in Australia (5). Given the aforementioned linguistic and coordination issues with follow-up of migrant workers and the potential gravity of inappropriate clinical follow-up, it may be prudent to consider Q fever vaccination for all employees who work within UK meat-processing industries.

Public health practitioners should be aware of the continuously evolving multinational makeup of the local population and this should stimulate constant review of local translation services because census data seriously underrecognize the ethnic minority migrant worker population. Furthermore, many migrant workers are unsure of their rights to access primary and hospital care and the structure of healthcare is unfamiliar to many. GPs should consider zoonotic infections, such as Q fever, when patients with acute febrile illness report occupational livestock exposure, especially because migrant workers have become an important source of labor (sometimes preferred over domestic workers) in the agricultural workforce in the United Kingdom (2).

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Fatal Streptococcus equi subsp. ruminatorum Infection in a Man

To the Editor: Streptococcus equi belongs to the pyogenic group of streptococci and to group C of the Lancefield classification. It consists of 3 subspecies of zoonotic agents rarely reported as human pathogens (1,2): S. equi subsp. equi, S. equi subsp. zooepidemicus, and S. equi subsp. ruminatorum. We report here a case of human infection caused by S. equi subsp. ruminatorum. (3).

A 53-year-old man was admitted to an intensive care unit of our hospital (University Teaching Hospital, Montpellier, France) on April 28, 2006, with a high fever and in a comatose state. The day before, he had experienced headache and neck pain. He had been infected with HIV for 9 years but had not had an opportunistic infection. His ongoing HIV treatment consisted of ritonavir, lopinavir, abacavir, lami-vudine, and co-trimoxazole; 3 weeks before admission, his body CD4+ T-cell count was 133/μL, and viral load was 118,000 copies/mL. At the time of admission, his body temperature was 38.9°C, heart rate was 105 beats/min, and blood pressure was 55/35 mmHg. He exhibited a fixed pupil in 1 eye, neck stiffness, and was nonresponsive. He had bilateral pulmonary infiltrates and severe hypoxemia. Treatment consisted of mechanical ventilation, fluid therapy, and norepinephrine. Laboratory investigations found the following: leukocyte count 9,600/mm³ with 90% neutrophils, hemoglobin level 9.0 g/dL, platelet count 32,000/mm³, C-reactive protein value 159 mg/L, and blood lactate concentration 3.2 mmol/L. Computed tomographic scanning of the brain showed no hemorrhage or edema. Lumbar puncture produced turbid cerebrospinal fluid (CSF) with 300 leukocytes/mm³ (95% neutrophils), protein 5.6 g/L, glucose <0.1 mmol/L, and gram-positive cocci. Three sets of aerobic-anaerobic blood cultures and bronchial aspirates were sampled, and intravenous treatment with dexamethasone (10 mg/6h/day), cefotaxime (2 g/4 h/day), and vancomycin (30 mg/kg/day) was initiated. On day 2, the hemodynamic state was stabilized, but brain death occurred.

All sets of aero-anaerobic blood cultures, CSF, and bronchial aspirate fluid yielded the growth of a catalase-negative, β-hemolytic, gram-positive cocci belonging to the Lancefield group C of streptococci. Antimicrobial susceptibility testing showed a bacterium fully susceptible to antibiotics tested. MICs of penicillin, amoxicillin, and cefotaxime were 0.047, 0.125, and 0.125 mg/L, respectively. The isolates were identified as S. equi by using the Vitek2 system, rapid ID32 STREP, and API 20 STREP strips (bioMérieux, Marcy l’Etoile, France), but phenotype was inconclusive for subspecies identification. The strains were identified as S. equi subsp.
zooepidemicus by Vitek2, but aesculin was not hydrolyzed, and D-ribose fermentation was noted, as previously described for S. equi subsp. ruminatorum. 16S rRNA gene–based identification was performed as previously described (4) on strain ADV 6048.06 from blood. The 1,396-bp sequence (GenBank accession no. EF362949) was compared with databases by using the BLAST program (5); the sequence differed by only 1 nucleotide position (>99.9% identity) from the sequence of S. equi subsp. ruminatorum CECT 5772T. Other primarily related sequences were from S. equi subsp. ruminatorum strains of animal origin (99.5%–99.9% identity) and from S. equi subsp. zooepidemicus, (98.7% identity). Phylogenetic trees clustered the clinical isolate with S. equi subsp. ruminatorum strains to form a robust lineage, well separated from other strains of S. equi and supported by a high bootstrap value (Figure).

S. equi subsp. equi and S. equi subsp. zooepidemicus are zoonotic agents implicated in diverse animal infections such as strangles, mastitis, abscesses, wounds, and respiratory and uterine infections. Human infections caused by S. equi subsp. equi, and S. equi subsp. zooepidemicus included outbreaks of foodborne diseases (6,7), meningitis, septicemia, arthritis, pneumonia, glomerulonephritis, and streptococcal toxic shock syndrome, in both immunocompromised and immunocompetent patients (1,2,8,9).

S. equi subsp. ruminatorum was described in 2004 in domestic sheep and goats with mastitis (3). More recently, it was isolated during severe infections in spotted hyenas and zebras (10). No human isolate has been reported to date. Moreover, none of the 3 subspecies of S. equi has been isolated from HIV-infected patients. The current case underlines the conclusion that molecular identification of S. equi subsp. ruminatorum is essential. S. equi subsp. ruminatorum could have been underestimated due to its potential misidentification as S. equi subsp. zooepidemicus by phenotypic tools. Despite the rare occurrence of group C streptococci in human infections, a high death rate is reported for invasive infections (7–9). S. equi subsp. zooepidemicus produce superantigen exotoxin that may have been implicated in the pathogenesis of fatal infection (2); S. equi subsp. ruminatorum should also be investigated for potential virulence factors for humans.

Epidemiologic investigations were unsuccessful in tracing the patient’s infection to an animal source. The respiratory tract, from which S. equi subsp. ruminatorum was recovered in pure culture, could be considered the most probable portal of entry.

The mode of S. equi subsp. ruminatorum transmission to humans remains unknown. More information is needed on its reservoirs, but they likely resemble those of S. equi subsp. equi, and S. equi subsp. zooepidemicus (2,6,7). Prevention of human infections due to S. equi should include frequent microbiologic sampling of lactating animals and control measures for unpasteurized dairy products (7). Better characterization of underlying conditions that increase risk of invasive S. equi infections is also needed. This knowledge could help define high-risk

![Figure](Image)

Figure. Neighbor-joining tree showing the phylogenetic placement of strain ADV 6048.06 (boldface) among members of the Streptococcus equi species in the pyogenic group of streptococci. Twenty-three 16S rRNA gene sequences selected from the GenBank database were aligned with that of strain ADV 6048.06 by using ClustalX 1.83 (available from http://bips.u-strasbg.fr/fr/documentation/ClustalX). Alignment of 1,263 bp was used to reconstruct phylogenies by using PHYLIP v3.66 package (http://evolution.genetics.washington.edu/phylip.html). The neighbor-joining tree was constructed with a distance matrix calculated with F84 model. Numbers given at the nodes are bootstrap values estimated with 100 replicates. S. pneumoniae is given as outgroup organism. Accession numbers are indicated in brackets. The scale bar indicates 0.005 substitutions per nucleotide position. Maximum likelihood and parsimony trees were globally congruent with the distance tree and confirmed the placement of the strain ADV 6048.06 in the S. equi subspecies ruminatorum (SER) lineage. SEZ, S. equi subspecies zooepidemicus.
groups of persons and could lead to
generation of specific preventive rec-
mandations.

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LETTERS

Rabies Prophylaxis for Pregnant
Women

To the Editor: Rabies poses a
100% risk for death to pregnant wom-
en and an indeterminate risk to the
fetus (1,2). Although a theoretical risk
exists for adverse effects from rabies
immune globulin and killed rabies vi-
rus vaccines, several studies assessing
the safety of this treatment have failed
to identify these risks (3–6). Indeed,
the consensus is that pregnancy is not
an indication per se (3–6). However,
many recent human rabies patients have
no known history of exposure to a ra-
bid animal (9,10). Of the 21 cases of
bat-associated rabies in the United
States during 1980–1999, 12 (57%)
occurred in persons with apparent bat
contact but no detectable bites (8).
Our patient woke up with a bat fly-
ing in her room and did not know how
long it had been there. The best course
of action would have been to test the
bat for rabies. However, because the
animal had already been disposed of,
laboratory testing for rabies was not
possible. Furthermore, given that 5%–
9% of bats tested in Washtenaw Coun-
ty, Michigan, are positive for rabies
vaccines, several studies assessing
the safety of this treatment have failed
to identify these risks (3–6). Indeed,
the consensus is that pregnancy is not
an indication per se (3–6). However,
many recent human rabies patients have
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9% of bats tested in Washtenaw Coun-
ty, Michigan, are positive for rabies
(www.mdch.state.mi.us/pha/epi/cded/
cd/batcoframe.htm), the exposure risk
was not insignificant. Therefore, it