
Tracking MRSA Evolution and Transmission: Revolutionary Strategy for Control and Prevention of Infection

The ability to track strains in this way will enable researchers to understand how strains can spread so rapidly, and should lead to novel infection control strategies, not only for MRSA but also for other emerging superbugs.

The team used new very high-throughput DNA sequencing technologies to compare individual MRSA isolates from patients to precisely show their genetic relatedness. Very quickly they were able to spot single-letter changes in the genetic code and to identify differences between even the most closely related of MRSA isolates.

"We looked at two very different sets of samples," explains Dr Simon Harris, from the Wellcome Trust Sanger Institute and co-lead author on the study. "We have 42 samples taken from people across the globe, who became infected with MRSA between 1982 and 2003. The second set is from a single hospital in northeast Thailand, and consists of 20 samples from patients who developed MRSA infection within 7 months of each other, all possibly linked by a chain of person-to-person transmission".

"We wanted to test whether our method could successfully zoom in and out to allow us to track infection on a global scale -- from continent-to-continent, and also on the smallest scale -- from person-to-person."

The team sequenced the whole genomes of all the samples using a next-generation DNA sequencing technology. This technique reveals the minutiae of single-letter genetic changes in the hospital samples, and showed that no two infections were caused by entirely identical bacteria. Based on these subtle genetic differences, the researchers divided the Thai hospital samples into two groups. In the larger group of 13 bacteria they found five which were extremely similar and differed altogether by just 14 single-letter changes.

"This group of five related MRSA strains caused infections in patients who were resident in intensive care units in adjacent blocks of the hospital," explains Dr Ed Feil, from the Department of Biology and Biochemistry at the University of Bath and co-lead author on the study, "and all were isolated within a few weeks of each other. By contrast, bacteria from patients housed in other parts of the hospital were much less similar."

"This cemented our theory -- based on the sequence comparison -- that there were two different groups of isolates that had had been introduced to the hospital separately."

Importantly, the team was also able to determine the rate at which DNA sequence typically mutated, providing an unprecedented insight into the rate of evolution in vivo. The particular MRSA strain studied acquired about one single-letter change every six weeks.

To understand better the evolution and global spread of MRSA over several decades and large geographic distances, the team looked at samples from hospitals in North and South America, Europe, Australia and Asia collected over a period of more than twenty years by the CEM/NET Initiative, an international project in molecular epidemiology organized by Instituto de Tecnologia Qu

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