MRSA strain resistant to tetracycline.

Genotypic analysis

All MRSA isolates tested by the Animal Disease Diagnostic Laboratory of the Ohio Department of Agriculture were confirmed to be MRSA after culture and genetic analysis. The *Sma*I macrorestriction fragment profiles of the 19 *S. aureus* isolates were determined by PFGE. A dendrogram of percent similarity calculated with Dice coefficients from the PFGE data using a cut-off of 80% (in addition of the phenotyping and SCC*mec* typing). All MRSA isolates obtained from the small animal section carried the *mecA* gene and SCC-type II, and based on their PFGE patterns, 15 of them were classified as USA100 and two had PFGE patterns that do not conform to any CDC categorized ones. The unique isolate obtained from the equine section was also a *mecA* carrier, but was classified as a SCC-type IV, USA500. The findings revealed that

TABLE 1. HUMAN AND ANIMAL ENVIRONMENTAL CONTACT SURFACES SAMPLED FOR METHICILLIN-RESISTANT *STAPHYLOCOCCUS AUREUS* CONTAMINATION, INCLUDING SAMPLING TECHNIQUE USED WITH EACH SURFACE, IN THE SMALL ANIMAL, EQUINE, AND FOOD ANIMAL SECTIONS AT THE OHIO STATE UNIVERSITY-VETERINARY MEDICAL CENTER

	Small animal section	Equine section	Food animal section
Human contact surfaces	Swab sampling		
	Addressographs	Anesthesia machine ^b	Anesthesia machine ^b
	Clippers (handle)	Computer keyboards/mice ^a	Computer keyboards/mice ^a
	Computer keyboards/mice ^a	Hoist controls for surgery and examination tables	
	Examination table knobs		
	Fax/phones		
	Light switches ^a		
	Microscopes ^a		
	Otoscopes		
	Paper towel dispensers ^a		
Animal contact surfaces	Hand sanitizer dispensers ^a		
	Soap dispensers		
	Surgery table knobs ^a		
	iv pumps		
	Swiffer [®] sampling		
	Doors	Chairs (surgery) ^b	Chairs (surgery) ^b
	Drawer handles ^a	Doors	Doors
	Exam lights ^a	Drawer handles/countertops ^a	Drawer handles/countertops
	Water faucets	Exam lights ^{a,b}	Exam lights ^{a,b}
		Endoscope (controls)	Faucets + towel dispensers ^b
General surfaces		Faucets + towel dispensers ^b	Phones ^b
		Phones ^b	Refrigerator
	Swab sampling		
	Clippers (blade) ^a	Hair brushes ^a	Halters
	Muzzles (per ward) ^a	Endoscope controls	Milking machine (teatcups) ^a
	Oxygen monitors ^a	Twitches	Nose tongs ^a
	Washer	Ultrasound	
	Swiffer sampling		
	Cages (per ward) ^a	Anesthesia prep stalls (pads)	Chute
	Carts/gurneys	Endoscope probes	Cushion pads ^a
General surfaces	Exam tables ^a	Exam/preparation tables (pads) ^a	Exam/preparation tables (pads) ^a
	Floor (exam) ^a	Examination stocks	Head catcher ^a
	Warming pads ^a	Recovery stalls (pads)	Mobil chutes
	Water bowls (per ward) ^a	Ultrasound (probe)	Pneumatic table
	Air vents ^c	Not applicable	Water + food bowls ^a
	Vacuum equipment ^c		Not applicable

^aThese surfaces were sampled as a pool if more than one was located in a room or location.

^bSome of these equipments are shared between the equine and food animal sections.

^cAir vents and vacuum equipment (hoses) were sampled using swiffers and swabs, respectively.

TABLE 2. PREVALENCE OF METHICILLIN-RESISTANT *STAPHYLOCOCCUS AUREUS* IN HUMAN AND ANIMAL CONTACT SURFACES IN THE SMALL ANIMAL, EQUINE, AND FOOD ANIMAL SECTIONS AT A LARGE REFERRAL VETERINARY HOSPITAL

Section	Human contact MRSA/samples collected	Animal contact MRSA/samples collected	General surfaces ^a	Total MRSA/samples collected
Small animal (1st sampling)	5/29 (17.9%)	6/25 (24%)	0/3	11/57 (19.2%)
Small animal (2nd sampling)	2/28 (7.1%)	5/24 (20.8%)	0/1 ^b	7/53 (13.2%)
Sub total small animal section				18/110 (16.4%)
Equine	1/13 (7.7%)	0/10 (0%)	—	1/23 (4.3%)
Food animal	0/8 (0%)	0/16 (0%)	—	0/24 (0%)
Total	8/78 (10.3%)	11/75 (14.7%)	0/4	19/157 (12.1%)

^aAir vents and vacuum equipment (hoses) in the small animal section.

^bAll Air vents and vacuum equipment were sampled together as a pool on the 2nd sampling date.
MRSA, methicillin-resistant *Staphylococcus aureus*.

majority of the tested isolates were clonally related and distributed in among two major clusters (Cluster 1 [C1] with seven pulsotypes and cluster 2 [C2] with two pulsotypes, Fig. 1) and three individual pulsotypes (PFT 10–12) outside these clusters. Of the 19 MRSA isolates, 84.2% (16/19) were grouped within two clusters, with the majority of the isolates (12/19, 63.2%) belonging to C1. The remaining three MRSA isolates (VTH-0164, -00128, and -0091) had different pulsotypes (PFT-10, -11, and -12, respectively) to the predominant isolates in C1 and C2. The sole MRSA isolate from the equine section (VTH-0164) was distinctly different from those located in the small animal section. The results of SCCmec typing, antimicrobial resistance profiles, date of sampling, location of the isolates, and type of contact surfaces are also summarized in Figure 1. Of the eight MRSA isolates circulating among human contact surfaces, six of them had similar pulsotypes and all of the isolates belong to genotypic cluster type C1. In contrast, 11 MRSA isolates from animal contact surfaces had more diverse pulsotypes (e.g., at least four different types noted), with the majority of patterns corresponding to clusters C1 and C2. In any case, a slight higher diversity of MRSA strains in animal contact surfaces than in human contact surfaces was observed.

Discussion

The present report was a cross-sectional study to determine the estimated prevalence MRSA in the environment from different sections of the OSU-VMC during a nonoutbreak period. In the present study, MRSA was detected in numerous animal and human contact surfaces across different sections and areas of the hospital, identifying in some cases multiple areas sharing a common MRSA clone. The majority of MRSA isolates detected at the veterinary hospital were USA100 carrying SCCmec type II, which is also one of the most common MRSA types reported in human hospital settings (Deurenberg and Stobberingh 2009). The results have lead to the design of an active surveillance system to monitor MRSA contamination of the OSU-VMC environment.

PFGE results showed that all isolates from the first sample collection in the small animal section in March were clonally related, suggesting a horizontal dissemination or an independent acquisition from a common source. In contrast, isolates from the second day of collection (45 days apart) from the same areas and surfaces in the small animal section were more diverse and significantly distinct suggesting multiple sources. This switch from a prevalent clone on the first day of

FIG. 1. Dendrogram based on the *Sma*I macrorestriction fragment profiles of 19 *Staphylococcus aureus* isolates obtained from the environment at the Ohio State University Veterinary Teaching Hospital on two separated dates. The percent similarity was calculated with Dice coefficients from the pulsed-field gel electrophoresis data. Band position tolerance and optimization were set at 1.5%. A similarity coefficient of 80% was selected to define the pulsed-field type (PFT) clusters after including the phenotyping and Staphylococcal chromosome cassette *mec* (SCCmec) typing associated with each of the isolates.

sampling (PFT-3) to a diverse group of MRSA strains on the second day of collection is very interesting, as it apparently shows entry of new strains from multiple sources and reservoirs replacing the previous MRSA strains. Because during the sampling dates (and up to 1 week before collection) there was no known MRSA outbreak or current hospitalization of known clinical cases of MRSA-infected animals, the presence of MRSA in the environment suggest that unidentified infected/colonized animals were likely entering the hospital on a regular basis, contaminating the environment. The observation of USA100 MRSA strains may also suggest that colonized/infected personnel (including faculty, staff, and students) and visitors were probably also contributing to the MRSA environmental contamination. Similar conclusions in regard to the potential sources and movements of MRSA in a veterinary hospital were presented by other authors (Heller et al. 2009).

It was also interesting to observe that the predominant clone in the first day of collection was widely detected across multiple locations and type of surfaces (animal and human) in the small animal section. For example, the same MRSA strains (VTH-0054 and -0058) were detected the same day on the bathroom faucets as well as at the doors of the intensive care unit, locations that are physically separated by multiple doors and approximately 50 m of distance. Therefore, for these clonal strains to spread across the different surfaces and areas in the small animal section, direct as well as indirect transmission may have occurred by sharing of equipment or movement of personnel and patients among such areas. Such cross contamination apparently did not occur between the small animal and equine sections, as the MRSA isolate detected in the equine section was distinctly different from all the others, clearly indicating a different source. In any case, it is obvious that there was a dynamic movement of MRSA strains across different areas and surfaces. This finding triggered a revision of the movement of animals, shared equipment, and personnel across the hospital, especially when dealing with MRSA cases, in an attempt to avoid the contamination and spread of this nosocomial and zoonotic pathogen.

MRSA is not part of canines' regular bacterial flora; therefore, we expected only to detect a low contamination level and few strains of MRSA on the animal contact surfaces. On the other hand, there is great diversity of MRSA strains circulating in humans; therefore, it was expected to detect a higher number of human contact surfaces contaminated with a higher diversity of isolates than animal contact surfaces. However, MRSA was unexpectedly detected in animal contact surfaces (14.7% of samples) in similar numbers as in human contact surfaces (10.3% of samples) ($p > 0.4$), and with almost even number of PFT detected among the two type of surfaces (six PFT in animal contact surfaces vs. seven PFT in human contact surfaces). The common factor among the contaminated surfaces was that all were frequently used throughout the day by multiple animals and/or humans. For example, doors proved to be, as is the case in human hospitals, an important hot spot for MRSA contamination (6 isolates of 19). Several studies have also reported the presence of MRSA on doors in human (Oie et al. 2002, Cimolai 2008) and veterinary hospitals (Loeffler et al. 2005, Heller et al. 2009), indicating that they may be one of the most important sources for dissemination of this pathogen in a hospital setting even during a nonoutbreak period.

Animal contact surfaces that were also MRSA positive were carts or gurneys, as well as cages and examination tables, which in many cases showed the exact same MRSA clone even though they were in separate locations. As the doors, all of these surfaces have in common that they are regularly exposed to multiple patients and individuals during the routing activities of the hospital. The presence of MRSA in similar animal contact surfaces has been reported in other veterinary hospitals (Weese et al. 2004, Loeffler et al. 2005, Heller et al. 2009), which clearly indicate that this equipment or these locations must be closely monitored. Such results suggest that surfaces frequently touched by multiple patients or individuals that are not cleaned regularly could be potential hot spots for the presence of MRSA. Consequently, effective cleaning and disinfection of these common surfaces and equipments must be done between each patient. In addition, the presence and movement of MRSA strains in human contact surfaces, such as doors, computer keyboards, and faucets, indicates a need for increased MRSA awareness among faculty, staff, students, and clients in regard to proper hand hygiene practices and regular cleaning and disinfection of such surfaces.

In regard to a specific hospital surveillance program or established hygiene practices in place at the time of this cross-sectional study, there was no active environmental surveillance program in place at the small animal hospital; however, routine cleaning and disinfection of the different areas was applied daily. At the end of each day (or as needed), a cleaning crew would clean the cages and floors of the different rooms and wards using water and detergents (as needed), followed by an application of a sodium hypochlorite solution (floors were mopped with such solution). Cages and other surfaces were also disinfected on a need-by-need basis using quaternary ammonium disinfectants. Equipments such as muzzles and gurneys, and other contact surfaces such as computer key boards and doors were cleaned and disinfected as needed. With respect to MRSA-positive animals, at the time of this study these animals did not receive any special handling such as isolation or additional extraordinary barrier precautions. They were allowed to enter the hospital and were examined or managed in the respective section to which they were admitted.

One of the limitations of this study is that even though there is evidence to suggest the movement of single MRSA clones between areas and surfaces, the source and directionality of such movement (from animals to the environment or humans to the environment) cannot be determined. Therefore, it is difficult to determine if MRSA-positive humans or animals are more likely to be contributing to the environmental contamination in our hospital.

The results from this study indicate that MRSA could be present in the environment even during nonoutbreak periods, and that this pathogen can be equally distributed among animal and human contact surfaces. This study also shows a dynamic movement and distribution of unique MRSA strains across multiple locations and surfaces at a veterinary hospital. In light of this study, the OSU-VMC established an active MRSA surveillance for the small animal section to determine the real level of contamination of the environment overtime. Therefore, every month the same animal and human contact surfaces, which were identified as important targets for surveillance in the present study, would be sampled and screened for the presence of MRSA. In addition, the OSU-VMC reviewed and designed specific protocols to handle and

manage MRSA-positive animals entering the hospital and their associated environment, as well as improved and applied specific cleaning and disinfection protocols to be used regularly to the most likely contaminated areas here identified. These hot spots, such as gurneys and doors, in a veterinary hospital environment, need to be targeted specifically in environmental surveillance programs to monitor the presence and spread of this emerging veterinary nosocomial and zoonotic occupational pathogen, as well as when designing and executing infection control programs in veterinary hospitals.

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Disclosure Statement

No competing financial interests exist.

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