

New method helps researchers piece together the puzzle of antibiotic resistance

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Associate Professor Lachlan Coin, Devika Ganesamoorthy, Dr Minh Duc Cao.
Credit: University of Queensland

Researchers from The University of Queensland's Institute for Molecular Bioscience (IMB) have developed a faster and more accurate method for assembling genomes which could help clinicians rapidly identify antibiotic-resistant infections.

IMB Centre for Superbug Solutions Deputy Director Associate Professor Lachlan Coin said arming clinicians with this information could help them prescribe the most effective antibiotic for their patient.

"Antibiotic resistance is a global challenge that threatens our ability to treat common infections," he said.

"Sequencing a bacterial [genome](#) using standard techniques resulted in a genome splitting into hundreds of fragments which was impossible to piece together.

"In particular, pathogenicity islands—which are crucial to identifying antibiotic resistance—usually split across multiple pieces.

"For the past two years, we have used cutting-edge Oxford Nanopore Technologies sequencing devices to sequence bacterial genomes and understand how antibiotic resistance develops.

"Because this technology is so new, we needed to develop a powerful method that could help us make the most of its results and really understand the genetic drivers of antibiotic resistance," Associate Professor Coin said.

IMB Postdoctoral Researcher Dr Minh Duc Cao said the team developed a new method for analysis of sequencing data on the fly, which allowed them to quickly and accurately piece together complete genomes.

"With our method, we can reconstruct an entire bacterial genome shortly after you switch on the machine and put in the DNA sample.

"The speed is key as we're interested in predicting [antibiotic resistance](#) in real time on clinical samples, because when it comes to diagnosing and treating infections, every minute counts," he said.

Associate Professor Coin said the method could be applied to help unravel the genomic causes of other diseases.

"We would like to work towards finding new ways to apply this approach to help unravel other diseases, particularly cancer.

"Cancer genomes are about 1000 times larger than bacterial genomes, so the powerful combination of this leading technology and our improved [method](#) holds enormous potential for rapid assembly of personalised tumour genomes," Associate Professor Coin said.

The research was published in *Nature Communications* and was funded by The University of Queensland, National Health and Medical Research Council and the Australian Research Council.

The University of Queensland's Institute for Molecular Bioscience Centre for Superbug Solutions will host the Solutions for Drug-Resistant Infections conference in Brisbane from 3-5 April 2017.

The conference will bring international experts and advocates in the field to network and discuss new ways to solve the global challenge of drug-resistant infections.

More information: Minh Duc Cao et al. Scaffolding and completing genome assemblies in real-time with nanopore sequencing, *Nature Communications* (2017). [DOI: 10.1038/ncomms14515](https://doi.org/10.1038/ncomms14515)

Provided by University of Queensland

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