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Ventilator-associated Pneumonia and MRSA ST398, Italy

To the Editor: Methicillin-resistant *Staphylococcus aureus* (MRSA) sequence type (ST)398 has become increasingly common in livestock, particularly pigs, in some countries in Europe, such as Spain and Germany (1). In Italy, prevalences as high as 14% and 21.6% in pig-breeding facilities and meat-processing sites, respectively, have been recently reported (1).

Possible association of MRSA in animals with infection in humans has been investigated. One study showed a strong relationship between contact with pigs or calves and carriage by persons having direct contact with animals and families of persons who handle animals (2). Moreover, an MRSA prevalence $\geq 11.9\%$ has been described by de Boer et al. (3) in meat, with 85% of isolates belonging to the ST398 lineage.

MRSA ST398 has been described as a lineage with limited virulence and ability to spread between humans, but severe clinical manifestations, such as wound infections and endocarditis, have been recently attributed to this clone (1,4). Cases of nosocomial

ventilator-associated pneumonia have also been reported in Germany (1). Moreover, an outbreak of infection with MRSA ST398 occurred in a surgical ward of a hospital in the Netherlands in 2007 (5).

MRSA ST398 is an infrequent cause of human infections in Italy. No isolates belonged to this lineage in 2 studies of MRSA in Italy during 2006–2007 (6) or in hospitals during 1990–2007 (7). Only 1 invasive infection has been recently reported in a pig farm worker (8). We report a case of ventilator-associated pneumonia caused by MRSA ST398 in a patient in Palermo, Italy. The patient and his household members did not report any exposure to companion or livestock animals.

The case-patient was a 78-year-old man admitted to a cardiac intensive care unit (ICU) of ARNAS Ospedale Civico Di Cristina e Benfratelli in Palermo on January 31, 2009, because of a recent history of unstable angina pectoris and acute anemia caused by duodenal ulcers. After cardiocirculatory arrest, he was transferred to a general ICU on February 3. The patient had type 2 diabetes and ischemic-hypertensive cardiomyopathy. MRSA nasal colonization at admission was not investigated because the patient lacked risk factors for screening at admission, e.g., antimicrobial drug therapy, hospitalization for >48 hours or time in a long-term care facility within the past 6 months, need for long-term nursing care, presence of indwelling devices, or chronic skin lesions.

The clinical course of the patient's illness was characterized by serious hemodynamic instability and difficulty in weaning from mechanical ventilation. Two bronchial aspirate specimens were cultured on February 4 and 9, when he was being treated with a third-generation cephalosporin (ceftriaxone). These cultures showed *Staphylococcus epidermidis* and *S. saprophyticus*. On the 14th day in the ICU, clinical signs of ventilator-

associated pneumonia developed in the patient. He had increased sputum production, fever (38.8°C), leukocytosis, and infiltrates were seen on a chest radiograph.

Empiric antimicrobial drug therapy with glycopeptides and a β -lactam/ β -lactamase inhibitor combination was started. Culture of bronchial secretions yielded MRSA that was susceptible to glycopeptides, rifampin, linezolid, macrolides, and sulfamethoxazole and resistant to fluoroquinolones and tetracyclines. Three days later, linezolid was given, but the patient died after an acute myocardial infarction.

The isolate was identified genetically by *mecA* PCR. It was not typeable by pulsed-field gel electrophoresis after digestion with *Sma*I, negative for Pantone-Valentine leukocidin, and carried staphylococcal cassette chromosome *mec* (SCC*mec*) type IVa (9). Multilocus sequence typing, performed according to a recommended procedure (<http://saureus.mlst.net/misc/info.asp>), identified the isolate as ST398.

A 1-year epidemiologic survey on MRSA isolates from 4 general hospitals in Palermo, which had begun on February 2009, did not identify any MRSA isolate carrying SCC*mec* type IV or V in patients admitted to the ICU until September 2009. However, colonization or infection by MRSA ST398 in the ICU patients before the study period could not be ruled out. Although an MRSA screening policy for the ICU staff members was not being carried out, a nosocomial chain of transmission appeared to be unlikely.

Our results indicate that a new zoonotic clone of MRSA is emerging as a potential cause of serious human infections. Screening at hospital admission would likely help efforts to determine whether exposure to pet animals and livestock had occurred. However, the absence of specific exposure to zoonotic clonal lineages, as in our case-patient, is a matter of concern in terms of screening and contact tracing policy for MRSA in-

fections. Prevalence of MRSA and distribution of MRSA sequence types in livestock in Italy are not known. However, surveys of foods of animal (pig) origin have showed an MRSA prevalence of 3.7% (1,10). In view of the low prevalence of MRSA ST398 in patients with no exposure to animals, food products currently seem to play a negligible role. However, this clone is likely spreading because of the large animal reservoir of ST398 and the global market for meat and livestock. The changing epidemiology of MRSA indicates that collaborative surveillance plans integrating human and animal information should be increased.

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Panton-Valentine Leukocidin-Positive MRSA, Shanghai, China

To the Editor: The development of methicillin resistance in community strains of *Staphylococcus aureus* is a notable step in the evolution of this pathogen. Unlike their equivalents in the hospital environment, community-associated methicillin-resistant *S. aureus* (CA-MRSA) strains tend to cause infections in children and young adults who have few known healthcare risks (1). CA-MRSA strains usually possess the Panton-Valentine leukocidin (PVL) genes and staphylococcal cassette chromosome (SCC) *mec* type IV or V (1,2).

We studied 72 *S. aureus* isolates (49 MRSA and 23 methicillin-susceptible [MSSA]) by pulsed-field gel electrophoresis and by SCC*mec*, staphylococcal protein A (*spa*), and multilocus sequence typing (1,3). These isolates were recovered from clinical specimens (52 respiratory specimens, 9 wound, 4 urine, 2 blood, and 5 other body fluids) from 72 patients treated in 5 district hospitals in Shanghai, People's Republic of China, during October 2005 through January 2007. The isolates were randomly chosen. In the hospitals, ≈1,000 *S. aureus* isolates were recovered annually during the time period of our study. The 5 hospitals are estimated to serve a population of 3.4 million, equivalent to one fourth of the total population in Shanghai. Hospital D is a children's hospital. The other 4 hospitals (A, B, C, and E) have all the major clinical specialties, emergency departments, and outpatient clinics.

The isolates were identified as *S. aureus* by Gram stain, latex agglutination (Slide StaphPlus; bioMérieux, Marcy l'Etoile, France), and tube coagulase, mannitol, ornithine, and deoxyribonuclease reactions (1,4). Methicillin resistance in the isolates was