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 shown 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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References

1. European Food Safety Authority. Analysis of the baseline survey on the prevalence of methicillin-resistant Staphylococcus aureus (MRSA) in holdings with breeding pigs, in the EU, 2008. European Food Safety Authority Journal. 2009;7:1376.
2. van Loo I, Huysdens X, Tiemersma E, de Neeling A, van de Sande-Buuma N, Beaujoup D, et al. Emergence of methicillin-resistant Staphylococcus aureus of animal origin in humans. Emerg Infect Dis. 2007;13:1834–9.
3. de Boer E, Zwaartkruis-Nahuis JT, Wit B, Huysdens WX, de Neeling AJ, Bosch T, et al. Prevalence of methicillin-resistant Staphylococcus aureus in meat. Int J Food Microbiol. 2009;134:52–6. DOI: 10.1016/j.ijfoodmicro.2008.12.007
4. Ekelenkamp MB, Sekkat M, CarpinEx N, Troels A, Bonten MJ. Endocarditis due to methicillin-resistant Staphylococcus aureus originating from pigs [in Dutch]. Ned Tijdschr Geneeskd. 2006;150:2424–7.
5. Wulf MW, Markstein A, van der Linden FT, Voss A, Klaassen C, Verduin CM. First outbreak of methicillin-resistant Staphylococcus aureus ST398 in a Dutch hospital, June 2007. Euro Surveill. 2008;13:8051.
6. Campanile F, Bongiorno D, Borbone S, Stefani S. Hospital-associated methicillin-resistant Staphylococcus aureus (HA-MRSA) in Italy. Ann Clin Microbiol Antimicrob. 2009;8:22. DOI: 10.1186/1476-0711-8-22
7. Marchese A, Gualco L, Maioli E, Debbia E. Molecular analysis and susceptibility patterns of methicillin-resistant Staphylococcus aureus (MRSA) strains circulating in the community in the Ligurian area, a northern region of Italy: emergence of USA300 and EMRSA-15 clones. Int J Antimicrob Agents. 2009;34:424–8. DOI: 10.1016/j.ijantimicag.2009.06.016
8. Pan A, Battisti A, Zoncada A, Bernieri F, Boldini M, Franco A, et al. Community-acquired methicillin-resistant Staphylococcus aureus ST398 infection, Italy. Emerg Infect Dis. 2009;15:845–7. DOI: 10.3201/eid1505.081417
9. Zhang K, McClure JA, Elsayed S, Louie T, Conly JM. Novel multiplex PCR assay for characterization and concomitant subtyping of staphylococcal cassette chromosome mec types I to V in methicillin-resistant Staphylococcus aureus. J Clin Microbiol. 2005;43:5026–33. DOI: 10.1128/JCM.43.10.5026-5033.2005
10. Normanno G, Corrente M, La Sandra G, Dambrosio A, Quaglia NC, Parisi A, et al. Methicillin-resistant Staphylococcus aureus (MRSA) in foods of animal origin product in Italy. Int J Food Microbiol. 2007;117:219–22. DOI: 10.1016/j.ijfoodmicro.2007.04.006

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 SCCmec, 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
included 8 infants with pneumonia and 4 (17.3%) of the 23 MSSA isolates were attributed to 2 clones with genotypes t318/ST30-IV (or t318/ST1114-V) and t1376/ST88-V. Detection of t318/ST30 strains in 4 patients with healthcare-associated infections suggested hospital transmission of this CA-MRSA clone, corroborating reports elsewhere (9). Worldwide, ST30 is a common CA-MRSA genetic lineage (1,2). Besides t318, strains related to the ST30 clone have been reported to be spa types t019, t021, and t1273 (2). ST88 PVL-positive MRSA is relatively less common but has been found in Wenzhou (People’s Republic of China), Bangladesh, Belgium, and Nigeria (2,7,8,10).

Because the number of isolates tested in this study is relatively small, no firm conclusion could be drawn on the prevalence of PVL-positive CA-MRSA among *S. aureus* isolates. Nonetheless, our findings agree with previous reports that the genotypes of MSSA isolates are more diverse than those for PVL-positive and -neg-
tive MRSA isolates and that genotypes for some CA-MRSA strains are shared by a few of the MSSA strains (1).

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References

1. Ho PL, Chuang SK, Choi VF, Lee RA, Lit AC, Ng TK, et al. Community-associated methicillin-resistant and methicillin-sensitive Staphylococcus aureus: skin and soft tissue infections in Hong Kong. Diagn Microbiol Infect Dis. 2008;61:245–50. DOI: 10.1016/j.diagmicrobio.2007.12.015

2. Tristan A, Bes M, Meugnier H, Lina G, Bozdogan B, Courvalin P, et al. Global distribution of Panton-Valentine leukocidin-positive methicillin-resistant Staphylococcus aureus, 2006. Emerg Infect Dis. 2007;13:594–600. DOI: 10.3201/eid1304.061316

3. Ho PL, Lai EL, Chow KH, Chow LS, Yuen KY, Yung RW. Molecular epidemiology of methicillin-resistant Staphylococcus aureus in residential care homes for the elderly in Hong Kong. Diagn Microbiol Infect Dis. 2008;61:135–42. DOI: 10.1016/j.diagmicrobio.2007.12.017

4. Ho PL, Wang TK, Ching P, Mak GC, Lai E, Yam WC, et al. Epidemiology and genetic diversity of methicillin-resistant Staphylococcus aureus strains in residential care homes for elderly persons in Hong Kong. Infect Control Hosp Epidemiol. 2007;28:671–8. DOI: 10.1086/517951

5. Finlay JE, Miller LA, Poupard JA. Interpretive criteria for testing susceptibility of staphylococci to mupirocin. Antimicrob Agents Chemother. 1997;41:1137–9.

6. Perez-Roth E, Claverie-Martin F, Villar J, Mendez-Alvarez S. Multiplex PCR for simultaneous identification of Staphylococcus aureus and detection of methicillin and mupirocin resistance. J Clin Microbiol. 2001;39:4037–41. DOI: 10.1128/JCM.39.11.4037-4041.2001

7. Denis O, Deplano A, De Beenhouwer H, Hallin M, Huymans G, Garrino MG, et al. Polyclonal emergence and importation of community-acquired methicillin-resistant Staphylococcus aureus strains harbouring Panton-Valentine leukocidin genes in Belgium. J Antimicrob Chemother. 2005;56:1103–6. DOI: 10.1093/jac/dki379

8. Yu F, Chen Z, Liu C, Zhang X, Lin X, Chi S, et al. Prevalence of Staphylococcus aureus carrying Panton-Valentine leukocidin genes among isolates from hospitalised patients in China. Clin Microbiol Infect. 2008;14:381–4. DOI: 10.1111/j.1469-0691.2007.01927.x

9. Zaoutis TE, Toltzis P, Chu J, Abrams T, Du M, Kim J, et al. Clinical and molecular epidemiology of community-acquired methicillin-resistant Staphylococcus aureus infections among children with risk factors for health care–associated infection: 2001–2003. Pediatr Infect Dis J. 2006;25:343–8. DOI: 10.1097/01.inf.0000207403.67197.cc

10. Ghebremedhin B, Olugbosi MO, Raji AM, Layer F, Bakare RA, Konig B, et al. Emergence of a community-associated methicillin-resistant Staphylococcus aureus strain with a unique resistance profile in Southwest Nigeria. J Clin Microbiol. 2009;47:2975–80. DOI: 10.1128/JCM.00648-09

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Clostridium difficile in Ground Meat, France

To the Editor: Clostridium difficile is a toxigenic enteropathogen responsible for 15%–20% of antimicrobial drug–associated diarrhoea and for almost all cases of pseudomembranous colitis. Two protein toxins (TcdA and TcdB) play a major role in the pathogenesis of infections. C. difficile is also recognized as a cause of disease in several animal species, which could be potential reservoirs (1). In the past few years, the presence of C. difficile in raw diets for dogs and cats and in retail meat sold for human consumption has been reported in the United States and Canada at rates from 6% to 42% (2–5). To determine C. difficile contamination of meat in France, we evaluated 105 packages of ground beef (vacuum packed or not), 59 pork sausages, and 12 packages of feline raw diet meat purchased from 20 urban and suburban Paris retail stores and supermarkets during September 2007–July 2008.

C. difficile spores or vegetative forms in samples were found as described by Rodriguez-Palacios et al. (4). Briefly, 5 g of each sample was cultured in 100 mL of prereduced brain–heart infusion (BHI) broth supplemented with cefoxitin (10 μg/mL), cycloserine (250 μg/mL), and taurocholate (0.1%). After the samples were incubated under anaerobic conditions at 37°C for 72 h, subculturing with and without alcohol shock for spore selection was performed. The BHI broth culture was treated with 2 mL of absolute ethanol (1:1 vol/vol) for 30 min and centrifuged at 3,800 × g for 10 min, and the pellet was resuspended in 200 μL of prereduced BHI broth. Serial dilutions of the BHI broth and the pellet were injected onto Columbia cysteine agar supplemented with cefoxitin–cycloserine, taurocholate, and 5% horse blood and incubated anaerobically for 48 h at 37°C.