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# Hospital genomics initiative tackles dangerous superbug

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By **Pulse+IT**



Peter Doherty Institute for Infection and Immunity (Doherty Institute), Melbourne. Image supplied.

Australian researchers are using real-time genome sequencing in routine hospital care for patients with severe *Staphylococcus aureus* infections – otherwise known as ‘golden staph’, a superbug responsible for more than one million deaths globally each year.

In partnership with seven major Victorian hospitals, researchers from the Peter Doherty Institute for Infection and Immunity (Doherty Institute), have been the first to show that tracking bacterial changes using genome sequencing during serious infection can give clinicians immediate insights to personalise treatment and improve patient outcomes.

Golden staph can cause life-threatening infections such as sepsis, pneumonia, bone and joint infections and endocarditis. The bacteria is known for its ability to adapt quickly and build resistance to antibiotics.

Researchers said that unlike standard hospital laboratory tests – which only identify the type of bacteria – genome sequencing revealed a complete genetic profile, including traits that influence its response to treatment.

University of Melbourne Doherty Institute director of the Microbiological Diagnostic Unit Public Health Laboratory (MDU PHL) and senior author of the study Professor Benjamin Howden said the work had “significant implications” for the future of infectious disease management.

“These findings represent a major step toward targeted therapy for bacterial infections and open the door to future clinical trials that could make this approach standard practice in hospitals worldwide,” Prof Howden said.

MDU PHL was now exploring a new service to provide advanced genomic investigations for cases where treatment was failing.

Victorian hospitals would be the first to access the technology, in what the researchers said would be a world-first implementation of precision microbiology in clinical care.

Led by University of Melbourne’s Dr Stefano Giulieri, infectious diseases physician and clinician researcher at the Doherty Institute and lead author of the study published in [Nature Communications](#), the team collected golden staph samples from patients with severe, recurring infections at the time of treatment failure.

The strains were compared to strains obtained at the beginning of the infection, with the findings returned to the treating physicians.

Previously, studies on bacterial evolution during infection had only been conducted retrospectively – often years after treatment.

Dr Giulieri said while these previous studies had provided valuable insights to researchers, tracking evolution during infection could be “extremely beneficial” for clinicians.

Dr Giulieri said the study found that in one-third of cases, the bacteria had picked up dangerous mutations that made treatment more likely to fail.

“In one case, after initially controlling a golden staph infection, the patient returned to hospital two months after stopping antibiotics,” Dr Giulieri said.

“Samples were referred to us for sequencing and we discovered that, during infection, the golden staph bacteria had become 80 times more resistant to the antibiotic used. Each time they reappeared in blood, the bacteria had picked up a new dangerous mutation.

“Using this information, the clinical team was able to choose a new treatment that was able to finally cure the infection.

“Our study is the first to show that by tracking bacterial evolution in real-time, genome sequencing can reveal tricks bacteria use to survive, giving doctors the power to stay one step ahead and tailor treatment to the specific bacterial strain. This helps avoid unnecessary treatments, minimise side effects for patients and prevent further antibiotic resistance – ultimately giving patients the best chance of recovery.”

To assess the value of this approach, the researchers surveyed 25 infectious disease specialists across Australia, Switzerland, the UK and the US. Clinicians rated the genomic reports as “highly useful” (80 out of 100) and indicated that the information influenced their choice of antibiotic treatment in more than a third of cases.

University Hospital Geelong infectious diseases consultant and survey participant Professor Eugene Athan said the approach offered the opportunity for infectious diseases to “enter the era of precision medicine, just as cancer genomics has done in oncology.”

“The ability to track bacterial evolution in real-time during severe infections is a game-changer for clinicians,” Prof Athan said.

Benjamin Howden

Doherty Institute

Dr Stefano Giulieri

Eugene Athan

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