

## New method for measuring gut microbiota

Gut microbiota have an effect on human health, but how they work is not known well enough. The behaviour of microbiota at protein level is studied at the University of Turku by means of metaproteomics.



Previous studies have mainly focused on discovering the composition of microbiota, while there is still very little information about the behaviour of gut microbiota at protein level. Proteins perform most cell operations, and studying them in more detail may help us understand the interaction between cells and their environment. Metaproteomics is a good method for studying human gut microbiota, because it can identify and categorise the proteins involved.

“Previously only the composition of gut microbiota has been profiled. However, it tells us nothing about what is really going on in the gut. There may be dead bacterial mass involved, or the bacteria are not otherwise active. In order to discover how they

function, we need metaproteomics. This has only recently become technically possible to measure,” says researcher **Tomi Suomi**.

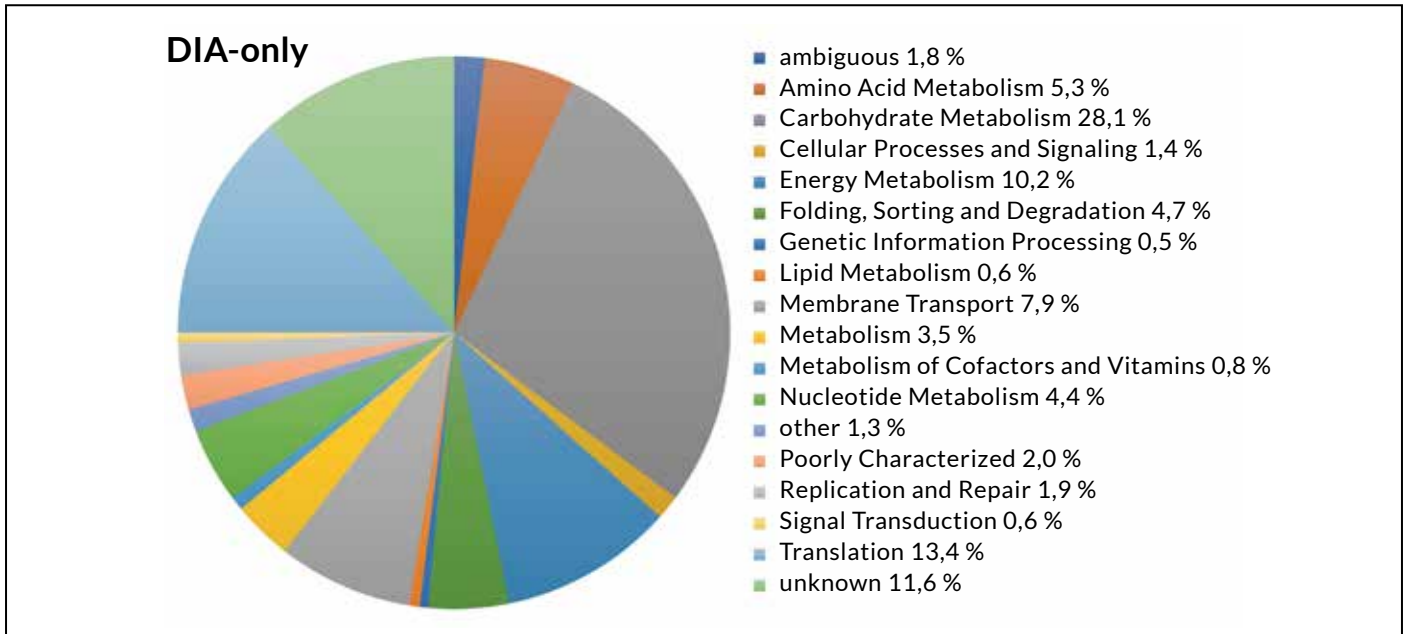
### Studying microbiota at protein level

Suomi works at the University of Turku in Professor **Laura Elo**’s research team that has developed a new method for studying microbiota at protein level. Suomi says that the key question is which processes can be detected in gut microbiota. Only now is information becoming available on the metabolic activity of bacteria at protein level. This makes it possible to analyse many dietary factors, such as how baby formulas affect the gut microbiota.

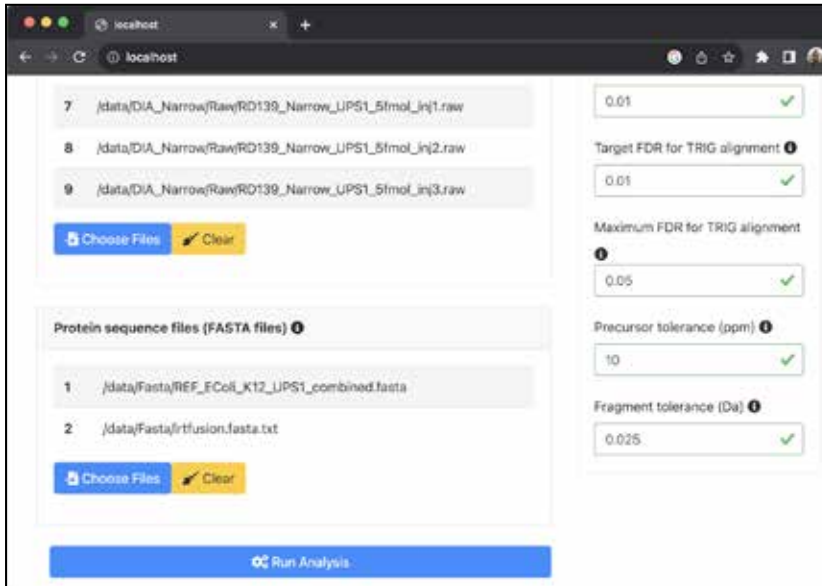
“This enables us to measure and study like never before what happens in the intestine. How do bacteria interact with each other and what determines which bacteria are active? The method we have developed makes use of the latest mass spectrometry technology and computational methods. It enables us to comprehensively measure the protein levels of complex microbial samples.”

The importance of gut microbiota for human health and their role in various illnesses has been identified in recent studies. Potential diseases that can be studied by means of metaproteomics include Crohn’s disease, ulcerative colitis, colorectal cancer or diabetes.

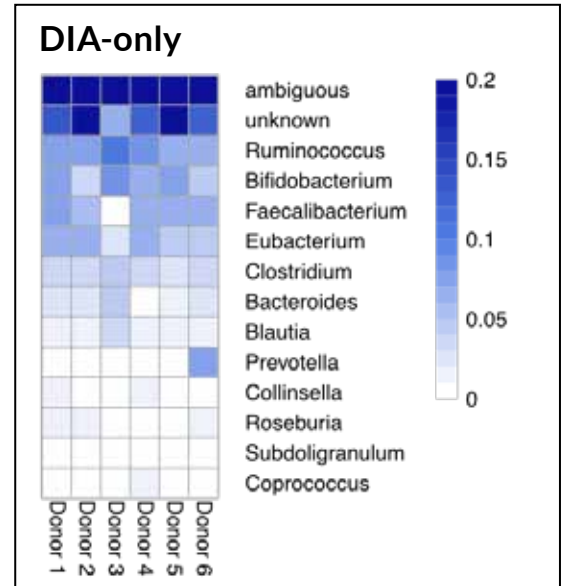
“Other areas of application may include



Functional groups identified from human stool samples by means of DIA spectrometry as fractions of identified peptides.



Screenshot of the user interface of the research team's glaDIator application for the study of data produced by a mass spectrometer.



Composition of six stool samples at genus level of the largest group in the previous figure (carbohydrate metabolism). Presented as fractions of the identified peptides.

allergies. There are a number of conditions with which a link with gut microbiota has been suggested at least on some level. The methods we have developed can be applied directly to such studies.”

### DIA method

Mass spectrometry is used to identify isolated proteins. Proteins in a sample are broken down into smaller amino acid chains, or peptides, which are then analysed with a mass spectrometer. Proteins are identified by de-

ducing the amino acid chains of the peptides on the basis of measured masses by means of computational methods. The measured masses are compared to databases containing, for example, known protein sequences that best match the peptide masses.



In the new DIA methods (data-independent acquisition), the aim is to measure and fragment all peptides contained in the sample for identification. However, identification is more difficult than normally, because individual spectrums may represent more than one peptide. A similar DIA-based mass spectrometry has not been used before in connection with metaproteomics. The research team has developed algorithms to identify peptide sequences and to search for them from databases.

According to Suomi, this is computationally difficult, because the new DIA methods attempt to measure everything in the sample: all peptides originating from various types of microbes contained in it.

“Metaproteomics requires massive computing power, because identification is so difficult. As reference, we have millions of possible proteins from thousands of bacteria, which we are trying to identify in the samples. However, we get really accurate and comparable measurements as a result.”

The research team is using the computing power of Finland’s ELIXIR node CSC – IT Center for Science. The virtual computers of CSC have been connected as an extension of the local computing cluster of the University of Turku.

According to Suomi, this measurement method seems to be working really well for clinical samples. Future applications may

include comparable measurements of stool samples in biobanks.

“We may have hundreds of samples from different individuals. At the moment, using this method alone, we are able to perform sufficiently comparable measurements between individuals, for example as part of studying how diseases develop. With the new method, it will be possible to study large cohorts.”

The new method offers a variety of applications, Suomi says.

“In theory, the methods could be used more extensively in metaproteomics applications, such as ocean and wastewater study or the analysis of soil samples, but we have not yet tested our methods for them.”

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#### MORE INFORMATION:

##### Turku Bioscience Centre

<https://bioscience.fi>

##### CSC – IT Center for Science

is a non-profit, state-owned company administered by the Ministry of Education and Culture. CSC maintains and develops the state-owned, centralised IT infrastructure.

<http://www.csc.fi>

<https://research.csc.fi/cloud-computing>

##### ELIXIR

builds infrastructure in support of the biological sector. It brings together the leading organisations of 21 European countries and the EMBL European Molecular Biology Laboratory to form a common infrastructure for biological information. CSC – IT Center for Science is the Finnish centre within this infrastructure.

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