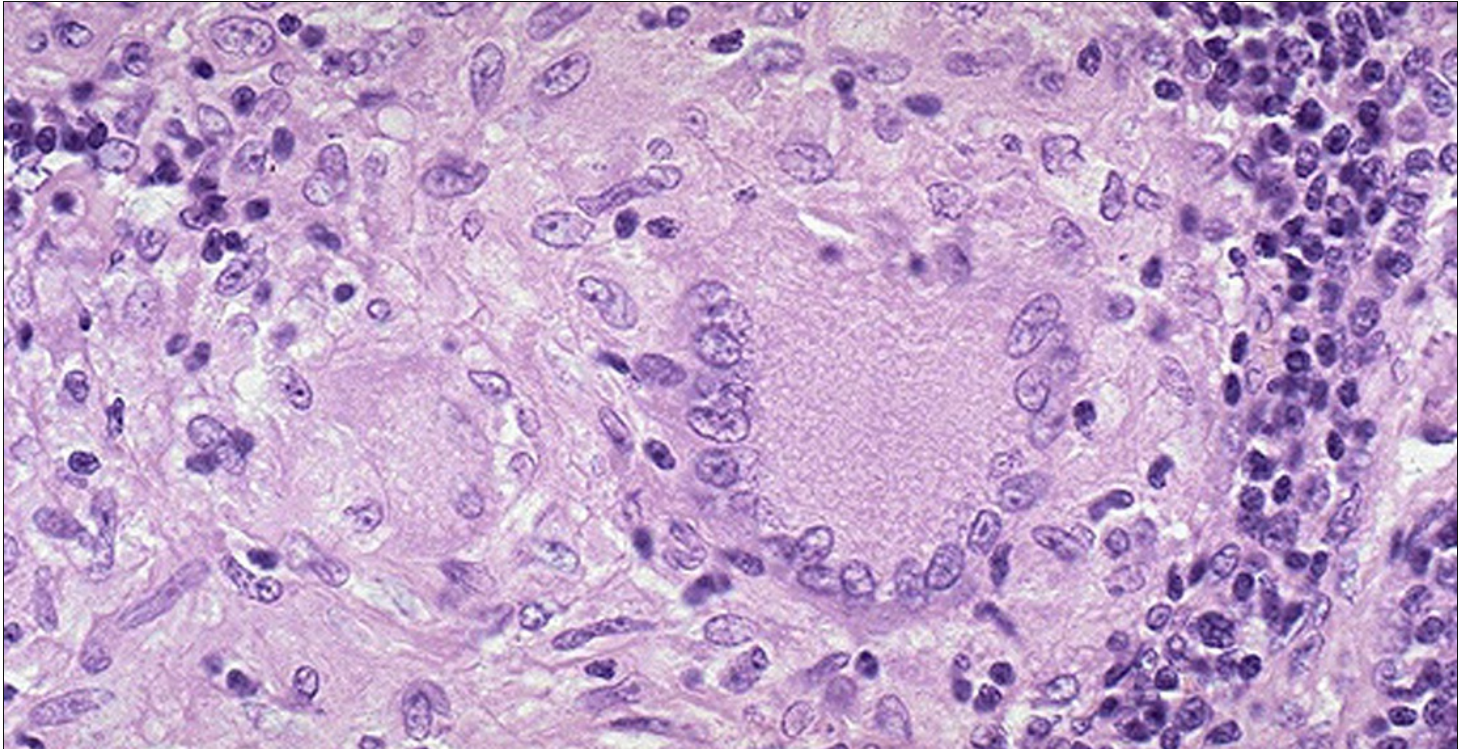


## DNA is de sleutel in de strijd tegen tuberculose

Onderzoekers stippelen richtlijnen uit voor volledige genomsequencing als enige methode voor de diagnose, de behandeling en de detectie van tuberculose.

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Dit is de omschrijving



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Er worden momenteel verschillende methoden gebruikt voor de detectie, de behandeling en het opsporen van tuberculose (tb). Sequentiebepaling van het hele genoom (WGS) zou al deze technieken kunnen vervangen. Een groep onderzoekers onder leiding van dr. Conor Meehan van het Instituut voor Tropische Geneeskunde (ITG) beschrijft in *Nature Reviews Microbiology* de voor- en nadelen van steeds vaker gebruikte moderne genomsequencingstechnologie. De

**onderzoekers formuleren een reeks aanbevelingen over standaardisatie en internationale normen voor goede WGS-praktijken in klinische zorg en volksgezondheid.**

The diagnosis, treatment and tracking of *Mycobacterium tuberculosis*, the bacterium that causes TB, is currently done through various techniques. With the arrival of cheap and reliable WGS, these different techniques could be replaced by one, single method. However, there is a risk that with no clear consensus and lack of international standards, the widespread use of WGS technology can lead to data and processes without harmonisation, comparability and validation.

"We call for extensive standardisation and validation efforts to be made, before implementing the WGS approach on a large scale," said Dr. Conor Meehan. "That will require political commitment and also the involvement of supranational laboratories and regulatory authorities. It is important to guarantee access to standardised and validated WGS techniques, especially in countries with a high burden of TB and where WGS will have the greatest impact."

Dr. Conor Meehan of ITM together with Dr. Inaki Comas from Biomedicine Institute of Valencia and Prof. dr. Annelies Van Rie from the University of Antwerp set up a consortium of more than 40 international scientists with TB expertise. Working together, they described the state-of-the-art of WGS in *Mycobacterium tuberculosis* and formulated a set of recommendations. These recommendations are of particular relevance in light of international developments.

"Currently, WGS techniques are mainly used in research activities, but the method is rapidly expanding into clinical care and public health tools to map the spread of tuberculosis. A streamlined method and standardised reporting are becoming more important by the day," said Meehan.

WGS is already recommended by the World Health Organization as a standard technique for global drug resistance surveys and is also increasingly being used as a method to provide personalised treatment. More and more countries are implementing WGS techniques.

Tuberculosis is a bacterial infection that kills around 1.6 million people each year, making it one of the top ten causes of death worldwide. ITM's research on tuberculosis is world-renowned. The Institute has the largest public collection of TB strains for research. It caused a breakthrough with a shorter combination treatment for resistant tuberculosis and researches new diagnostics and case detection techniques.

## Link

- [Whole genome sequencing of \*Mycobacterium tuberculosis\*: current standards and open issues](#) (Nature Reviews Microbiology)