ecologic interactions between genetically diverse strains (8). In this report, we describe a single case; comparison of disease severity of scrub typhus caused by mixed and single genotype infections should be studied further.

Simultaneous infection with multiple antigenic strains of *O. tsutsugamushi* was detected in an individual mite, *Leptotrombidium arenicola* (9), a probable vector of scrub typhus. Infection with multiple *O. tsutsugamushi* strains may be caused by being bitten by multiple mites or by multiple genotypes coexisting within individual mites (7). We ascribed the co-infection to the second cause because the 2 genotypes were simultaneously detected from an eschar sample associated with the bite of 1 mite examined in this study. There may be diverse genotypic co-infection patterns of *O. tsutsugamushi*. Mechanisms of in-host interactions between genetically diverse strains of *O. tsutsugamushi* and the initiated host response require the establishment of animal models for further research.

Acknowledgment

We thank Shu-Xia Li for her assistance with sample collection.

The work was supported by grants from the National Natural Science Foundation of China (no. 81273133 and no. 30972515).

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DOI: http://dx.doi.org/10.3201/eid2003.121349

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Of the 5 isolates from the horses, 1 was identified as methicillin-resistant *S. pseudintermedius* (MRSP) and 4 as methicillin-susceptible *S. delphini* (Table). The MRSP isolate was classified by direct repeat unit typing as dt11a, a predominant MRSP clone in dogs in North America (8). In addition to β-lactams, the MRSP isolate was resistant to chloramphenicol, clindamycin, erythromycin, gentamicin, tetracycline, and trimethoprim/sulfamethoxazole and susceptible to nitrofurantoin, rifampin, streptomycin, and vancomycin.

The 4 *S. delphini* isolates were initially identified biochemically as *S. pseudintermedius* but subsequently classified as group A (n = 1) and group B (n = 3) *S. delphini* by molecular methods (Table). One isolate (SD-4) was resistant to only erythromycin; the remaining isolates were susceptible to all tested antimicrobial drugs. PFGE showed that 2 of the *S. delphini* isolates (SD-1 and SD-2) were possibly related, with a 4-band difference. The remaining isolates were unrelated to each other and the 2 related isolates. Two of the horses (sources of isolates SD-2 and SD-3) had been recently acquired at the same auction and were sampled on the same day; however, PFGE showed that these samples were not related and came from different groups (A, B). No common epidemiologic links were identified for any of the horses.

The AHL database search identified 8 additional horses from which *S. pseudintermedius* was biochemically identified; on the basis of drug-resistance patterns, 6 (75%) of these isolates were determined to be MRSP (Table). One additional *S. delphini* isolate was identified by using MALDI-TOF. No common epidemiologic links were identified for these infections.

MRSP is an emerging pathogen in dogs and cats (1) but has been rarely identified in horses (2). The role of these bacteria in disease in horses is unclear, but given their ability to cause opportunistic infections in other species, these pathogens should not be dismissed. *S. pseudintermedius* rarely causes disease in humans (9), and transmission normally occurs from infected or colonized animals. Although rarely reported, infection with MRSP might be overlooked in horses; misidentification as *S. aureus* is possible if laboratories assume that coagulase-positive staphylococci from horses are *S. aureus*, and misidentification as methicillin susceptible is possible because the use of cefoxitin susceptibility and *S. aureus* breakpoints is ineffective for determination of methicillin resistance in *S. pseudintermedius* (10). Additionally, *S. pseudintermedius* generates coagulase-positive results by tube testing but coagulase-negative results by slide testing, which creates the potential for misidentification as coagulase-negative staphylococci. Given the rapid expansion of *S. pseudintermedius* infections among dogs, the potential for zoonotic transmission, and the highly resistant nature of this pathogen, ongoing surveillance is indicated in the equine population.

Recently, *S. delphini* has been divided into groups A and B (3). The typical hosts for group A are believed to be mustelidae (i.e., mink, ferret, badger), whereas hosts for group B

### Table. Results of investigation of *Staphylococcus delphini* and *S. pseudintermedius* infection in horses, Canada*

<table>
<thead>
<tr>
<th>Isolate ID or source</th>
<th>Species</th>
<th>Animal age and status</th>
<th>Medical history</th>
<th>Sample source</th>
<th>Date sampled</th>
<th>Mixed infection?</th>
<th>Identification method†</th>
</tr>
</thead>
<tbody>
<tr>
<td>MRSP-I</td>
<td>MRSP, dt11a</td>
<td>1 y, filly</td>
<td>Sinusitis</td>
<td>Frontal sinus surgery</td>
<td>2011 Aug</td>
<td>Yes</td>
<td>A</td>
</tr>
<tr>
<td>SD-1</td>
<td>S. delphini (group B)</td>
<td>8 y, mare</td>
<td>Chronic otitis externa Streptococcus equi surveillance</td>
<td>Ear canal swab</td>
<td>2011 Feb</td>
<td>Yes</td>
<td>B</td>
</tr>
<tr>
<td>SD-2</td>
<td>S. delphini (group B)</td>
<td>5 y, mare</td>
<td>Streptococcus equi surveillance</td>
<td>Nasopharyngeal wash</td>
<td>2011 Jun</td>
<td>No</td>
<td>B</td>
</tr>
<tr>
<td>SD-3</td>
<td>S. delphini (group A)</td>
<td>5 y, mare</td>
<td>S. equi surveillance</td>
<td>Nasopharyngeal wash</td>
<td>2011 Jun</td>
<td>No</td>
<td>B</td>
</tr>
<tr>
<td>SD-4</td>
<td>S. delphini (group B)</td>
<td>4 y, mare</td>
<td>S. equi surveillance</td>
<td>Nasopharyngeal wash</td>
<td>2011 Jul</td>
<td>No</td>
<td>B</td>
</tr>
<tr>
<td>AHLT</td>
<td>MRSP</td>
<td>4 y, mare</td>
<td>Cough</td>
<td>Respiratory tract Skin (pastern) Wound</td>
<td>2011 Mar</td>
<td>Yes</td>
<td>C</td>
</tr>
<tr>
<td>MRSP</td>
<td>S. pseudintermedius</td>
<td>24 y, UNK</td>
<td>Dermatitis (pustular) Chronic draining abscess</td>
<td>Upper respiratory tract Uterus</td>
<td>2011 Jun</td>
<td>Yes</td>
<td>C</td>
</tr>
<tr>
<td>MRSP</td>
<td>8 y, mare</td>
<td>Nasal/sinus swelling</td>
<td></td>
<td>Uterus</td>
<td>2011 June</td>
<td>Yes</td>
<td>C</td>
</tr>
<tr>
<td>MRSP</td>
<td>19 y, mare</td>
<td>Previous uterine infection</td>
<td></td>
<td>Neck wound</td>
<td>2011 June</td>
<td>No</td>
<td>C</td>
</tr>
<tr>
<td>MRSP</td>
<td>11 y, gelding</td>
<td>Draining sores on neck</td>
<td></td>
<td></td>
<td>2011 Jul</td>
<td>No</td>
<td>C</td>
</tr>
<tr>
<td>MRSP</td>
<td>4 y, mare</td>
<td>Wound (coronary band)</td>
<td></td>
<td>Coronary band wound Uterus</td>
<td>2011 Jul</td>
<td>Yes</td>
<td>C</td>
</tr>
<tr>
<td>S. pseudintermedius</td>
<td>UNK, mare</td>
<td>Prebreeding examination</td>
<td></td>
<td>Uterus</td>
<td>2011 Aug</td>
<td>No</td>
<td>C</td>
</tr>
<tr>
<td>S. delphini</td>
<td>3 mo, filly</td>
<td>Chronic pneumonia</td>
<td>Nasal passage</td>
<td></td>
<td>2012 Jun</td>
<td>No</td>
<td>D</td>
</tr>
</tbody>
</table>

*ID, identification; MRSP, methicillin-resistant *S. pseudintermedius*; AHLT, Animal Health Laboratory Database; UNK, unknown.†A, matrix-assisted laser desorption/ionization–time of flight mass spectrometry (MALDI-TOF); MRSP PCR, direct repeat unit typing, mecA PCR, penicillin-binding protein 2a latex agglutination test, broth microdilution; B, MALDI-TOF. S. delphini PCR, sodA sequence analysis, broth microdilution; C, standard biochemical methods, disk diffusion; D, MALDI-TOF, disk diffusion.
remain unknown. *S. delphini* has rarely been identified in horses, but, as we observed, it may be misidentified by conventional methods. Although colonization or contamination appeared most likely in the instances we describe, these findings suggest that this opportunistic pathogen can be found in horses and might be pathogenic in certain situations.

Our findings highlight the importance of using additional identification methods (e.g., MALDI-TOF, *Staphylococcus* species-specific PCR) for differentiation of SIG members (notably *S. delphini* and *S. pseudintermedius*) to effectively document the emergence of these species in horses. In addition, these findings indicate the need to ensure proper differentiation of *S. aureus* from SIG in equine isolates, despite the historical predominance of *S. aureus*, because of the differences in methods for determination of methicillin resistance. Future studies are needed to determine prevalence trends and disease roles for these species in equids.

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Kala-azar and Post–Kala-azar Dermal Leishmaniasis, Assam, India

To the Editor: Kala-azar (visceral leishmaniasis) is a fatal disease caused by a protozoan parasite *Leishmania donovani* and transmitted by the female sandfly, *Phlebotomus argentipes*. In the state of Assam, India, kala-azar epidemics occurred during 1875–1950 and resulted in thousands of deaths in the districts of Kamrup, Garo Hills, Goalpara, and Nagaon (1,2). The disease gradually disappeared from Assam because of the extensive use of DDT in the national malaria elimination program, and results of later entomologic studies indicated that there were no *P. argentipes* sandflies in this region after DDT use (3). However, sporadic kala-azar cases appeared again in Assam in 2004 (4), and in 2008, we reported a kala-azar outbreak in Kamrup (5), where kala-azar epidemics had occurred during the 1870s (1).

At bimonthly intervals during 2012, we conducted house-to-house surveys in 4 villages in the district of Kamrup, for a total of 845 households and 4,376 persons. Residents are socioeconomically poor and depend on agriculture and nearby brick kiln industries for their livelihood; persons involved in these industries generally keep cattle, and areas of cow manure provide breeding sites for sandflies. Persons reported with fever for >2 weeks, anemia, weight loss, and palpable spleen or liver and who were negative for malaria were tested for kala-azar by using the rK39 diagnostic kit (InBiOS, Seattle, WA, USA). We obtained bone marrow biopsy samples from selected persons who exhibited the symptoms listed above. A total of 162 persons had positive kala-azar results according to rK39...