During the past 50 years, *Staphylococcus aureus* has been a dynamic human pathogen that has gained the deepest respect of clinicians. Its incredible success in caus ing disease involves characteristics associated with host susceptibility (age, chronic disease, surgery, presence of invasive devices, or impaired immunity), the specific strain (genetics, ease of colonization, virulence, and antibiotic resistance), and epidemiology (carriage, transmission, and breaches in infection-control measures). Invasive *S. aureus* infections are clearly associated with increased morbidity, mortality, and costs. Our inability to control these infections highlights the need for increased awareness and better prevention and treatment strategies.

Since the first report of health care–associated methicillin-resistant *S. aureus* (MRSA) infection in the United States at Boston City Hospital in 1965, MRSA has become widespread [1]. MRSA strains are resistant to cephalosporins and carbapenems, in addition to semisynthetic penicillins, such as methicillin, oxacillin, and nafcillin; generally resistant to macrolides, clindamycin, and aminoglycosides; and usually susceptible to trimethoprim-sulfamethoxazole, tetracycline, rifampin, and the newer antibiotics (linezolid, quinopristin-dalfopristin, and daptomycin).

Despite widespread use of vancomycin after its introduction in 1956, an interval of ~30 years passed before vancomycin–intermediate *S. aureus* (VISA) and glycopeptide–intermediate *S. aureus* (GISA) isolates (MIC for both agents, >4 to 16 μg/mL) were first reported [2]. It was not until 2003 that the first of 5 vancomycin-resistant *S. aureus* (VRSA) isolates (MIC, ≥16–32 μg/mL) appeared [3]. Although vancomycin remains a reliable treatment for the vast majority of staphylococcal infections, the lack of universal susceptibility to vancomycin and to other glycopeptides is sobering, and the potential spread of GISA and VRSA is of great concern.

The logical first step in the emergence of GISA and VRSA strains as a global threat is entry into the health care environment, as described in this issue by de Lassence et al. [4]. The outbreak of GISA they report involved 21 patients in an intensive care unit who became colonized or infected during 1999–2000. The spread of infection was due, in part, to the initial failure in the microbiology laboratory to identify GISA, which underscores the importance of saving clinical isolates for proper microbiologic testing and molecular typing that may complement epidemiologic data.

Despite a number of methodologic weaknesses in the article, de Lassence and coworkers document their efforts to control a GISA outbreak. Two crucial points should be taken from this article. First, laboratory detection of these strains is difficult. Automated systems are commonly used to test clinical isolates for antimicrobial resistance, because they are faster and more cost-effective than manual methods. Unfortunately, there is a lag time between the recognition of a new type of resistance and the ability of automated systems to reliably detect the resistant organisms. Retrofitting systems with the suitable software “fix” that can reliably detect the new mechanism of resistance is difficult, as evidenced by failures of automated systems used to detect vancomycin–resistant enterococci, extended-spectrum β-lactamase–resistant Enterobacteriaceae, and, now, GISA isolates. The use of vancomycin agar screening plates that contain vancomycin, 6 μg/mL, has been recommended as an adjunct to standard testing methods that are used to detect vancomycin–resistant enterococci.

Significant hospital costs result from delays in the recognition of resistant bacteria, such as GISA. Laboratory costs associated with performing additional resistance testing, such as the Etest (noted in the article by de Lassence and colleagues), are minimal, compared with the costs to contain resistant organisms. In addition, eradication of GISA and MRSA is often difficult and may require multiple control strate-
gies. Clearly, compliance with effective infection-control standards, such as hand disinfection, is often suboptimal, and we lack standardized methods for culturing samples from the environment. Standardized environmental monitoring, possibly including quantitation of colonization, is essential for assessing the role of environmental colonization. Because of the relative rarity of these strains in 2005, the role of DNA fingerprinting to assess the number of strains involved is less critical.

Although it is unclear which control strategies are most cost effective, compliance with conventional prevention strategies (i.e., gown and glove use and hand washing with alcohol-based disinfection), along with maintaining rational nurse-to-patient ratios, are sensible but often breached. Successful strategies for control of MRSA, however, should be applicable for GISA and VRSA.

In contrast to health care–associated MRSA, community-acquired MRSA presents a new threat for serious infections in healthy children and adults [5, 6]. Most infections in these 2 groups have been severe skin and soft-tissue infections complicated by deep abscesses or necrotizing fasciitis and, less commonly, by pneumonia. Reported outbreaks involving schools, athletic teams (e.g., football and wrestling teams), prisons, homeless shelters, military facilities, and families should be noted by clinicians and public health officials. All community-acquired MRSA isolates are clonal and carry a unique gene, and nearly all possess the Panton-Valentine leukocidin virulence factor and are more susceptible to antibiotics than are health care–associated MRSA.

What questions should the changing epidemiology of MRSA infections in the United States introduce, and what should we do about them? Is it possible that patients with community-acquired MRSA could serve as vectors for the introduction of this strain to hospitals? Could changes in health care–associated MRSA and community-acquired MRSA infections increase the risk of bacterial superinfections following influenza outbreaks? If avian influenza virus infection becomes pandemic, could these isolates enhance the airborne spread of avian influenza and MRSA (“cloud adult”), increase rates of severe staphylococcal pneumonia, and create “the perfect storm” [7]? Prevention and containment would invariably require impeccable infection control, proper use of influenza vaccines, early identification of infection, and appropriate use of antibiotic and antiviral therapy.

Because times are a-changin” regarding the epidemiology of S. aureus, our response needs to change by adhering to established infection-control measures and staff education, while creating better prevention strategies. Protein-polysaccharide conjugate vaccines have been highly effective for control and prevention of disease due to other encapsulated pathogens, such as Haemophilus influenzae type b, Streptococcus pneumoniae, and Neisseria meningitidis, and initial studies of S. aureus conjugate vaccine containing capsular polysaccharide types V and VIII provided some protection against invasive disease for patients undergoing hemodialysis [8]. These data underscore the need to improve vaccine efficacy for this population and to study immune response and protection in other high-risk populations. S. aureus has been dynamic and creative in meeting new challenges during the past 50 years. Therefore, we must be more dynamic and demonstrate similar creativity and persistence in our response.

Acknowledgments


References