

Researchers report breakthrough in tuberculosis research

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Scientists from the PATHOGEN-TRACE project in Germany and France together with colleagues from the Oxford Biomedical Research Centre and the South African National Institute for Communicable Diseases developed a new genetic method, paving the way for a more effective treatment of tuberculosis (TB). The new method enables researchers not only to predict which antibiotics result in resistance but, it allows for a precise selection of compounds which are most effective in the treatment of TB.

Until now, detection of TB pathogens and the precise determination of antibiotic resistance were only possible using culture procedures, requiring up to six weeks until a first result is available. A long period, taking into account that TB is the most frequent deadly contagious disease worldwide. A further disadvantage of the conventional procedures using cultures is their proneness to error. They require ideal lab conditions in order to obtain reliable and comparable results, which are rarely known in most of the regions particularly hit by TB. Even the molecular-diagnostic quick tests used over the last 20 years could only provide information on a limited number of mutations and the resistances which result from them.

'We wanted to go one step further and give therapeutic pointers on which combinations of antibiotics are suitable for treating a certain pathogen,' summarizes Professor Stefan Niemann, Head of the Molecular Mycobacteriology research group at the Research Center Borstel and coordinator of the EU funded collaborative project,

PATHONGEN-TRACE, to describe the research approach. 'We are moving from 130 years of TB cultivation towards a new, digital era in microbiology.'

For its latest breakthrough the team successfully sequenced the whole genomes of approx. 3 500 TB strains. The researchers focused on changes to the genome which can be associated to [antibiotic resistance](#) and sensitivity. 'We have established a kind of dictionary for mutations in the genomes of TB pathogens,' explains Stefan Niemann, the coordinator of PATHONGEN-TRACE. 'If changes to the genetic code are found in a patient isolate, certain medications are no longer effective and should therefore not be used for treatment. This is an enormous advance in progress, particularly in terms of treating multi-resistant pathogens!'

It will take some time until the method can be applied by physicians and in daily routine. Nevertheless, Dr Thomas Kohl, co-author of the publication, is convinced that the method has great potential: 'In the long term, genome analysis is significantly easier and cheaper to carry out than developing cultures. Above all, with regard to the WHO EndTB strategy, which plans to successfully end tuberculosis by 2035, these new diagnostic approaches are very important.'

Tuberculosis (TB) is the most frequent deadly contagious disease in the world. Experts assume that around one third of the world's population is infected with the TB pathogen. Even if tuberculosis never breaks out among the majority of those infected, each year 9 million people contract TB and for about 1.5 million it has fatal consequences. Against this backdrop, increasing antibiotic resistances of the pathogens represent a particular challenge, considerably prolonging the treatment of patients and thereby increasing costs for society.

More information: "Whole-genome sequencing for prediction of

Mycobacterium tuberculosis drug susceptibility and resistance: a retrospective cohort study." *The Lancet Infectious Diseases*, [dx.doi.org/10.1016/S1473-3099\(15\)00062-6](https://doi.org/10.1016/S1473-3099(15)00062-6)

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