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Transmission of a Panton-Valentine Leucocidin-Positive, Methicillin-Resistant *Staphylococcus aureus* Strain between Humans and a Dog

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Panton-Valentine leucocidin-positive methicillin-resistant *Staphylococcus aureus* (MRSA) strains with identical resistance patterns were cultured from recurrent infections of a 51-year-old patient, her healthy husband, son, and dog, and pulsed-field gel electrophoresis showed that all MRSA strains were indistinguishable.

CASE REPORT

In 2002, a 51-year-old female patient with a diabetic foot was admitted to the surgical ward of a Dutch teaching hospital in the province Overijssel. Cultures were taken from the ulcer at admission, and a methicillin-resistant *Staphylococcus aureus* (MRSA) strain, resistant to fusidic acid and tetracyclines but susceptible to macrolides, trimethoprim-sulfamethoxazole, quinolones, rifampin, and aminoglycosides was cultured, while cultures from nose, throat, and perineum did not grow MRSA. The patient was treated successfully with trimethoprim-sulfamethoxazole. Two months later the patient was screened for the MRSA carrier state, and a sample from her throat was culture positive for an MRSA strain with the same resistance pattern, while nostril, perineum, and wound cultures were MRSA negative. She developed a urinary tract infection with a positive MRSA culture again 4 months after the initial treatment. Therapy with ciprofloxacin and rifampin was started, after which the MRSA infection was eradicated for half a year, based on monthly negative cultures of urine, nostrils, throat, wound, and perineum. However, the final screening for carrier state after this half-year revealed an MRSA strain again in cultures from the nose, throat, and perineum. After these findings a source of the recurrent MRSA carrier state was suspected at her home. Samples were taken from the nose and throat of the patient's husband (57 years old), son (25 years old), and their dog, a German Shepherd, who were all clinically healthy. The samples from the throat of the husband and from the nose of the son and dog were culture positive for MRSA. In a last effort to eradicate the patient's MRSA infection, all family members (including the dog) were treated simultaneously with ciprofloxacin and rifampin. This last treatment eradicated the MRSA carrier state of all persons and the dog. Follow-up cultures of nostrils, throat, and perineum of all persons and the dog were taken for 6 months, and all cultures remained negative.

All isolates were sent to the National Institute of Public Health and the Environment (RIVM) for identification and genotyping by pulsed-field gel electrophoresis (PFGE). The staphylococci isolated from the patient (isolates from the ulcer, throat, and urine), her husband and son, and the dog were all identified as *S. aureus* by conventional methods, Vitek 2 (bioMérieux, Marcy-l'Étoile, France) and Martineau PCR (8). Susceptibility testing was performed using the Vitek 2 assay according to the manufacturer's instructions. All isolates had the same resistance pattern: they were resistant to all beta-lactams, fusidic acid, and tetracycline and were susceptible to aminoglycosides, fluoroquinolones, erythromycin, clindamycin, vancomycin, rifampin, and trimethoprim-sulfamethoxazole. An Etest (AB Biodisk, Solna, Sweden) showed that the oxacillin MIC for the isolates of the dog and the family members was 192 mg/liter. The presence of the *mecA* gene was demonstrated by a positive *mecA* PCR for all isolates, as previously described (2). PFGE was carried out as described by Schwarzkopf et al. (12). PFGE showed that all MRSA isolates from the dog, the patient, and her family members had indistinguishable patterns and that they belonged to RIVM cluster 28, an epidemic human MRSA cluster. On the basis of these data, we believe that the woman had recurrent infections with the same MRSA strain; that she consequently transmitted this MRSA to her husband, her son, and the dog; and that she was reinfected by one of the family members and/or the dog. RIVM cluster 28 strains were first reported in The Netherlands in 1995. Multilocus sequence typing revealed that MRSA with PFGE cluster 28 belong to sequence type 80 (16, 17). All isolates in the present study were positive for the *S. aureus* Panton-Valentine leucocidin (PVL) toxin genes (*lukS-PV* and *lukF-PV*) by PCR, performed as described by Lina et al. (6). PVL is a bicomponent cytotoxin that causes leukocyte destruction and tissue necrosis. PVL is encoded by two cotranscribed genes, *lukS-PV* and *lukF-PV* (3). This virulence factor is associated with skin and soft-tissue infections such as furunculosis and abscesses as well as with severe necrotizing pneumonia in humans and has

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been found in community-acquired MRSA (CA-MRSA) infection in many countries (3, 4, 16, 17). Outbreaks of PVL-positive CA-MRSA infection have been reported from closed living communities (jail inmates, military recruits, and gay men) and also among health care staff and within families (17). PVL-positive CA-MRSA strains often afflict relatively young persons without apparent risk factors (3, 17). PVL-positive MRSA might also emerge in the hospital environment (16). In 2003, the PVL loci were detected in 8% (123/1601) of the human MRSA isolates sent to the RIVM by Dutch hospitals (16). Sequence type 80 was the predominant PVL-MRSA genotype found in humans in The Netherlands in the period from 2000 to 2003 (16, 17). This PVL-MRSA genotype is also predominant in other European countries but is rarely found outside of Europe (17). Recently, PVL-positive MRSA strains isolated from animals were reported for the first time (10). Eleven of a total of 23 MRSA isolates tested were shown to possess the PVL toxin genes. The PVL-positive strains originated from dogs ($n = 8$), one cat, one rabbit, and one parrot and were from clinical infections (10). The clinical conditions of these animals were similar to those reported in humans infected with PVL-positive MRSA. The authors suggested that animals infected with PVL-positive MRSA might act as a reservoir for humans and vice versa (10). In the present study we prove that dogs can be subclinical carriers of PVL-positive MRSA and that transmission of these strains can indeed occur between humans and animals.

The staphylococcal cassette chromosome *mec* (SCC*mec*) is a mobile genetic element that carries the *mecA* gene (5). Five SCC*mec* types have been identified to date (5). The SCC*mec* type IV is typically found in CA-MRSA strains (5, 13) and most CA-MRSA strains are PVL positive (17). RIVM cluster 28 isolates are known to carry SCC*mec* type IV (17). CA-MRSA infection is more difficult to control than health care-associated MRSA infection. SCC*mec* type IV is smaller in size than SCC*mec* elements I to III and has been found in MRSA with many different genetic backgrounds (3). Therefore, it is thought that they have a greater mobility (5). The presence of CA-MRSA in animals is concerning because this might imply that these strains can spread rapidly.

The transmission of MRSA between humans and companion animals within a household has been reported before (1, 7, 14). Recently, we reported the transmission of an MRSA strain of PGFE RIVM cluster 35 from a nurse to her baby and her dog (14). However, to our knowledge, this is the first report of transmission of a PVL-positive MRSA strain between humans and an animal. The fact that we found two cases in which an MRSA strain was transmitted from human to dog in a short period of time indicates that MRSA is an emerging problem in companion animals. Studies comparing MRSA isolates from human and animal origin using PFGE have shown that isolates from animals often correspond to recognized human PFGE types (9, 11, 15, 18). Rich et al. (11) recently reported the isolation of MRSA from 210 companion animals (mainly dogs and cats) from various geographical locations throughout the United Kingdom, mainly from wound infections. Of these isolates, 31 were randomly selected for PFGE, and 29 (93.5%) of these isolates were indistinguishable from human health care-associated epidemic MRSA strains currently prevalent in the United Kingdom. Middleton et al. (9) investigated 70 *S. aureus* isolates from 65 patients at seven veterinary teaching hospitals in the United States and found MRSA in 9 animals: 4 dogs, 1 cat, and 4 horses. Weese at al (18) reported 79 MRSA-positive horses and 27 MRSA-positive persons working with horses. Most cases were from one veterinary hospital and one horse farm. The majority of the equine and human isolates were subtypes of Canadian epidemic MRSA-5, suggesting transmission of MRSA between humans and horses (18). The fact that Canadian epidemic MRSA-5 is uncommon in humans might imply that this is a horse-adapted strain (18). Companion animals may therefore serve as reservoirs for MRSA infections or reinfections of humans and animals. In the present case it remained unclear if the patient was reinfected by the dog, the husband, or the son. To date, it is unknown whether animals are primary sources of human MRSA infections or whether most MRSA infections in animals are of human origin. Further research into this issue is crucial in order to establish appropriate infection control measures for MRSA.

In conclusion, MRSA seems to be an emerging pathogen of pets and horses. Animals can be a reservoir for MRSA including PVL-positive strains, and, consequently, protocols for screening the contacts of humans infected with or carrying MRSA should include animals. PVL-positive MRSA can cause serious infections in animals. Further research into the prevalence and the epidemiology of MRSA infections and carriage in veterinary medicine is warranted, and veterinary hospitals should have protocols for MRSA-infected patients.

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