UNIVERSITÉ
DE GENÈVE

PRESS RELEASE

Geneva | 25 August 2025

Gut bacteria can reveal colorectal cancer

UNIGE scientists developed an artificial intelligence-based approach to diagnose colorectal cancer from the gut microbiota.

High resolution pictures

Colorectal cancer is the second leading cause of cancer death worldwide. If detected early, it can be efficiently treated, but the cost and discomfort of colonoscopies - the main diagnostic method currently in use - often result in delayed diagnosis. Using machine learning algorithms, a team from the University of Geneva (UNIGE) identified for the first time all human gut bacteria to a level of detail that makes it possible to understand the physiological importance of the different microbial subgroups. This inventory was then used to detect the presence of colorectal cancer according to the bacteria present in simple stool samples, a non-invasive and low-cost screening tool. The potential applications are vast, ranging from the diagnosis of other cancers to a better understanding of the links between gut microbiota and health. These findings are published in *Cell Host & Microbe*.

Colorectal cancer is often diagnosed at an advanced stage when treatment options are limited. This underscores the need for simpler, less invasive diagnostic tools, particularly in the face of a still unexplained rise in cases among young adults. While it has long been known that gut microbiota plays a role in the development of colorectal cancer, translating these findings into clinical practice has proven challenging. This is because different strains of the same bacterial species can have opposite effects, with some promoting the disease and others having no effect.

“Instead of relying on the analysis of the various species composing the microbiota, which does not capture all meaningful differences, or of bacterial strains, which vary greatly from one individual to another, we focused on an intermediate level of the microbiota, the subspecies,” explains Mirko Trajkovski, full professor in the Department of Cell Physiology and Metabolism and in the Diabetes Centre at the UNIGE Faculty of Medicine, who led this research. “The subspecies resolution is specific and can capture the differences in how bacteria function and contribute to diseases including cancer, while remaining general enough to detect these changes among different groups of individuals, populations, or countries.”

With the help of machine learning

The first step was to analyse huge amounts of data. “As a bioinformatician, the challenge was to come up with an innovative approach for mass data analysis,” recalls Matija Trickovic, PhD student in the laboratory of Mirko Trajkovski and first author of this study. “We successfully developed the first comprehensive catalogue of human gut microbiota subspecies, together with a precise and efficient method to use it both for research and in the clinic.”

By combining this catalogue with existing clinical data, the scientists developed a model that can predict the presence of colorectal cancer solely based on the bacteria present in stool samples. “Although we were confident in our strategy, the results were striking,” enthuses Matija Trickovic. “Our method detected 90% of cancer cases, a result very close to the 94% detection rate achieved by colonoscopies and better than all current non-invasive detection methods.”

By integrating more clinical data, this model could become even more precise and match the accuracy of colonoscopy. It could become a routine screening tool and facilitate the early detection of colorectal cancer, which would then be confirmed by colonoscopy but only in a selected group of patients.

A new world of applications

A first clinical trial is being set up in collaboration with the Geneva University Hospitals (HUG) to determine more precisely the cancer stages and the lesions that can be detected. However, the applications go beyond colorectal cancer. By studying the differences between subspecies from the same bacterial species, researchers can now identify the mechanisms of action by which the gut microbiota influences human health. “The same method could soon be used to develop non-invasive diagnostic tools for a wide range of diseases, all based on a single microbiota analysis,” concludes Mirko Trajkovski.

contact

Mirko Trajkovski
Full Professor
Department of Cell Physiology and Metabolism
Faculty Diabetes Centre
Faculty of medicine
UNIGE
+41 22 379 52 56
Mirko.Trajkovski@unige.ch

Matija Trickovic
PhD Student
Department of Cell Physiology and Metabolism
Faculty of medicine
UNIGE
+41 22 379 01 55
Matija.Trickovic@unige.ch

DOI: 10.1016/j.chom.2025.07.015

UNIVERSITÉ DE GENÈVE
Communication Department
24 rue du Général-Dufour
CH-1211 Geneva 4

Tel. +41 22 379 77 17

media@unige.ch
www.unige.ch