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Correspondence

Emergence of Unusual Bloodstream Infections Associated with Pig-Borne-Like *Staphylococcus aureus* ST398 in France

TO THE EDITOR—*Staphylococcus aureus* ST398 is a zoonotic agent primarily described in Europe that is becoming a worldwide threat associated with livestock, their human contacts, and food products. In animals, carriage is frequent, but infections are rare. In humans, infections consist in nosocomial bloodstream and wound infections [1] that are associated with *spa* types 011 or 034, tetracycline resistance, and the absence of panton-valentine leukocidin (PVL). Recently, a new population of ST398 strains has been isolated in China and from children adopted from China [2] that is responsible for pneumonia and skin and soft-tissue infections in patients without association with animals or animal farming and which is characterized by *spa* type 571, tetracycline susceptibility, and variable presence of PVL [3].

Annual surveys of bloodstream infection are performed in the center region of France [4, 5]. In 2009, we observed the emergence of cases associated with t571, TetS, and PVL-negative ST398 strains. Examination of patient histories revealed exposure to animals in 1 case, a fatal idiopathic community-acquired bloodstream infection in an 84-year-old man who lived on a farm at which 1 pig was being raised. The remaining cases were hospital-acquired and included 1 case of catheter-associated infection observed in a 58-year-old man with advanced multiple myeloma, 1 case following elective digestive tract surgery in a 69-year-old

woman, and 1 case following cardiac surgery in a 68-year-old man.

Microarray and MLVA analysis [7] were performed to characterize the strains and compare them with European pig-borne methicillin-resistant *S. aureus* and virulent strains (USA300, MW2, TW20, COL, and Newman). Most characteristics of the present strains were similar to those of the pig-borne strain. All were of *accessory gene regulation* type I, and none contained the genes encoding the following virulence factors: EsxA and EsxB proteins; leukocidin F; Panton-Valentine Leukocidin; TSST-1; exfoliatins A and B; and enterotoxins A–E, G–R, and U. None harbored the lantibiotic epidermin/gallidermin genes *epiA–epiF* typically reported in virulent strains. In addition, similarly to the pig-borne strain, our strains harbored the *cna* gene, encoding a collagen adhesin associated with colonizing strains and involved in the pathogenesis of osteomyelitis and infectious arthritis [6]; the hyaluronidase gene, involved in the early stages of subcutaneous infections; and a factor SAV2371, associated with bacterial attachment to host cells and virulence. By contrast, unlike the pig-borne strain, the studied strains and the USA300 virulent clone shared *cadC–cadM* genes, which are responsible for cadmium resistance, and prophagic genes. In addition, the strains harbored remnants of staphylococcal cassette chromosome *mec* (IS1272 and Tn554), similar to the strains reported from China [2]. Importantly, the strains appeared to be deficient in the type I restriction system (*hsdS–hsdR*), the main function of which is to limit horizontal gene transfer [8, 9].

Our observations show the emergence of new ST398 strains in human infectious diseases that differ from pig-borne strains and share similarity with Chinese-type and USA300 strains. The similarity with the USA300 virulent clone highlights their high potential for virulence and alerts us about the need to develop an active surveillance strategy to study and control the rapid spread of this clone. Transmission of pig-borne ST398 between animals and humans, as well as between humans, has been described [10, 11]. In the present cases of bloodstream infection, which were identified at 4 unrelated health care institutions, our data do not clarify how the strains were transmitted, which highlights the need for further epidemiological studies.

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