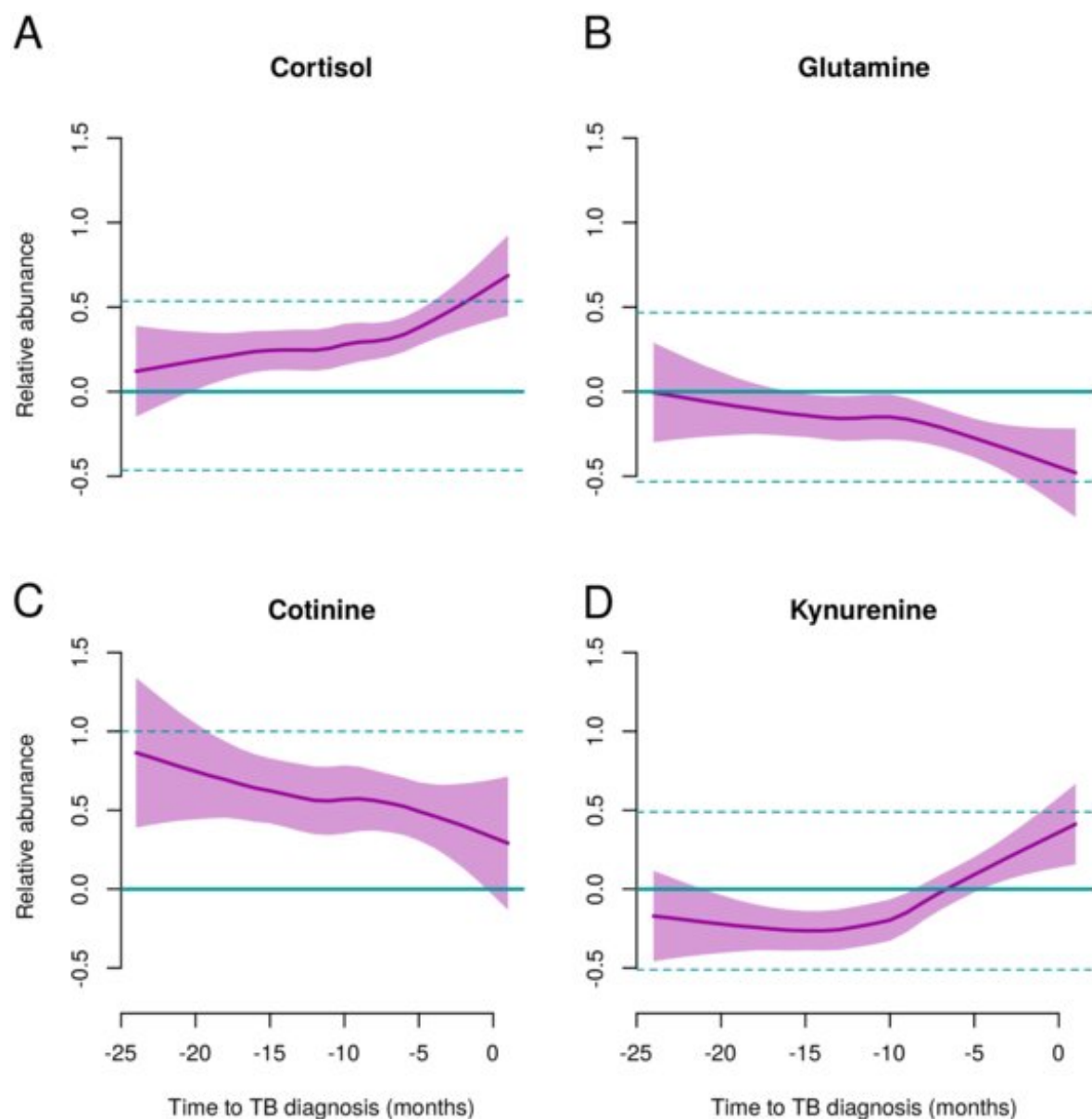


By analyzing the chemicals in the blood, scientists can find out who develops active tuberculosis

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/home/january/Projects/GC6-2013/metabolon/manuscript_25_naturecomm, press_release_figure_Weiner_EN.pdf, 2018-12-03 1

Changes in abundance of four selected metabolites: The steroid hormone cortisol, the amino acid glutamine, the metabolite cotinine and the signaling molecule kynurenine (X-axis: Months to the time point of the diagnosis of tuberculosis; green lines: Average levels and range in the healthy individuals). Three of the four metabolites show a significant change over time allowing prognosis of tuberculosis. The remaining risk factor shows a difference even at the beginning of the study. Credit: Weiner et al., 2018

Although a quarter of the world population is infected with the pathogen that causes tuberculosis, only about ten percent develop the disease during their lifetime. An international team of scientists, including some from the Max Planck Institute for Infection Biology in Berlin showed that the amounts of certain chemical compounds which circulate in the blood, change prior to the onset of the disease even months before a clinical diagnosis can be made. In the future, this may allow to predict tuberculosis based on a blood screening – a highly valuable progress in the fight against this life threatening disease.

Tuberculosis remains a major threat to humankind: each year, over 1.5 millions die of this [disease](#), making the responsible microbe – *Mycobacterium tuberculosis* – the deadliest one on Earth. Even though some [risk factors](#) are known – such as smoking – it is largely unclear who will develop the disease.

To fight tuberculosis successfully, an [early diagnosis](#) is extremely important. Earlier work of scientists from Max Planck Institute for Infection Biology revealed that tuberculosis patients can be identified based on a number of chemical compounds in blood. Their analysis showed that a number of amino acids have lower concentrations in the blood of tuberculosis patients than of the healthy individuals, while some

important signaling molecules – such as kynurenin or cortisol – are present at higher concentrations.

Disease prediction from blood samples

This study was performed by a consortium supported by the Grand Challenges program of the Bill and Melinda Gates Foundation. The team tested whether these and other molecules could be helpful to predict progression to tuberculosis in apparently healthy individuals. To this end, they recruited some 4,500 individuals from four African countries and followed them up for several years. During the study, around 100 individuals were diagnosed with active tuberculosis. Then, hundreds of chemical compounds were analyzed in [blood](#) samples taken from the recruited individuals. "We were able to predict who will develop tuberculosis in future. Furthermore, we were identified risk factors, such as molecules characteristic for smokers, who are at a higher risk for developing the disease" – so January Weiner from Max Planck Institute for Infection Biology.

The scientists validated their findings using independent data sets and thereby showed that the chemical compounds characteristic for progressors – those, who will develop tuberculosis at a later time point – are largely similar to the chemical compounds which allow distinguishing tuberculosis patients from healthy individuals. Moreover, the findings are specific to tuberculosis and the profiles of patients suffering from other respiratory diseases were different.

In future, these results may be the starting point for a rapid and inexpensive prognostic test. According to Stefan H.E. Kaufmann, director at the Max Planck Institute for Infection Biology in Berlin, "this type of screening can be used at a very [early stage](#) in suspected tuberculosis cases and will allow preventive therapy prior to disease onset. This would be an important step forward in fight against

tuberculosis."

More information: undefined undefined et al. Metabolite changes in blood predict the onset of tuberculosis, *Nature Communications* (2018). DOI: [10.1038/s41467-018-07635-7](https://doi.org/10.1038/s41467-018-07635-7)

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