Scientists to sequence DNA of cystic fibrosis superbug

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Scientists at the University of Liverpool are using the latest DNA sequencing technology to understand the diversity of a bacterium that causes severe lung infection in cystic fibrosis patients.

The bacterium, called Pseudomonas *aeruginosa*, is the most common cause of persistent and fatal lung infections in cystic fibrosis patients. Scientists at Liverpool identified a particularly virulent strain of the bacteria that is transmissible between patients. The Liverpool Epidemic Strain (LES), referred to as a cystic fibrosis 'superbug', can cause aggressive infection and results in progressive lung decline.

The team from the University's Institute of Infection and Global Health took samples from patient sputum and cough swabs to understand why the infection is so aggressive in people with cystic fibrosis. They found that during chronic infections the bacteria has the ability to mutate rapidly, resulting in huge diversity. Tests also show that the bacteria produce a molecule that could be the trigger for episodes of acute infection in patients.

Dr Craig Winstanley, member of the National Institute of Health Research (NIHR) Biomedical Research Centre (BRC) at Liverpool, explains: "Patients with LES need to be separated from others in hospitals, so that infection does not spread between cystic fibrosis patients on wards. Once established, these chronic infections can never be cleared. We found that the bacteria have the ability to diversify into hundreds of distinct sub-types, making it very difficult to decide which

antibiotic to use for a successful outcome.

"Using the latest DNA technology we have the unique opportunity to study the behaviour of bacteria during chronic infection in real time. This will allow us to get a clearer picture of how it adapts so efficiently to cystic fibrosis patients. If we can understand how and why it behaves the way that it does we may be able to target more effective treatments for the infection."

Working with scientists at the University's Centre for Genomic Research, the team will use new DNA sequencing technology to read the genetic code of the infection. The first of its kind in the UK, the machine works 250,000 times faster than technology used to sequence the human genome 10 years ago.

Dr Steve Paterson, from the University's Institute of Integrative Biology, said: "Each cystic fibrosis patient can be infected with a diverse population of bacteria and it is therefore essential to test samples of the disease from a number of patients in order to understand how it evolves. The technology we are using can read 30 billion letters of DNA sequence per day, compared to four billion using current machines. It will allow us to investigate the mutations of the infection in precise detail, giving us valuable information about the progress of this serious medical condition."

Provided by University of Liverpool