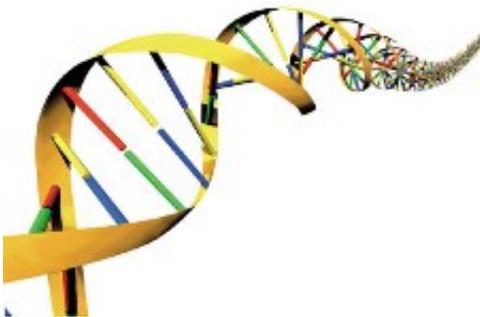


Researchers uncover new knowledge about our intestines

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Researchers from Technical University of Denmark Systems Biology have mapped 500 previously unknown microorganisms in human intestinal flora as well as 800 also unknown bacterial viruses (also called bacteriophages) which attack intestinal bacteria.

To map the [microorganisms](#), the researchers have developed a new principle for analysing DNA sequence data, which they have named the co-abundance principle. A principle which basically assumes that different pieces of DNA from the same organism will occur in the same amount in a sample, and that this amount will vary over a series of samples.

"Using our method, researchers are now able to identify and collect

genomes from previously unknown microorganisms in even highly complex microbial societies. This provides us with an overview we have not enjoyed previously," says Professor Søren Brunak who has co-headed the study together with Associate Professor Henrik Bjørn Nielsen.

So far, 200-300 intestinal bacterial species have been mapped. Now, the number will be more than doubled, which could significantly improve our understanding and treatment of a large number of diseases such as type 2 diabetes, asthma and obesity.

Viruses—not antimicrobial agents

The two researchers have also studied the mutual relations between bacteria and viruses.

"Our study tells us which bacterial viruses attack which bacteria, something which has a noticeable effect on whether the attacked bacteria will survive in the intestinal system in the long term," says Henrik Bjørn Nielsen

Previously, bacteria were studied individually in the laboratory, but researchers are becoming increasingly aware that in order to understand the [intestinal flora](#), you need to look at the interaction between the many different bacteria found.

And when we know the [intestinal bacteria](#) interactions, we can potentially develop a more selective way to treat a number of diseases.

"Ideally we will be able to add or remove specific bacteria in the intestinal system and in this way induce a healthier intestinal flora," says Søren Brunak.

It is particularly interesting in relation to the increasing problem of antimicrobial resistance which many consider a real threat to global health.

"We have previously been experimenting with using bacteria and viruses to fight disease, but this was shelved because antimicrobial agents have been so effective in combating many infectious diseases. If we can learn more about who attacks who, then bacterial viruses could be a viable alternative to [antimicrobial agents](#). It is therefore extremely important that we now can identify and describe far more relations between [bacteria](#) and the viruses that attack them," says Henrik Bjørn Nielsen.

The research findings will be published in *Nature Biotechnology*.

More information: An integrated catalog of reference genes in the human gut microbiome, *Nature Biotechnology*, [DOI: 10.1038/nbt.2942](https://doi.org/10.1038/nbt.2942)

Provided by Technical University of Denmark

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