These differences could be ascribed to the prison’s being situated in a natural setting, with the flock grazing for 1 month in the meadows nearby.

*C. burnetii* is an infrequent cause of community-acquired pneumonia in our region. These data suggest that the infected sheep were the source of this large outbreak. None of the patients had any contact with animals, except for the Veterinarian Service personnel, which suggests airborne transmission of infected dust particles from contaminated soil, favored by the dry weather recorded in that period. To our knowledge, this is the second outbreak of Q fever reported in northern Italy (5). Since 1999, neither the Department of Prevention nor the Veterinary Service had received any reports of Q fever in Como. In Italy, the total number of cases of rickettsial diseases, which includes Q fever, reported to the Ministry of Health was 769 in 2002 and 739 in 2001, with 5 and 13 cases, respectively, from Lombardia, which includes Como. This Q fever epidemic in Como is thus an exceptional event in our area.

The collaboration between epidemiologists and veterinarians of the Department of Prevention and staff from Saint Anna Hospital allowed us to share epidemiologic and medical information, which proved useful in diagnosing the outbreak and treating patients. Our experience emphasizes the necessity of a greater awareness of this occupational zoonosis in areas with a high rate of urbanization.

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**Correction Vol. 9, No. 6**

In "Clinical Implications of Varying Degrees of Vancomycin Susceptibility in Methicillin-Resistant Staphylococcus aureus Bacteremia, by Mitchell J. Schwaber et al., errors occurred in some reference numbers. In the Discussion, fourth paragraph, p. 661, the last sentence should read as follows: ‘It is possible that some or all of the isolates from our cases are potential precursors of truly heteroresistant isolates (hetero-VISA), which may in turn be forerunners of VISA (6,18,32).’ In the final paragraph, pp. 662-663, the next to last sentence should read as follows: ‘These results add weight to assertions that clinical microbiology laboratories need not routinely screen for vancomycin heteroresistance in S. aureus isolates with vancomycin MICs in the susceptible range (1,7).’

**Correction Vol. 9, No. 11**

In “Genetic Variation among Temporally and Geographically Distinct West Nile Virus Isolates, United States, 2001, 2002, by C. Todd Davis, et al., errors occurred in Tables 1 and 2. The correct title for Table 1 is “Nucleotide mutations in sequences of the prM gene of 22 West Nile virus isolates obtained during 2001 and 2002 compared to WN-NY99.” In Table 1, line 6, Nueces Co., Tx-1, under “prM 491” should read “G (Arg)”; line 19, Galveston Co., TX-2, under “prM 679” should read “A (Thr).” The correct title for Table 2 is “Nucleotide mutations in sequences of the E gene of 22 West Nile virus isolates obtained during 2001 and 2002 compared to WN-NY99.” In Table 2, line 3, Harris Co., TX, under “Envelope 2,392,” should read “A (Thr)”; line 8, Nueces Co., TX-2, under “Envelope 1,118,” should read “U (Val)”; line 12, Randall Co., TX, under “1,192” should read “C (Asn)”; line 24, Galveston Co., TX-3, under “Envelope 1,192” should read “G (Ala).” Corrected versions of Tables 1 and 2 are available at: URL: http://www.cdc.gov/ncidod/EID/vol9no11/03-0301.htm

We regret any confusion these errors may have caused.