Website address:
https://www.gesundheitsindustrie-bw.de/en/article/press-release/personalisierte-antibiotika-behandlungsstrategie-bei-tuberkulose-erkrankten

Personalised antibiotic treatment strategies for tuberculosis patients

Tuberculosis is one of the leading causes of death worldwide, with an estimated 1.4 million deaths and ten million people infected annually. Resistant and multidrug-resistant (MDR) variants of the tuberculosis pathogen Mycobacterium tuberculosis pose a major threat to tuberculosis control and global health. The genomes of M. tuberculosis bacteria isolated from MDR tuberculosis patients have been found to harbour antibiotic resistance-associated mutations in various combinations. Rapid detection of these patient-specific resistance patterns is therefore crucial for targeted treatment as well as successful containment of transmission of antibiotic-resistant tuberculosis bacteria. An international study published in the journal Lancet Microbe has now brought researchers a big step closer to this goal.

In the multicentre observational study, DZIF scientists from the Research Center Borstel and University Hospital Heidelberg sequenced the genomes of a large number of clinical *M. tuberculosis* isolates from around the world. The researchers found that certain changes (mutations) in the bacterial genome correlated closely with the efficacy of antibiotics in the respective tuberculosis patients. Identification of certain mutations in the bacterial genome therefore potentially allows prediction of which antibiotics are still effective in a patient, or whether the dose should be increased. With this knowledge, the success of initial antibiotic therapy can be increased and further transmission of the pathogen can be prevented.

"This large-scale study is the result of close collaboration between DZIF scientists in Borstel and Heidelberg, the global diagnostics alliance FIND, and partners in five countries where tuberculosis is highly endemic. The sequence analysis enables us to better understand the genetic basis for resistance to anti-tuberculosis drugs and therefore to provide faster, personalised anti-tuberculosis treatment," summarises Dr Claudia Denkinger, last author of the publication.

"In the comparative genome analysis, we also observed, for example, changes in the genetic makeup of the bacteria that do not always lead to unambiguous results in classical bacterial culture-based resistance testing, but may potentially influence therapy," says Dr Matthias Merker, one of the study's first authors and Schleswig-Holstein Excellence-Chair junior research group leader at the Research Center Borstel.

"Our study also shows that genetic analysis of the bacteria already enables precise prediction of resistance to important tuberculosis antibiotics and can replace many of the classical and often lengthy tests," adds Prof. Stefan Niemann of the National Reference Center for Mycobacteria at Borstel, one of the study's final authors. "In the future, we plan to further expand this bacterial genomic analysis technique specifically in tuberculosis focal points in southern Africa, Eastern Europe and Central Asia."

The work was supported by the Bill & Melinda Gates Foundation, the German Center for Infection Research (DZIF) and the Schleswig-Holstein Cluster of Excellence "Precision Medicine for Chronic Inflammatory Diseases."

Publication

Finci I, Albertini A, Merker M, et al. Investigating resistance in clinical Mycobacterium tuberculosis complex isolates with genomic and phenotypic antimicrobial susceptibility testing: a multicentre observational study [published online ahead of print, 2022 Jul 27]. *Lancet Microbe*. 2022;S2666-5247(22)00116-1. doi: 10.1016/S2666-5247(22)00116-1

Press release

01-Sept-2022
Source: Deutsches Zentrum für Infektionsforschung e.V. and Heidelberg University Hospital

Further information

- Heidelberg University Hospital
- German Center for Infection Research