MedicalXpress

Tracking MRSA in real time: Study highlights benefits of rapid whole-genome sequencing

June 13 2012

In a new study released today in *New England Journal of Medicine*, researchers demonstrate that whole genome sequencing can provide clinically relevant data on bacterial transmission within a timescale that can influence infection control and patient management.

Scientists from the Wellcome Trust Sanger Institute, University of Cambridge, and Illumina collaborated to use whole genome sequencing to identify which isolates of methicillin-resistant Staphylococcus aureus (MRSA) were part of a hospital outbreak.

Current laboratory techniques often cannot distinguish between MRSA isolates. This study indicates that whole genome sequencing can provide precise information in a fast turnaround time, and could make a clear distinction between MRSA isolates in a way that was not previously possible.

MRSA infection is a major public health problem. For example, in the United States, an estimated 89,785 invasive MRSA infections associated with 15,249 deaths occurred in 2008. Even when the disease is treated, MRSA infections double the average length of hospital stay and increase healthcare costs. Fast and accurate detection of bacterial transmission is crucial to better control of healthcare-associated infection.

"An important limitation of current infection control methodology is that

the available bacterial typing methods cannot distinguish between different strains of MRSA," explains Professor Sharon Peacock, lead author from the University of Cambridge and clinical specialist at the Health Protection Agency. "The purpose of our study was to see if whole genome sequencing of MRSA could be used to distinguish between related strains at a genome level, and if this would inform and guide outbreak investigations."

The team focused on an outbreak in a neonatal intensive care unit that had already ended. They took the samples and sequenced them as if they had been working in real time. They found they could distinguish between strains that were part of the outbreak and strains that were not, and showed that they could have identified the outbreak earlier than current clinical testing, potentially shortening the outbreak.

"This study demonstrates how advances in whole genome sequencing can provide essential information to help combat hospital outbreaks in clinically relevant turnaround times," says Dr Geoffrey Smith, co-lead author and Senior Director of Research at Illumina. "As sequencing has become increasingly accurate and comprehensive, it can be used to answer a wide range of questions. Not only could we distinguish different MRSA strains in the hospital, we were also able to rapidly characterise antibiotic resistance and toxin genes present in the clinical isolates."

The team constructed a list of all the MRSA genes that cause antibiotic resistance. Rapidly identifying drug resistance in MRSA strains will guide healthcare professionals to give each infected patient the most appropriate treatment possible. This also provides a powerful tool for the discovery of new drug resistance mechanisms.

MRSA produces numerous unique toxins that can inflict severe clinical syndromes, including septic shock, pneumonia, and complicated skin

and soft tissue infections. The team created a list of toxin genes to rapidly identify those present in the MRSA strains, which currently can only be identified with multiple assays in reference laboratories.

"Distinguishing between strains is important for infection control management," says Dr Julian Parkhill, lead author from the Wellcome Trust Sanger Institute. "Quick action is essential to control a suspected outbreak, but it is of equal importance to identify unrelated strains to prevent unnecessary ward closures and other disruptive control measures. Healthcare needs better, more efficient ways of identifying an outbreak and then processing the data."

"Current clinical methods to make links between related strains compare the pattern of bacterial susceptibility to a profile of antibiotics. We found this method to be inaccurate. We showed that two MRSA strains, which seemed by current methods to be identical, were genetically very different."

The use of whole genome sequencing will ultimately become part of routine health care. This study indicates that whole genome sequencing in real time will be valuable in controlling MRSA and other outbreaks in a hospital setting.

"The next stage is to develop interactive tools that provide automated interpretation of genome sequence and provide clinically meaningful information to healthcare workers, a necessary advance before this can be rolled out into clinical practice," adds Professor Peacock.

More information: Köser CU, Holden MTG, Ellington MJ, Cartwright EJP et al. (2012) A neonatal MRSA outbreak investigation using rapid whole genome sequencing. *New England Journal of Medicine*, doi: 10.1056/NEJMoa1109910

Medical Xpress

Provided by Wellcome Trust Sanger Institute

Citation: Tracking MRSA in real time: Study highlights benefits of rapid whole-genome sequencing (2012, June 13) retrieved 27 April 2024 from https://medicalxpress.com/news/2012-06-tracking-mrsa-real-highlights-benefits.html

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.