

Real-time genome sequencing helps control hospital outbreak

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Pioneering use of whole genome sequencing in real time to help control a hospital outbreak is reported in an article published in the open access journal *Genome Medicine*. The research corroborates the use of the technique as a rapid and cost-effective way of tracking and controlling the spread of drug-resistant hospital pathogens.

Acinetobacter baumannii is a multi-drug resistant pathogen found in hospitals across the globe and emerged as a significant threat to casualties in the Iraq and Afghanistan wars. It affects severely ill patients, particularly trauma and [burns patients](#), often leading to pneumonia and bloodstream infections. Healthcare-associated infections (HAIs) are estimated to cost the UK £1 billion a year and, at any given time, one in every 15 patients will have a HAI.

Whole [genome sequencing](#), which sequences an organism's entire DNA, is thought to be a promising new addition to the toolkit for controlling HAIs. Conventional methods are often applied retrospectively and yield limited information about a pathogen's DNA, making it difficult to compare whether patients are carrying the same bacteria and track transmission of outbreaks.

In this paper the researchers from the University of Birmingham, University of Warwick, and the National Institute for Health Research Surgical Reconstruction and Microbiology Research Centre, report how [whole genome sequencing](#) was used to control an [outbreak](#) of *A. baumannii* at Queen Elizabeth Hospital Birmingham in 2011. The

outbreak began following the admittance of a military patient from Afghanistan with blast injuries and lasted for 80 weeks - making it one of the longest outbreaks ever described for this pathogen. The patient was carrying a novel strain of the bacterium that had not previously been observed in the region's hospitals. After first using traditional methods to try and contain the pathogen, the researchers decided to switch to whole genome sequencing mid-way through the outbreak.

Sampling patients and the environment, the researchers were able to identify 74 patients belonging to the outbreak. They then determined the detailed genetic makeup of the bacteria carried by each of these patients and used this data, with information about the ward that the patients were housed in, and the date of their first positive tests, to identify nearly 70 possible transmission events. Armed with this detailed information, the researchers were able to pinpoint transmission hot spots within the [hospital](#), which included an operating theatre and a specialised bed for burns [patients](#).

Deep cleaning of these transmission sites followed and new decontamination protocols were put in place by the hospital. In May 2013 the outbreak was declared closed. Lead author of the study, Mark Pallen from the University of Warwick, said: "We have demonstrated how whole genome sequencing can be applied in a clinically helpful timeframe to track and control the spread of drug-resistant hospital [pathogens](#). In this case, it helped understand and control what was probably longest running *A. baumannii* outbreak ever seen in this country."

More information: Genomic Epidemiology of a Protracted Hospital Outbreak caused by Multi-Drug-Resistant *Acinetobacter baumannii* in Birmingham, England, Mihail R Halachev, Jacqueline Z-M Chan, Chrystala I Constantinidou, Nicola Cumley, Craig Bradley, Matthew Smith-Banks, Beryl Oppenheim and Mark J Pallen , *Genome Medicine*,

genomemedicine.com/content/6/11/70

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