

Whole genome sequencing found to rapidly enhance infection control

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Whole genome sequencing can quickly isolate the specific strain of bacteria causing an outbreak, identify the source of contamination, and enable rapid infection prevention to stop the spread of infection, according to a study published today. The findings, based on the examination of an outbreak of *Pseudomonas aeruginosa* in an Australian neonatal unit, appear in *Infection Control & Hospital Epidemiology*, the journal of the Society for Healthcare Epidemiology of America.

"Bacteria, such as *P. aeruginosa*, have evolved into many strains and frequently contaminate the healthcare environment, which makes it difficult to determine the source of an outbreak and control it using traditional methods," said Rebecca Davis, MD, the study's lead researcher. "Whole [genome sequencing](#), determining the organism's entire DNA sequence in real time, changes that. Our study found this technology allows us to implement rapid-response infection control protocols and stem the outbreak, which is critical for vulnerable patients, such as those in a neonatal intensive care unit."

Researchers at Royal Prince Alfred Hospital in Sydney investigated an outbreak of *P. aeruginosa* colonization in babies, as an increase was seen in the numbers of babies carrying this [bacteria](#) on their skin. Only one baby, however, had become ill with infection from the bacteria.

During the outbreak, researchers conducted enhanced screening practices for all babies by collecting nasal swabs. They also swabbed common areas that were possible [sources](#) of transmission, such as areas

in and around sinks, including splash-backs and soap dispensers. They found 18 infants were colonized with the bacteria, which in extreme cases can be fatal.

The investigators performed real-time DNA sequencing on specimens collected from twelve babies and seven environmental locations. They found that all babies except one were colonized by a specific strain of *P. aeruginosa*, ST253, and that two environmental samples obtained from different sinks also tested positive for the same strain. Upon this discovery, infection control personnel took active measures including isolating the babies infected with *P. aeruginosa* and cleaning and/or replacing equipment associated with the sink areas that tested positive. No further babies became ill with the bacteria.

"Whole genome sequencing gave us the ability to see that all but one of the babies were infected by the same strain of *P. aeruginosa*, something that would not have been recognized otherwise," said Davis. "When trying to stem infection, the ability to exclude a patient from the outbreak is just as important as the recognition of the [outbreak](#) itself. Additionally, the thorough information provided about factors of each strain, like antibiotic resistance mutations if present, and the quick processing time make it a superior tool in infection control."

More information: Rebecca Davis, Slade O. Jensen, Sebastian Van Hal, Bjorn Espedido, Adrienne Gordon, Rima Farhat, Raymond Chan. "Whole genome sequencing in real-time investigation and management of a *Pseudomonas aeruginosa* outbreak on a Neonatal Intensive Care Unit." *Infection Control & Hospital Epidemiology*. Web (June 8, 2015)

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