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MRSA outbreak mapped by DNA sequencing

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Scientists have used DNA sequencing for the first time to effectively track the spread of, and ultimately contain, an outbreak of methicillin-resistant Staphylococcus aureus (MRSA), according to new research published in *The Lancet Infectious Diseases*.

The technique allowed researchers to map and control an MRSA outbreak in a special care baby unit (SCBU) much more effectively than traditional infection control techniques alone would have allowed, leading to hopes that in future, the management of MRSA and other harmful bacterial infections could be vastly improved by the routine use of DNA sequencing technologies.

Researchers from the Wellcome Trust Sanger Institute, the University of Cambridge and Cambridge University Hospitals initially performed a type of DNA sequencing known as whole-genome sequencing on MRSA isolates taken from 12 babies known to have been carrying MRSA during a 6 month period in 2011.

When the MRSA infections first arose, an infection-control team working in the hospital suspected that the cases were linked, but this could not be proven using conventional methods to track and characterise outbreaks, nor was it clear how the infection was spreading and what its source might be. In an attempt to halt the spread of infection, the infection control team recommended standard measures of decolonisation treatment to eradicate MRSA from carriers and a deep clean of the ward where the infections had occurred.

When the scientists retrospectively performed DNA sequencing on these MRSA isolates, they were able to confirm that the MRSA strains were closely related, and that the MRSA cases observed were therefore part of an outbreak. Moreover, by widening their analysis to include samples from parents and visitors to GP's surgeries, they were able to determine that the outbreak had spread into the community, infecting twice as many people as previously suspected.

While this retrospective analysis was taking place, the hospital infection-control team identified a new case of MRSA carriage in the special care baby unit, more than 2 months after the last MRSA-positive patient had left the unit and the ward had been deep-cleaned. The researchers used rapid DNA sequencing to show that the new case of MRSA was related to the earlier outbreak, leading them to hypothesise that a member of staff in the hospital might be unwittingly carrying the MRSA strain identified months earlier, allowing the same strain to infect another patient months after the initial outbreak and infection control measures.

As a result of this, 154 health care workers were screened for MRSA, and one member of staff was found to be carrying the same strain of MRSA linked to the outbreaks. The worker was then treated to eradicate their MRSA carriage, and the outbreak was contained.

According to Professor Julian Parkhill, lead author from the Wellcome Trust Sanger Institute in Cambridge, UK, "Routine use of DNA sequencing could have detected this MRSA outbreak 6 months earlier than standard techniques, and might well have prevented substantial illness and costs arising from MRSA transmission and subsequent infection. Whole-genome sequencing of MRSA could make an important contribution to infection-control investigation and practice, allowing quicker identification, tracking and isolation of outbreaks than is currently possible."

This is the first study in which DNA sequencing has been used alongside conventional methods in real time, allowing scientists to directly compare the two and to understand how DNA sequencing might be effectively used alongside existing techniques in future.

"Before this technology can be used in routine clinical practice, we will require automated tools that interpret sequence data and provide information to healthcare workers and people without specialist sequencing knowledge" says Professor Sharon Peacock, lead author from the University of Cambridge, who adds that "we are currently working on such a system".

Writing in a linked Comment, Dr Binh Diep, from the University of California, San Francisco, USA, states that, "The advent of high-throughput whole-genome sequencing has the potential to revolutionise outbreak investigations by providing a substantial advance in our ability to discriminate between different strains, compared with traditional molecular methods."

More information: Simon R. Harris, Edward J.P. Cartwright, M. Estée Török, Matthew T.G. Holden, Nicholas M. Brown, Amanda L. Ogilvy-Stuart, Matthew J. Ellington, Michael A. Quail, Stephen D. Bentley, Julian Parkhill, Sharon J. Peacock (2012). 'Using whole genome sequencing to dissect the cause and effect of a meticillin-resistant Staphylococcus aureus outbreak: a descriptive study' http://www.thelancet.com/journals/laninf/article/PIIS1473-3099(12)70268-2/abstract

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