

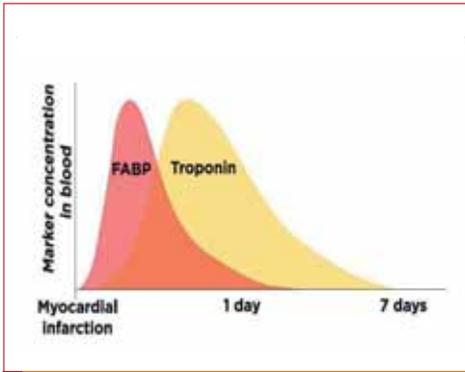
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by Siemens Healthineers

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Genomic tracking of MRSA outbreaks could help infection control

Bernard Leger
M.D.



Hospital-acquired infections (HAIs) today rank among the major causes of death and morbidity in hospitalized patients and are estimated to be responsible for 175,000 deaths per year in industrialized countries. HAIs have been growing exponentially worldwide since the 1980s primarily because of the indiscriminate use of antibiotics which have triggered the growth of multidrug resistant bacterial strains – also known as superbugs – and the transmission of such strains between patients, as well as between patients and hospital staff and vice versa. Methicillin-resistant *Staphylococcus aureus* (MRSA) is a superbug that is resistant to several widely used antibiotics. In the general community, MRSA mostly causes skin infection, is spread by skin-to-skin contact and, if left untreated, can also get deeper into the body, causing potentially life-threatening infections. It is generally estimated that about 3 percent of the population chronically carries MRSA. However, in a healthcare setting such as a hospital or nursing home, MRSA infection is more frequent and often more severe, leading to pneumonia, surgical site infections, bloodstream infections and possibly sepsis. The risk factors are indeed much higher in hospitals because of the increased vulnerability of some patients (the elderly and those with weakened immune systems) and because of the multiple potential pathways for MRSA entry into the body provided by wounds (including surgical wounds), burns as well as feeding tubes, intravenous lines or urinary catheters. MRSA is also prevalent in nursing homes where healthy carriers have the opportunity to spread it among the resident population and staff.

A very recent study, published in the October 25 edition of *Science Translational Medicine*, used genomic sequencing technology for the genomic surveillance of MRSA in the East of England. A team at the Wellcome Trust Sanger Institute sequenced the genetic code of every single MRSA-positive sample processed over a 12-month period by

a routine clinical microbiology lab receiving samples from three hospitals and 75 general practitioner practices. Samples from 1465 people were analysed, revealing a total of 173 transmission clusters involving 598 people and ranging from outbreaks affecting two patients up to 44.

These findings shed some new light on MRSA transmission within and between hospitals and the community and could pave the way for more targeted, efficient and effective infection control practices. While genomic surveillance of MRSA cannot by itself prevent an outbreak from occurring,

it can certainly help to reduce the numbers of infected people. The cost-effectiveness of implementing this strategy needs to be carefully evaluated. Although the whole genome of a bacterium can now be sequenced for around 140€, this might still prove too much for many healthcare systems.

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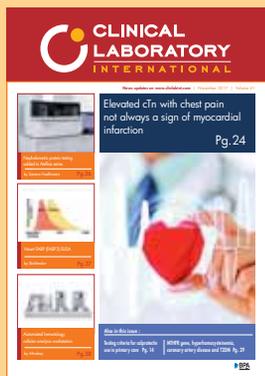
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