

Researchers develop methods to understand how tuberculosis bacterium consumes its favourite foods

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Scanning electron micrograph of *Mycobacterium tuberculosis* bacteria, which cause TB. Credit: NIAID

Mycobacterium tuberculosis is incredible in that it can survive for decades within its human host. It does this by varying its diet to successfully steal nutrients from the human host including immune cells; it is known to acquire and absorb multiple carbon sources from the body during infection.

In a paper published in the journal *Molecular Systems Biology*, Surrey scientists detail how they measure the flow of metabolites or 'fluxes' through [metabolic pathways](#) when *Mycobacterium tuberculosis* is consuming some of its favorite nutrients. Measuring these fluxes could help scientists advance new tuberculosis drugs as well as understand why the bacterium survives so long in humans and why current antibiotics are often ineffective.

By growing *Mycobacterium tuberculosis* in specialized bioreactors that allow the [environmental conditions](#) and [growth rates](#) to be tightly controlled, and then analyzing the resulting data with bespoke, cutting-edge computing, Surrey scientists were able to determine the speed of the chemical processes that the bacterium uses to turn the host's nutrients into new bacteria. By measuring these metabolic fluxes, scientists can identify which reactions are critical for the bacteria's growth and thus direct the design of new tuberculosis drugs to effectively kill the bacterium.

The work is a collaboration between Surrey scientists Dr. Khushboo Borah, Dr. Tom Mendum, Professor Johnjoe McFadden and Dr. Dany Beste.

Dr. Dany Beste, the lead author of the study and Senior Lecturer in Microbial Metabolism at the University of Surrey, said: "The decline of tuberculosis deaths in recent years is positive news. However, the current

Covid-19 pandemic is estimated to set back TB control decades and therefore we urgently need novel treatments. Our basic science study advances our understanding of the metabolism of this pathogen which can ultimately be capitalized in developing more effective tuberculosis drugs and accelerate progress towards eliminating this infection globally."

More information: Khushboo Borah et al, Metabolic fluxes for nutritional flexibility of *Mycobacterium tuberculosis*, *Molecular Systems Biology* (2021). [DOI: 10.15252/msb.202110280](https://doi.org/10.15252/msb.202110280)

Provided by University of Surrey

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