

New technique identifies pathogens in patient samples faster, in great detail

December 2 2013

A team of Danish investigators has shown how to identify pathogens faster, directly from clinical samples. The research, published online ahead of print in the *Journal of Clinical Microbiology* appears in the journal's January 2014 issue.

The investigators used a technique known as whole genome sequencing to identify and completely characterize bacteria causing [urinary tract infections](#). In just 18 hours, they identified the culprit microorganisms, characterized the pathogens' patterns of antibiotic susceptibility, and identified specific strains.

"Using conventional methodologies this would have taken several days to weeks, and even using [whole genome sequencing](#) on cultured bacteria would have taken an extra day," says Frank M. Aarestrup of the Technical University of Denmark, Lyngby, an author on the study.

Their work will help [patients](#) heal more quickly and avoid unnecessarily prolonged illness and even death. It will also help prevent outbreaks of hospital-acquired disease, and identify emerging infections.

"Rapid identification of the causative agent, and of any [antibiotic resistance](#) is crucial to choosing the correct treatment for individual patients," says Aarestrup. "Choosing the wrong antibiotic will lead to longer infections and in the worst case, deaths."

The investigators also identified bacteria in the patient samples that they

did not detect using conventional techniques. "*Lactobacillus iners*, *Gardnerella vaginalis*, *Prevotella*, and *A. urinae* have all been implicated in [urinary tract infections], even though their precise roles as pathogens and normal colonizers of the genital tract have not been firmly established," write the researchers. They note that by conventional methods *A. urinae* is rarely identified but frequently misclassified.

The ability to identify strains in patients with repeated infections enables the doctor to know whether the patient's infection is new, or recurrent. And the typing of bacterial strains enables rapid comparison of bacteria from different patients, so that doctors can detect the spread of infections within the hospital, and identify emerging infections.

"Whole [genome sequencing](#) may still be too expensive for routine use in most clinical microbial laboratories," the researchers write. But they predict that rapidly falling prices and automation will render it a standard technology for infection detection and control, in and out of the hospital.

More information: www.asm.org/images/Communicati.../1113wholegenome.pdf

Provided by American Society for Microbiology

Citation: New technique identifies pathogens in patient samples faster, in great detail (2013, December 2) retrieved 11 May 2024 from <https://medicalxpress.com/news/2013-12-technique-pathogens-patient-samples-faster.html>

<p>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.</p>
--