A Brief Note on Antibiotic Resistance in Staphylococcus Aureus

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Editorial Note

Methicillin-Resistant Staphylococcus Aureus (MRSA) isolates came into existence soon after the introduction of methicillin. Historically, MRSA isolates have been associated with nosocomial infections and rapidly developed resistance to multiple drug classes. However, in recent years, different strains with unique phenotypes have emerged in the community, and the reservoir of community-associated MRSA is rapidly expanding. Community-associated pathogens are likely to cause life-threatening systemic infections, especially in children and elderly individuals, and may also cause serious skin and soft-tissue infections in healthy individuals. Compared with nosocomial strains, community-associated MRSA isolates are associated with increased virulence and currently are more likely to be susceptible to a variety of antibiotics. The epidemiological and microbiological differences between community-associated and nosocomial MRSA infections necessitate different strategies to prevent and treat the 2 types of infections. Vancomycin nonsusceptibility in S. aureus is on the increase, further complicating therapy.

Methicillin-resistant Staphylococcus aureus (MRSA) is a major pathogen worldwide; MRSA infections are associated with increased morbidity and mortality, in comparison with other S. aureus infections. Over the past decade, the changing pattern of resistance in S. aureus has underscored the need for new antimicrobial agents. Once confined to health care—associated environments, MRSA has now migrated into the community. Community-associated strains share some characteristics with nosocomial strains but also differ in antimicrobial susceptibility and potential virulence. of concern is the probable increasing prevalence of heterogeneous vancomycin-intermediate S. aureus (hVISA) and vancomycin-intermediate S. aureus (VISA) MRSA strains in Europe, Asia, and the United States. Although 7 cases of infection with vancomycin-resistant S. aureus (VRSA) strains have been described in the United States, the clinical and epidemiological significance of this resistance phenotype is unclear at the present time.

Study of early isolates of MRSA showed that a key genetic component responsible for resistance, mecA, is not native to the S. aureus genome. The staphylococcal chromosome cassette mec (SCCmec) has been characterized as a novel, mobile resistance element that differs from both transposons and bacteriophages. MRSA typically spreads through clones; however, it is known that the mec gene has been transmitted between S. aureus strains and, possibly, between other staphylococcal species. Recently, the British Society for Antimicrobial Chemotherapy, the Hospital Infection Society, and the Infection Control Nurses Association published guidelines for the laboratory diagnosis and susceptibility testing of MRSA. Routine identification of S. aureus should be performed via tube coagulase tests or latex agglutination tests; routine use of molecular tests for identification is not currently practical for most diagnostic laboratories. However, molecular testing may be useful when there is a high index of suspicion for MRSA. Susceptibility testing may be performed through any standard recognized method, and latex methods to detect PBP 2a and/or PCR tests to detect the mecA gene can provide confirmation of equivocal results. DD testing with cefoxitin has been well correlated with the presence of mecA-mediated oxacillin resistance in S. aureus and has excellent sensitivity (98%) and specificity (100%).

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