MRSA Transmission between Cows and Humans

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We isolated methicillin-resistant Staphylococcus aureus (MRSA) from cows with subclinical mastitis and from a person who worked with these animals. The bovine and human strains were indistinguishable by phenotyping and genotyping methods and were of a low frequency spa type. To our knowledge, this finding indicates the first documented case of direct transmission of MRSA between cows and humans.

Since the introduction of β-lactamase–stable antimicrobial drugs into clinical use, methicillin-resistant Staphylococcus aureus (MRSA) strains have emerged worldwide as important nosocomial pathogens; their prevalence in the community is increasing substantially. Although S. aureus is known to be one of the most common causes of bovine mastitis and other severe animal diseases such as septicemia and wound, bone, and joint infections, MRSA strains have been rarely isolated from animals. MRSA strains have been isolated from cows with mastitis, horses and dogs with lesions, and dogs and cats that were carriers (1). Transmission of MRSA between humans and animals (e.g., dogs, horses, pigs) has been reported (2–4), but transmission between cows and humans has not, to our knowledge. We describe a first putative case of transmission of MRSA between cows and a person.

From January 2002 through December 2004, 595 milk samples were collected from cows with subclinical mastitis on a farm in Hungary and sent for bacteriologic analysis to the Bacteriologic Department of the Hungarian Central Veterinary Institute. Samples were streaked onto a Columbia agar plate (Merck, Darmstadt, Germany) containing 5% sheep blood and 0.01% esculin and a Baird-Parker (BP) agar plate (Oxoid Ltd., Basingstoke, England). After incubation at 37°C for 24 h, the colonies were tentatively identified according to morphologic features, pigment production, Gram stain results, catalase test results, type of hemolysis, and characteristic growth on BP agar. The isolates initially characterized as staphylococci were tested for coagulase production (in tubes) and with Slidex Staph Plus test (bioMérieux, Marcy l’Etoile, France) to confirm their identification as S. aureus. From this farm, 375 S. aureus strains were isolated. The strains were tested for antimicrobial drug susceptibility, production of β-lactamases, and presence of mecA by PCR (5). The first MRSA strain was isolated in spring 2002; during the next 15 months, 26 additional MRSA strains were isolated from this dairy herd.

In December 2002, tonsil swabs were collected once from 12 workers on this farm who were in close contact with the cows (veterinarian, milkmen, and attendants) and who gave informed consent. (The study was approved by the Ethical Committee of the National Center for Epidemiology, Budapest, Hungary.) Culturing and identification of S. aureus were carried out by the above-described method. S. aureus was isolated from 3 samples. One of these isolates was resistant to methicillin by disk diffusion and E-test, and the presence of the mecA gene was confirmed by PCR.

All 28 MRSA strains (27 bovine and 1 human) produced PBP2a, according to latex agglutination test (Oxoid Ltd.). Eight of 27 randomly chosen bovine strains and the human strain containing the mecA gene, as well as 4 bovine and 2 human mecA–negative isolates, were phage typed with MRSA phages (6) at the Institute of National Public Health and Medical Officers Service in Hajdú-Bihar County. The phages were used in 2 concentrations: routine test dilution (RTD), and 100× RTD. None of the MRSA or methicillin-susceptible S. aureus (MSSA) strains were lysed by phages in RTD. All MRSA strains showed a similar lysis pattern with the 100× RTD MRSA phages (Table).

Susceptibilities to 7 antimicrobial agents were assessed by a disk diffusion method that used the Clinical and Laboratory Standards Institute (CLSI; formerly National Committee for Clinical Laboratory Standards) breakpoints for 7 mecA–positive bovine strains and the human mecA–positive strain. All tested strains showed the same susceptibility pattern (resistant to ampicillin, cephalaxin, tetracycline, and erythromycin and susceptible to enrofloxacin, gentamicin, and trimethoprim/sulfamethoxazole). Pulsed-field gel electrophoresis was performed on the 7 mecA–positive bovine strains, 1 human mecA–positive strain, 4 bovine MSSA strains, and 2 human MSSA strains, as described by McDougal et al. (7). The patterns of the Smal–digested DNA of the strains are presented in the Figure. All bovine mecA–positive strains and the human mecA–positive strain (human 3) showed indistinguishable Smal patterns. All mecA–negative isolates showed a pulsed-field gel electrophoresis pattern different from that of the MRSA strains.

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For further identification, 1 human and 4 bovine MRSA isolates (29509, 24069/2, 24069/4, 30195; Table) underwent spa typing (8). All these isolates showed spa-type t127. Because the strains were indistinguishable by all methods, multilocus sequence typing (MLST) (9) and typing of the staphylococcal cassette chromosome (SSCmec) (10) were performed on just 1 strain (29509). This strain showed MLST sequence type (ST) 1 and SCCmec type IVa. The strain did not carry the Panton-Valentine leukocidin (PVL) toxin genes lukF–lukS as tested by PCR (11).

In this study, both phenotyping and genotyping showed that the MRSA isolates of bovine origin and the single human isolate were indistinguishable. The database of the European network for spa typing (www.seqnet.org) shows that MLST ST 1/spa-type t127 has a relative global frequency of 0.7%; according to this database, this type has not previously been reported in Hungary. A study of 135 human MRSA isolates collected in Hungary during 2001–2004 showed human epidemic clones of types other than ST 1 and spa-type t127 (12). We conclude that the bovine and human MRSA strains described in our study are epidemiologically related, which indicates transmission from either cow to human or human to cow. This strain is negative for the PVL genes, which differentiates it from community-associated MRSA ST 1, which is positive for PVL genes (11).

Several cows had positive test results for MRSA, which indicated that MRSA was spread within the farm. On the farm, cases of clinical mastitis were treated with intramammary infusions containing penicillin, aminopenicillins, or cephalosporins. Each cow also received drying-off therapy with cloxacillin or cephalosporins. The use of antimicrobial drugs may have contributed to the emergence of MRSA in this dairy farm.

MSSA strains with ST 1 and spa-type t127 have been reported from human sources (13). MSSA strains may be induced to pick up the mecA gene from coagulase-negative staphylococci. Alternatively, mastitis may be caused by human MRSA strains or bovine MRSA strains already present in small numbers and selected for by the frequent use of long-acting antimicrobial preparations, especially β-lactams. S. aureus usually shows limited host specificity, and transfer between different host species may occur (14). The transmission of milk-associated S. aureus strains between cows and humans was suggested by Lee (15), whose study showed MRSA in milk samples with comparable antibiotypes as those in humans, but the transfer to humans was not proven. The risk for spread of MRSA from bovine sources into the human population is low. Generally, persons are not at risk as long as raw milk is not consumed. However, persons in close contact with MRSA-infected cattle, including veterinarians, farmers, milkers, and persons working at slaughterhouses, may become colonized from the bovine source.

We conclude that several cases of subclinical mastitis in cows on a farm in Hungary were caused by MRSA and that these strains were indistinguishable from MRSA isolated from a carrier working in close contact with the cows. This suggests the transmission of these isolates between humans and cows, although the direction of transfer (cow to human or human to cow) could not be proven.

Acknowledgments

We thank A.C. Fluit for performing the PVL toxin gene PCR.

Dr Juhász-Kaszanyitzky is a veterinary microbiologist with special interest in antimicrobial resistance. She developed the

Table. Susceptibility of human and animal Staphylococcus aureus strains to phages and the presence of mecA by PCR*

<table>
<thead>
<tr>
<th>Strain no.</th>
<th>Reference no.</th>
<th>Identification of samples</th>
<th>mecA</th>
<th>MRSA 100× RTD†</th>
<th>ST</th>
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<tr>
<td>1</td>
<td>30195</td>
<td>795 LF</td>
<td>+</td>
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<tr>
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<tr>
<td>3</td>
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<td>490 RF</td>
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<td>616/617/623/626/630</td>
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<td></td>
</tr>
<tr>
<td>4</td>
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<td>723 RH</td>
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<td>8</td>
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†See Figure for DNA analysis. Strain no. 29509 was not included in the DNA analysis; thus, no strain no. was assigned.
‡Reaction pattern with 100× routine test dilution (RTD) methicillin-resistant Staphylococcus aureus (MRSA) phages (7). +, positive in mecA PCR; –, negative in mecA PCR.

Figure. Pulsed-field gel electrophoresis patterns of SmaI-digested DNA of bovine and human strains of Staphylococcus aureus isolated from cows with subclinical mastitis, Hungary, January 2002–December 2004. Strains are numbered as shown in Table.
Hungarian national antibiotic resistance monitoring system, based on samples from healthy slaughter animals, and since 2001 has coordinated this system.

References

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