Editorial

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Community-Associated Methicillin-Resistant *Staphylococcus aureus* in Nosocomial Infections

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Methicillin-resistant *Staphylococcus aureus* (MRSA) first emerged in the 1960s, shortly after the introduction of methicillin, and outbreaks of MRSA were reported in the early 1960s [1, 2]. In the 1990s, community-associated MRSA (CA-MRSA) emerged as an epidemic of skin and soft tissue infections in patients without any prior healthcare contact and was associated with serious morbidity and mortality [3].

Methicillin resistance is mediated by PBP-2a, a penicillin-binding protein encoded by the *mecA* gene, which permits the organism to grow and divide in the presence of methicillin and other beta-lactam antibiotics. The *mecA* gene is located on a mobile genetic element called staphylococcal chromosome cassette (SCC*mec*). A single clone probably accounted for most MRSA isolates recovered during the 1960s; by 2004, six major MRSA clones emerged worldwide, labeled as SCC*mec* I to VI [4].

Healthcare-associated MRSA (HA-MRSA) and CA-MRSA differ with respect to their clinical and molecular epidemiologies. HA-MRSA is associated with severe, invasive disease, including skin and soft tissue infections, bloodstream infection (BSI), and pneumonia in hospitalized patients [5]. HA-MRSA strains tend to have multidrug resistance and carry SCC*mec* type II. HA-MRSA has been a cause for concern in hospital settings since the 1960s; since then, the prevalence of antimicrobial resistance in hospital-acquired *S. aureus* infections has progressively increased. Risk factors of HA-MRSA infection include antibiotic use, prolonged hospitalization, intensive care, hemodialysis, MRSA colonization, and proximity to individuals with MRSA colonization or infection.

CA-MRSA is defined as MRSA infection that occurs in the absence of healthcare exposure. CA-MRSA is most often associated with skin and soft tissue infections in young, healthy individuals with no recent healthcare exposure [3]. The most common infections caused by CA-MRSA are skin and soft tissue infections, although more invasive infections involving the respiratory tract, with and without bacteremia, and septic shock can occur. Affected individuals often lack traditional risk factors of MRSA infection. Most CA-MRSA strains are sensitive to non-beta-lactam antibiotics, although a multidrug-resistant isolate has been described. Most CA-MRSA strains frequently carry SCC*mec* type IV or V; in addition, they frequently carry genes for the cytotoxin Panton-Valentine leukocidin (PVL) that confers enhanced virulence [6]. Many strains produce toxins, such as the PVL, and other virulence factors that may play a role in the increased severity of disease associated with

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CA-MRSA. CA-MRSA has emerged as an important cause of healthcare-associated infection, and introduction of these strains into the healthcare setting has led to a significant change in the epidemiology of MRSA. CA-MRSA clones have replaced classic hospital MRSA clones in many countries and have shown higher potential in transmission and virulence than hospital MRSA clones.

The CA-MRSA and HA-MRSA classifications are no longer distinct because patients can develop MRSA colonization in one setting and develop manifestations of infection in another. Although HA and CA-MRSA infections are convenient epidemiological terms, the line between them is significantly blurred. Community-onset, HA-MRSA infections have been observed with increasing frequency among patients in community settings. Similarly, patients with MRSA infections due to CA strains have also been observed with increasing frequency among patients in hospital settings. CA-MRSA strains may also cause hospital-onset, HA infections, as patients who become colonized with CA-MRSA strains in the community may require hospitalization and either transmit such strains to other hospitalized patients or develop infection while hospitalized (*e.g.*, following surgery or insertion of an invasive device) [7].

The blurring epidemiological distinction between HA-MRSA and CA-MRSA was also illustrated by the United States Active Bacterial Core surveillance network report of 8,987 invasive MRSA infections in 2005. The authors concluded that MRSA infections are primarily related to health care but are no longer confined to intensive care units, acute-care hospitals, or any healthcare institution [5]. CA-MRSA may be replacing traditional hospital-acquired strains. Molecular typing of 208 isolates from hospital-onset, HA-MRSA blood stream infections (BSIs) between 2000 and 2006 demonstrated that although the total number of MRSA BSIs was stable, community-acquired strains were responsible for an increasing proportion of cases (from 24% to 49%) [8].

The "Emergence of community-genotype MRSA in Korean hospitals: clinical characteristics of nosocomial infections by community-genotype strain" described clinical characteristics of nosocomial MRSA infections by a community-genotype of sequence type (ST) 72 [9]. As community-genotype MRSA strains spread into hospitals, the genotypes of the MRSA strains that cause hospital-acquired infections have become more diverse.

Conflicts of Interest

No conflicts of interest.

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