Staphylococci in animals: prevalence, identification and antimicrobial susceptibility, with an emphasis on methicillin-resistant *Staphylococcus aureus*

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ABSTRACT

Staphylococci form part of the normal flora of man and a wide variety of animals. Some staphylococcal species also cause a wide variety of pyogenic infections. The main pathogenic staphylococcus in man is *Staphylococcus aureus*. Increasingly, methicillin-resistant *S. aureus* (MRSA) has been a problem in the healthcare setting. Reports of MRSA in animals have been infrequent; however, evidence suggests that MRSA is being isolated increasingly from animals, in particular household pets and other companion animals. This article reviews the prevalence of pathogenic staphylococci in animals, with an emphasis on the emergence of MRSA as a possible animal pathogen.

KEY WORDS: Animals. Pets. Staphylococci. Staphylococcus aureus, methicillin-resistant.

Introduction

Staphylococci are facultative anaerobic, Gram-positive, catalase-positive cocci in the family *Micrococcaceae*. Staphylococci form part of the normal bacterial flora of the skin, mucous membranes and alimentary and urogenital tracts of a wide variety of mammals and birds. As well as making up part of the normal flora, some species of staphylococci may also cause a wide variety of usually pyogenic processes in various parts of the body (e.g., skin, wounds, ears and joints) in animals and humans.

In veterinary medicine, three staphylococcal species are of particular importance in specific diseases: *Staphylococcus aureus*, a cause of mastitis in animal species such as cattle, sheep, goats and horses and of dermatitis in sheep and goats; botryomycosis in pigs and horses; and suppurative conditions similar to those caused by *S. intermedius* in cats and dogs.

S. intermedius is a primary cause of pyoderma in dogs, and causes a range of other suppurative infections such as endometritis, cystitis and otitis externa in this species of animal. *S. intermedius* causes various pyogenic conditions in cats. *S. hyicus* causes exudative epidermitis (greasy pig disease) and arthritis in pigs. *S. aureus* subsp. *anaerobius* has been implicated in lymphadenitis in sheep, *S. schleiferi* subsp. *coagulans* in otitis externa in dogs and *S. delphini* as been reported as causing suppurative skin lesions in dolphins.[1]

The staphylococci mentioned above are loosely termed coagulase-positive staphylococci; however, care must be taken in the identification of these organisms as there is wide variation between the coagulase and thermonuclease reactions in some of these species. A variety of coagulase-negative staphylococci are also isolated from animals (Table 1). Most coagulase-negative staphylococci associated with animals, as with humans, are opportunistic pathogens that lack many of the virulence factors associated with coagulase-positive staphylococci.

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This review of the literature will consider the prevalence of coagulase-positive staphylococci in animals, and will concentrate on the data supporting evidence of the emergence of methicillin-resistant *S. aureus* (MRSA) as a pathogen in cats and dogs, the implications for human owners of MRSA-infected animals and the possibility of transfer between humans and animals.

Staphylococci in cats and dogs

The most prevalent *Staphylococcus* species in cats and dogs is *S. intermedius*. Raus *et al*.[2] used a range of biochemical procedures to identify 160 staphylococcal isolates from a variety of clinical diseases. A total of 123 strains were isolated from dogs, 10 from horses, 10 from cats and 17 from various other animals. After initial screening for coagulase production, all strains were tested for acid production from maltose, acid formation anaerobically from mannitol, production of acetoin, tellurite reduction, pigmentation of colonies, hyaluronidase activity and a modification of the coagulase test that inhibits the coagulase of *S. intermedius*.[3]

Of the strains studied, 27 were *S. aureus*, 115 were *S. intermedius* and 18 were either coagulase-negative by the original method or were unidentified to species level using this battery of tests and were not identified further. The study found that the most useful discrimatory tests were acid production from maltose and production of acetoin; however, it did not indicate which *Staphylococcus* species were isolated from which animals. This is significant

deficiency as different staphylococci are more prevalent in certain species of animals.

Biberstein *et al*.[4] assessed the species distribution of 268 isolates of coagulase-positive staphylococci among various animals, of which 91.8% of 195 isolates from dogs and 46.6% of 15 isolates from cats were *S. intermedius*. The remaining isolates in both cases were *S. aureus*. In this study, all staphylococcal isolates were screened for coagulase production using a tube coagulase test with rabbit plasma. Further biochemical characterisation was carried out using the API Staph-Ident system (Analytab Products, Plainview, NY, USA).

Incidentally, the study also assessed the site of infection of the original isolate and the susceptibility pattern of the isolates tested. It concluded that there were no meaningful differences in the site of infection or the susceptibility pattern between *S. aureus* and *S. intermedius* and questioned the clinical value of routine distinction between the two species.

Cox *et al*.[5] investigated 100 clinical isolates of staphylococci from animals, identifying them using a commercial biochemical micromethod. Of these isolates, 79 were from a canine source and 70 (88.6%) were confirmed as *S.intermedius*. In a further study in 1988 by Cox *et al*.,[6] 11 healthy dogs were followed up over a one-year period by monthly sampling of 12 sites (five skin, seven mucous membranes), and a total of 804 isolates of *Staphylococcus* species were recovered. *S. intermedius* accounted for 40.2% of the isolates (12 other species of staphylococci were identified). Nine dogs completed the yearlong study and *S. intermedius* was a persistent isolate from eight of the dogs. In a similar study in cats, Cox *et al*.[7] also found that *S. intermedius* was the most commonly isolated coagulase-positive staphylococcus.

Lilenbaum *et al*.[8] assessed 98 strains of staphylococci from cats in Brazil. Coagulase-positive staphylococci were isolated from 40 cats, 26 (65%) of which were *S. intermedius*. In Japan, Igimi *et al*.[9] isolated nine (42.9%) *S. intermedius* from a total of 21 coagulase-positive staphylococci (the remainder being *S. aureus*) out of a total of 93 staphylococci recovered from cats.

A small study carried out by Krogh and Kristensen[10] in Norway investigated the microflora on normal skin in 10 dogs and 10 cats. Interestingly, they isolated *S. aureus* from nine (90%) of the dogs and four (40%) of the cats, with no isolates of *S. intermedius*. However, Hajek published '*Staphylococcus intermedius*, a new species isolated from animals'[11] in the same year. With this in mind, it is possible that a proportion of the *S. aureus* isolates in Krogh and Kristensen's study may have been *S. intermedius*, which, at that time, would not have been recognised as a separate species.

Susceptibility of coagulase-positive stapylococci in animals

Increasing antimicrobial resistance in clinical bacterial isolates is of growing concern in both human and veterinary medicine. Although antimicrobial resistance is fairly stringently monitored in human medicine, both on a national and international level, there is little information in the literature on trends in antimicrobial resistance in bacteria isolated from companion animals, nor is there currently a single-source database from which this information can be obtained. A summary of a selection of studies carried out on antimicrobial susceptibility of coagulase-positive staphylococci isolated from companion animals is shown in Table 2.

Table 1. Coagulase-negative staphylococci isolated from animals (modified from ref. 1).

Species	Host/source
S. arlettae	Goats/nares, poultry/skin
S. capitis	Cattle/milk
S. caprae	Goats/skin
S. caseolyticus	Cattle milk, milk products
S. chromogenes	Cattle/milk, pigs, poultry/skin
S. cohnii	Cattle/milk
S. epidermidis	Cattle/milk, dogs, horses/wound infections
S. equorum	Horses/skin
S. felis	Cats/otitis externa, skin infections
S. gallinarum	Poultry/skin infections
S. haemolyticus	Cattle/milk
S. hominis	Cattle/milk
S. lentus	Pigs, sheep, goats/skin infections
S. saprophyticus	Cats/skin
S. sciuri	Cats and other animals/skin infections
S. simulans	Cattle/milk, dogs, cats, pigs/skin
S. vitulinus	Cattle, sheep, pigs/skin
S. warneri	Cattle/milk
S. xylosus	Cattle, sheep/milk, cats, poultry, pigs, horses/skin

In 1984, Biberstein assessed the susceptibility of 268 coagulase-positive staphylococci from various clinical sources from dogs (n=195), horses (n=25), cats (n=15), monkeys, (n=11), goats (n=6), cattle (n=7) and four other species.[4] Of these isolates, 63 were identified as *S. aureus* and 200 as *S. intermedius*. Biberstien concluded that there was no demonstrable significant difference between the susceptibility patterns between these strains.

Kruse *et al*., in Norway, retrospectively analysed the susceptibility of *S. intermedius* over two periods, 1986–1987 and 1993–1994.[12] A significant increase in resistance to penicillin was seen between the two periods. from 46% to 58.6%. This was accompanied by in a significant rise in resistance to lincomycin (3% to 24.8%), clindamycin (2.1% to 19.5%) and erythromycin (3.3% to 24.8%).

Werckenthin *et al*.[13] reviewed three studies carried out in 1986 in the USA,[14] in 1992 in the UK[15] and in 1992 in both the USA and Germany.[16] The study carried out in the USA reported the highest rates of penicillin and tetracycline resistance (83% and 52%, respectively).

Pellerin[17] compared 131 *S. intermedius* strains from apparently healthy animals and 187 *S. intermedius* strains from dogs with pyoderma. These strains were collected during three one-year periods (1986, 1992 and 1995). Minimum inhibitory concentration susceptibility testing was performed and results categorised as susceptible or resistant according to National Committee for Clinical Laboratory Standards (NCCLS) guidelines.

Table 2. Summary of selected studies of susceptibility of coagulase-positive staphylococci.

Organism	Number in study	Penicillin	Ampicillin	Amoxicillin/ Clavulanate	Cephalexin	Erythromycin	Clindamycin	Enrofloxacin	Trimethoprim/ sulphonamide	Tetracycline	Gentamicin	Reference
SA	22-30	30	–	–	100	95.8	–	–	100	74.7	96.5	4
SI	117-163	38.7	–	–	99.2	89.5	–	–	96.3	60.1	98.8	
SI	197	17.3	–	–	–	73.6	75.1	–	91.4	47.2	100	14
SI	96	19.8	–	–	–	90.6	–	–	-	47.9	-	15
SI	116	–	–	–	–	87.1	87.1	–	-	70	99.1	16
SI	1538	38	–	–	100	70	74.3	96.4	97.6	67.2	-	12
SI	100	–	–	99	98	74	77	95	64	65	98	17
SI	51	19.6	–	100	–	55	57.1	98	78	45.3	98	18
SI	67	52.4	55.2	98.5	–	76.1	–	80.6	–	80.6	94	19
SI	6575	31	31	97	95	90	90	97	97	70	98	Unpublished

SA: *S. aureus*; SI: *S. intermedius*

Comparison of susceptibility data between the 1986 and 1995 groups in the healthy dogs showed little difference in resistance rates, except for chloramphenicol susceptibility, which dropped from 78% in 1986 to 53% in 1995. This was reflected in the isolates from the dogs with pyoderma, in which chloramphenicol susceptibility rates dropped from 76% in 1986 to 60% in 1995. Further reduction was also seen in the susceptibility of *S. intermedius* for tetracycline (81% in 1986, 60% in 1995) and trimethoprim/sulphonamide (94% in 1986, 64% in 1995) in the pyoderma group. Pellerin suggested that there are similarities and differences between the resistance in these strains and in human strains.

It was stated that an increase in the prevalence of resistance follows increased use of antimicrobial agents, and also that resistance to the penicillins, tetracycline and erythromycin is the most frequent. It was suggested that a key difference is the location of the resistance genes, with chromosomal genes more prevalent in *S. intermedius* and plasmid resistance genes more common in *S. aureus*.

A study carried out in Switzerland by Boerlin *et al*.[18] investigated 77 *S. intermedius* strains isolated from routine diagnostic submissions from four cats and 73 dogs. Disc diffusion susceptibility testing was performed using NCCLS guidelines. The main focus of the study was to assess the genetic linkage of macrolide and aminoglycoside resistance in *S. intermedius*. The susceptibility profile of the main battery of antimicrobial agents tested did not reveal anything remarkably different from previous studies. Also, all 23 isolates shown to be erythromycin-resistant were also resistant to the aminoglycosides streptomycin and neomycin and the macrolide spiramycin.

All the erythromycin-resistant isolates showed reduced susceptibility to clindamycin. Susceptibility testing using adjacent erythromycin and clindamycin discs showed the typical D-shaped inhibition around the clindamycin disc, indicative of inducible resistance.

According to Boerlin, erythromycin resistance to *S. intermedius* is due to the presence of the *erm* (B) gene. This study found that the *erm* (B) gene is linked physically to adjacent aminoglycoside resistance genes in all the isolates tested.

Tejedor *et al*.[19] found no significant difference between the susceptibility of coagulase-positive staphylococci (mainly *S. intermedius*) from 22 healthy dogs and 45 dogs suffering from otitis media. Overall, 35.8% of the 67 strains were susceptible to all of the antibiotics tested, with penicillin and ampicillin showing the lowest activity.

This study also demonstrated that polymixin B had low activity against the isolates tested. Although polymixin B is primarily an agent that acts against Gram-negative organisms, it does have *in vitro* activity against *S. intermedius* (although not against *S. aureus*). The paper claimed to have used NCCLS guidelines for the interpretation of the susceptibility tests performed, but NCCLS does not provide guidelines for topical agents such as polymixin B. However, with the concentration present in a topical application, it is likely that this agent would be effective against *S. intermedius in vivo*. Unpublished data from a commercial veterinary diagnostic laboratory (IDEXX Laboratories) demonstrate a similar pattern of resistance to the above studies among 6575 *S. intermedius* strains tested.

Erythromycin and clindamycin resistance in staphylococci are mediated by a group of similar methylases that are the products of a class of genes termed erm (erythromycin ribosome methylation).[20] Approximately 30 *erm* genes have been identified. Previous reports show that *erm* (C) is the major methylase gene in staphylococci of human origin, followed by a minority of *erm* (A)-positive isolates and a very few *erm* (B)-positive isolates. Boerlin[18] showed that the erythromycin resistance methylase encoded by the *erm* (B) gene is the major macrolide determinant in *S. intermedius*.

Tetracycline resistance is encoded by tetracycline resistance (*tet*) genes, of which there are 18 different types. These genes are located on mobile elements, which favours their exchange with other organisms.[20] To date, four different *tet* genes, assigned to classes K, L, M and O, have been detected in staphylococci of animal origin.[14]

Schwartz *et al*.[21] analysed 228 tetracycline-resistant staphylococci from a total of 838 staphylococci isolated from a wide range of animals. This study demonstrated that all strains carried either the *tet* K, L, M or O gene. Only fourteen isolates carried more than one *tet* gene.

Table 3. Mechanisms of resistance among the main antibiotic classes (modified from ref. 21).

Antimicrobial family	Mechanism of action	Mechanism of resistance	Type of resistance
β-lactams	Prevent formation of the cell wall	β-lactamases Diminished permeability	Acquisition of DNA Mutational Target alterations
Aminoglycosides	Inhibition of protein synthesis	Methylation of ribosomal targets Modifying enzymes	Acquisition of DNA Mutational
Macrolides	Inhibition of protein synthesis	Methylation of 23S RNA	Acquisition of DNA Mutational
Tetracyclines	Inhibition of protein synthesis	Efflux mechanism Altered binding Altered target	Acquisition of DNA Mutational
Sulphonamides	Competitive inhibition of p-aminobenzoic acid (PABA)	Reduced uptake Altered metabolic enzymes Increased production of PABA	Acquisition of DNA Mutational
Quinolones	Avoid DNA coiling	Mutations in target genes *gyrA* and *parC* Efflux mechanisms	Mutational
Rifampicins	Inhibition of RNA polymerase	Altered RNA polymerase	Mutational
Glycopeptides	Inhibition of cell wall synthesis	Altered targets	Acquisition of DNA Mutational
Polymixins	Destruction of cell membrane	Increased permeability	Mutational

Aminoglycoside resistance is usually conferred by three different mechanisms. First, ribosome alteration leads to high-level resistance resulting from single-step mutations in chromosomal genes (*rpsL*, *rpsD* or *rpsE*) encoding ribosomal proteins. Second, decreased permeability as a result of an absence or alteration in the aminoglycoside transport system. Third, modification in the lipopolysaccharides phenotype can result in cross resistance to all aminoglycosides.

Aminoglycosides may also be inactivated by three main enzymes: acetyltransferases, nucleotidyltransferases and phosphotransferases. Clinically, deactivation of aminoglycosides is of most importance because the genes encoding aminoglycoside-modifying enzymes can be disseminated by plasmids or transposons.[22]

Resistance to sulphonamides is caused primarily by plasmids and, less frequently, by chromosomal mutations. Plasmids code for proteins that interfere with drug penetration, for change in enzyme affinity or for a high production of para-aminobenzoic acid (PABA). In Gram-positive bacteria, the primary target for fluoroquinolones is DNA topoisomerase IV, and the secondary target is DNA gyrase. These are encoded by the genes *gyrA*, *gyrB*, *parC* and *parD*. Resistance is usually chromosomally mediated so the spread of resistant bacteria contributes to the numbers of resistant strains rather than the transfer of resistance plasmids.[23]

Although a common form of penicillin-resistance, β-lactamase production is not the only mechanism of penicillin/β-lactam resistance. Susceptibility of staphylococci to β-lactam antibiotics is due to these antibiotics binding proteins known as penicillin-binding proteins (PBPs), which are membrane-bound enzymes responsible for cell-wall synthesis.

β-lactamase catalyses the opening and hydrolysis of the β-lactam ring of β-lactam antibiotics, with intrinsic resistance due to the modification of the PBPs. This takes place following the production of PBP2a, which is encoded by the *mecA* gene. β-lactam antibiotics are not capable of binding to this form of PBP, thus strains carrying the *mecA* gene are resistant to the β-lactamase-stable penicillins (e.g., the methicillin, oxacillin, cloxacillin group).[24] *S. aureus* isolates with this form of resistance are popularly known as methicillin-resistant *S. aureus* (MRSA).

Currently, MRSA is one of the most important infection-control issues in the UK and in many countries worldwide. The isolation of MRSA from companion animals is a relatively new phenomenon. Thus, the remainder of this review will focus on the emergence of MRSA as an issue in animals.

Methicillin-resistant staphylococci in animals

Methicillin-resistant *S. aureus* in animals has been reported in the literature since 1975.[25] Devriese reported 68 MRSA isolates from mastitis milk samples originating in 20 Belgian dairy herds, and suggested that these strains might have come from a single human source. Transmission of 'human' strains of *S. aureus* to farm animals was also reported by Moeller *et al*.[26] in 1963. In this study, phage types of staphylococci found in hospitals were compared to the phage types of staphylococci found in the milk of dairy herds owned by recently discharged patients. Moeller found that recently discharged hospital patients who could have been responsible for transfer of staphylococci to their animals were present on 7% of 122 farms studied.

In 1997, Hartmann *et al*.[27] reported a post-operative wound from a horse that had become infected with MRSA. In light of the increasing incidence of MRSA in both hospitals and

the community, it was thought likely that infections in animals would become more frequent.

The possibility of humans being primarily involved in the transfer of MRSA to animals was supported by Seguin *et al*.[28] in 1999. Eleven horses admitted to a veterinary teaching hospital for various medical and surgical procedures over a 13-month period were assessed. All the animals were re-admitted to the hospital with wound infections in the site of the original procedure two to three weeks after initially being discharged.

Follow-up screening was carried out on five members of the medical and surgical staff involved with the surgery. Three of the human screening swabs were culture-positive for MRSA. All isolates were subjected to pulsed-field gel electrophoresis (PFGE) typing. This revealed that all 11 equine stains and the strains isolated from the three members of the medical team were considered to have originated from the same strain. Seguin concludes that the initial source of the outbreak was probably of human origin, as the horses arrived at the hospital over a 13-month period from a variety of locations and with no apparent staphylococcal infection at the time of arrival.

Lee[29] collected 1913 specimens over a two-year period from cattle, pigs and chickens. Of these specimens, 421 contained *S. aureus* and of the 28 that showed increased minimum inhibitory concentration (MIC, >2 g/mL) to oxacillin, 15 strains (12 from dairy cattle and three from chickens) were confirmed to possess the *mecA* gene, confirming them as MRSA. Random amplified polymorphic DNA (RAPD) patterns were generated for these 15 isolates.

Four human MRSA isolates that were representative of 38 strains collected from hospitals during the time of the study were also analysed by RAPD. Typing revealed eight visually distinct RAPD patterns from the animal isolates. Comparison of these patterns with those of the human strains did give concordant results in some cases; however, the study showed little in the way of conclusive proof that animals were the source of infection in humans. This study was carried out in Korea, where it was reported that the rate of methicillin-resistance among *S. aureus* was around 50%. It was suggested that once interspecies transfer of this organism has occurred, these isolates can become widespread in the veterinary environment.

In Belgium. Cheirs *et al*. isolated 75 strains of *S. aureus* from 512 samples obtained from horses with skin disorders.[30] Of these, two (2.6%) were found to carry the *mecA* gene and were therefore confirmed as MRSA. No attempt was made to follow-up the source of MRSA, but the possibility of human origin was suggested.

However, the relationship between animal and human MRSA isolates has been disputed by Shimizu *et al*. in a study in Japan.[31] Fifteen equine isolates of MRSA were compared with nine human isolates of MRSA using PFGE. Although this showed that all 15 equine MRSA strains were closely related, none of the nine human isolates showed any similarity to the equine strains. A weakness in this study was that the human strains were taken from a source unrelated to the 15 equine strains.

All the human strains were similar to the most prevalent genotype at the time of the study, which accounted for over 70% of all MRSA isolates across Japan in the 1990s. The equine strains were similar to a genotype that was prevalent in Japan in the early 1980s but which declined in incidence dramatically in the 1990s. Clearly, screening and typing of strains isolated from humans associated with the horses involved would have proved of greater value, especially if a rare genotype were to be detected by the human screens.

Weese *et al*.[2] collected nasal swabs from 2283 horses at admission to a veterinary teaching hospital in Canada. One hundred and twenty MRSA isolates (5.3%) were detected. A similar detection rate was found in a study carried out in the north-west of England by Williams *et al*.[33] Eight horses out of a total of 106 were found to carry strains of MRSA. These were distinct from the most prevalent MRSA strains in the UK at the time (EMRSA-15 and EMRSA-16). Williams proposed that the acquisition of the *mecA* gene in these cases was either by transfer of the original strain from the human sources or by acquisition of the *mecA* gene from coagulase-negative strains that harboured it.

Another possible source of MRSA for animals is the environment. Weese *et al*.[34] collected 260 samples from stalls, examination and treatment rooms, public areas, personal items, medical equipment and handling equipment at a veterinary teaching hospital.[34] Overall, MRSA was isolated from 25 (9.6%) of the 260 sites. The most commonly contaminated sites were in stalls housing MRSA-positive horses, where 18 (62%) out of 29 surfaces were contaminated. Incidentally, a clinician's mobile phone was also MRSA-positive and subsequently the owner was identified as an asymptomatic nasal carrier of MRSA. Due to the manner in which horses explore their surroundings, it is possible that this could be a source of either contamination by MRSA carriers or of spread via the environment.

A recent national newspaper article[35] focused attention on the potential for companion animals, mainly cats and dogs, to act as a reservoir for the carriage of MRSA. Links with MRSA infection in a companion animal were reported from a ward cat that was heavily colonised with MRSA on a geriatric ward in which intensive screening of the patients and staff revealed an unusually high MRSA carriage rate (38%).[36] Appropriate infection control measures and the removal of the cat led to a rapid reduction in human carriage.

Cefai *et al*.[37] reported a case of MRSA conjunctivitis in a pet dog that was associated with human carriage of MRSA. Lillenbaum *et al*. in Brazil examined samples taken from 148 adult cats for the presence of staphylococci.[8] *S. aureus* was isolated in 14 (9.5%) samples, with three (2%) isolates proving to be MRSA.

Tomlin *et al*.[38] described the diagnosis and management of MRSA infection in 11 dogs. Three originated in the United Kingdom and eight were from two different locations in the United States. The dogs comprised a variety of breeds and ages. According to the clinical history, six infections developed after surgical treatment, two as a complication of wounds and three in dogs with recurrent pyoderma. Typing by PFGE was only performed on the three isolates from the UK, and revealed that these had similar PFGE band patterns. As discussed later, larger studies have since found that this is not unusual.

Antibiotic treatment based on the susceptibility patterns of the organisms involved improved or resolved the MRSA infection in nine out of the 11 dogs. Detailed evaluation of the environment and human contacts involved was not carried out and hence the origin of the MRSA in these dogs was uncertain.

In a study in Korea in 1999,[39] 12 strains of MRSA recovered from dogs hospitalised with underlying disease were

characterised by PFGE and the organisms were investigated for their toxin production profiles. Ten out of the 12 isolates produced one or more toxins. Six strains produced staphylococcal enterotoxin B (SEB), one produced toxic-shock syndrome toxin-1 (TSST-1) and three produced both TSST-1 and staphylococcal enterotoxin C (SEC). Typing by PFGE revealed six different PFGE patterns, one of which accounted for six of the isolates. This study concluded that there were several different strains involved at the veterinary hospital. Again no environmental or human carriage screening was undertaken to investigate the source of these isolates.

As demonstrated by Simoons-Smit *et al.*,[40] typing of stains isolated from human contacts may be beneficial in determining the source of possible infection. In this study, six strains of *S. aureus* (methicillin-sensitive) isolated from a 20-year-old woman suffering from pyoderma, her boyfriend, her mother, two isolates from her cat and one from her dog were collected. All isolates were analysed using an amplified fragment length polymorphism (AFLP) technique. This is based on the selective polymerase chain reaction (PCR) amplification of restriction fragments from a total digest of genomic DNA.

Analysis of the strains revealed indistinguishable patterns at a high correlation level. All the strains were clearly distinguishable from unrelated strains run as controls. Although the isolates in this study were MSSA and not MRSA, the transmission of *S. aureus* between humans and animals in a single household was demonstrated and there is no reason why this might not occur with MRSA.

Further evidence of possible human-to-animal transmission of MRSA is provided by Oughton *et al.*[41] This study describes 14 cases of MRSA in animals where transmission was most likely derived from community sources. Six equine and two feline cases were followed up. The feline strains were isolated from cats within the same household and were shown to be indistinguishable. Of the six canine isolates included in the study, one dog and its owner were each infected by indistinguishable (by PFGE) strains of MRSA. The owner had been hospitalised for surgery the previous year and had positive screening swabs for MRSA. This isolate was also indistinguishable from the strains obtained from subsequent screening swabs from the owner and the isolate from the pet dog.

Of the remaining five canine cases, four dogs had been exposed to healthcare environments, either through their owners or by attendance at various therapeutic centres. As is the case with human outbreaks, Oughton suggests that contact tracing and attempts at MRSA eradication would be highly advisable.

A study in Canada, undertaken by Willey *et al.*,[42] investigated a cluster of MRSA isolates from horses, and included a follow-up human and equine surveillance programme. Nasal MRSA isolates from horses (n=82) and from human contacts (n=29) were characterised by a variety of methods, including PFGE. Typing showed that 95% of equine and 93% of human MRSA strains were indistinguishable. No single route of transmission was demonstrated and it was concluded that a combination of human-to-horse, horse-to-human and horse-to-horse transmission was likely.

Manian[43] described the case of a 48-year-old diabetic with a leg-stump infection that subsequently proved to be MRSA. Four months later the patient's wife developed a skin infection and the MRSA isolated proved indistinguishable from that which was grown from her husband's stump. The only other household member was a healthy 18-month-old Dalmatian dog that frequently slept in the couple's bed. Nares cultures were performed on the dog and these revealed an MRSA indistinguishable from those obtained from the owners.

Treatment and decolonisation of the owners and the dog failed to clear the MRSA infection from all, with the original patient, the patient's wife and the dog being re-infected or recolonised in the nares over a six-month period until full decolonisation was achieved. All remained free of MRSA infection four months after the completion of decolonisation therapy. Manian suggested that the evaluation of patients with recurrent MRSA colonisation or infection that does not have an obvious source should prompt enquiries about regular contact with household pets and further investigation of such hidden carriers.

Rich *et al.*[44] reported 95 isolates of MRSA from companion animals over a 12-month period from January 2003. These isolates originated mostly from post-operative and wound infections in 69 dogs, 24 cats, one horse and one rabbit. Twelve isolates were investigated by phage and PFGE typing and were found to belong to the two most prevalent strain types currently carried by humans in the UK (epidemic-MRSA-15 and epidemic-MRSA-16). The authors suggested that MRSA carriage in companion animals was most likely a result of acquisition from a human source.

In The Netherlands, Duijkeren *et al.*[45] reported MRSA isolated from two dogs that underwent surgery in a foreign country. One of the isolates was said to be similar to a human MRSA cluster, which the authors described as unusual. In response to this article, Rich *et al.*[46] state that, far from being unusual, this is a common occurrence. Thirty-one randomly selected MRSA isolates from a total of 210 MRSA strains isolated from companion animals were characterised by a range of phenotypic and genotypic tests. In contrast to the findings of Duijkeren *et al.*, 29 (93.5%) of the animal isolates in the study were indistinguishable from human healthcare-associated epidemic MRSA strains currently prevalent in the United Kingdom. Rich *et al.* suggested that detailed characterisation of such strains may be prudent, not only from a public health perspective but also to provide insight into the transmission dynamics of MRSA in human and animal populations.

It is clear that there is a need for continued vigilance and systematic study to further our understanding of the origins and epidemiology of MRSA in companion animals. It is hoped that further planned study will determine whether or not an association exists between MRSA infection in dogs and cats, and MRSA colonisation or infection in humans closely associated with the affected animals. Specific objectives are to determine risk factors for MRSA infection in dogs and cats, the relationship between animal carriage and human carriage, and the genetic relationship of animal and human strains. □

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