

BBC NEWS

Human gut microbes hold 'second genome'

By Doreen Walton
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The human gut holds microbes containing millions of genes, say scientists.

In fact, there are more genes in the flora in the intestinal system than the rest of our bodies. So many that they are being dubbed our "second genome".

A study published in the journal Nature details the analysis of the genes, carried out to better understand how the gut flora is affected by disease.

"Basically, we are a walking bacterial colony," said Professor Jeroen Raes, one of the researchers involved.

"There is a huge diversity. We have about 100 times more microbial genes than human genes in the body. We also have 10 times more bacterial cells in our body than human cells," he told BBC News. Most of the microbes present in our bodies live in the gut.



Clostridium difficile bacteria, a normal inhabitant of the human gut

The study was led by Professor Jun Wang from the Beijing Genomics Institute-Shenzhen.

Scientists from Germany, Belgium, Denmark, Spain, France and the UK also took part in the international effort, named the European MetaHIT consortium, which has been co-ordinated by Dr Stanislav Dusko Ehrlich.

"Everyone was so motivated," said Dr Dusko Ehrlich. "To have such an exciting project to run - it's a piece of cake. The work went much faster than we expected."

Professor Raes, who works at Vrije Universiteit Brussel, explained why the microbes warranted such an intensive study: "Gut flora is crucial for our

health. We're basically living in symbiosis with these microbes.

"The bacteria help digest food, provide vitamins, protect us from invading pathogens. If there's a disturbance, people get all sorts of diseases such as Crohn's disease, Ulcerative colitis, and a link has also been made to obesity."

Untangling a mess

The researchers have developed what is called a metagenome, a combined genome of all the bacteria sequenced at once.

"This creates a huge dataset that has to be disentangled," explained Professor Raes. "The untangling of this mess is what I do; it's my role in the study."

“ We're basically living in symbiosis with these microbes” Professor Jeroen Raes

The team analysed faecal matter from 124 Europeans and found each person had about 160 bacterial species. The samples were more alike than they had expected and a significant fraction of the bacteria was shared between all the people who took part.

By mapping the genes, the scientists have found a way around the problem of having to culture bacteria in order to study them.

Many bacteria are very difficult to grow in cultures in the lab. From looking at the genes, the researchers hope to be able to investigate how the flora changes when a person has a disease.

“ We already have very exciting results in terms of differences between healthy and sick people” Dr Stanislav Dusko Ehrlich

"It will allow us to understand diseases better," said Professor Raes. "We know there is a microbial component but we don't know exactly how [it works]. We will use it for prognostic and diagnostic markers so we can predict disease severity or sensitivity to these diseases."

Dr Dusko Ehrlich said the work was showing promising results: "We have extremely interesting findings based on the results of this gene catalogue. We already have very exciting results in terms of differences between healthy and sick people."

Professor Elaine Holmes from Imperial College, London, who was not

involved in the research, said it was a welcome advance on previous studies.

"The article is extremely timely given the escalating interest in the influence of the gut microbiota in many aspects of health ranging from Irritable Bowel Disease, sepsis and obesity to autism," she told BBC News.

"It uses a large number of participants and therefore one assumes it is more representative of the 'real' microbial composition than previous studies. Also, it is an amazing feat of data processing."