Whole-Genome Sequencing Analysis: An Essential Tool for Shedding Light on the Obscure Evolution of Staphylococcus aureus USA300

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(See the major article by Von Dach et al on pages 1370–9.)

The editorial commentary discusses the changing epidemiology of methicillin-resistant Staphylococcus aureus (MRSA) infections and the role of the USA300 clone in causing infections. The USA300 clone, first identified in the United States, has expanded to other continents, including Africa and South America. This clone is characterized by the presence of a mobile element (ACME), which carries genes encoding resistance to antibiotics. The editorial highlights the importance of whole-genome sequencing (WGS) in understanding the complex evolution of the USA300 clone and the potential for future spreading of this clone to other regions. WGS technology is essential for monitoring the spread of MRSA and informing the development of effective preventive measures, particularly in healthcare settings.

Epidemiological studies at the international, national, regional, and local levels are required to monitor the spread of USA300 and to identify the factors contributing to its success. Such knowledge will be essential for the development of effective measures to prevent the further uncontrolled spread of this clone, particularly in healthcare institutions. Over the past 2 decades, sequencing technology has opened up new possibilities for the analysis of genomes of pathogenic bacteria. The expanding field of genomics has provided powerful tools and insight for studies of pathogen epidemiology. Whole-genome sequencing (WGS) provides the means to detect minor variations, down to the level of single-nucleotide variants. These techniques are, therefore, likely to prove more discriminatory than conventional epidemiological typing.

The article by Von Dach et al. in this issue of The Journal of Infectious Diseases reports the application of such genomic typing tools to the study of S. aureus USA300 and USA300-like strains. With the aim of investigating the reasons for the observed increase in the prevalence of CA-MRSA USA300 in the Geneva region, Switzerland, the authors used WGS techniques on all their MRSA isolates. They demonstrated an absence of local spread of the USA300 clone and of healthcare-associated transmission for this clone, identified several intrafamilial transmission events, and showed that the strains responsible for colonization and infections in the region concerned were evenly distributed between 2 very different...
subpopulations of USA300 strains that may have evolved independently: first, a genetically homogeneous ACME-positive subpopulation, containing strains highly similar to those observed in the United States, and, second, a more heterogeneous subpopulation of ACME-negative strains similar to those reported in South America. By contrast, conventional typing tools (ie, antibiotic susceptibility, pulsed-field gel electrophoresis, and spa- and SCCmec-typing) provided evidence for ongoing CA-MRSA USA300 spread in the region. These results confirm the particular complexity encountered in the epidemiological evolution of the USA300 clone and demonstrate the limitations of conventional typing tools and their inadequacy for microepidemiological studies of CA-MRSA USA300. Further investigations of this clone will clearly require the use of genomic tools.

Another important goal of research on the troublesome USA300 clone is to increase substantially our understanding of its pathogenicity and its evolutionary adaptation during the transition from colonizer to invasive pathogen. The genetic features associated with the occurrence of infections caused by this clone, benign SSTIs and life-threatening diseases, have yet to be determined. Outside of outbreak settings, little is known about the prevalence of carriage of S. aureus USA300 in the general population in many countries and the specific characteristics of the colonizing strains. The article by Von Dach et al suggests a greater capacity of strains from the USA300 Latin variant subpopulation to cause infections. However, the strains of this subpopulation could not be distinguished from the USA300 ACME-positive strains on the basis of the presence of virulence-associated genes and mobile genetic elements in the genome. Further studies, expanding on this WGS analysis, with strains recovered from diverse geographic areas and epidemiological settings (colonization, SSTIs, and invasive infections) should rapidly extend our knowledge of the pathogenicity of the different subpopulations of strains within the USA300 clone. Fascinating times lie ahead!

Note
Potential conflict of interest. Author certifies no potential conflicts of interest. The author has submitted the ICMJE Form for Disclosure of Potential Conflicts of Interest. Conflicts that the editors consider relevant to the content of the manuscript have been disclosed.

References