

## Bacterial balance that keeps us healthy

EMBL scientists present genetic catalogue of our gut flora

**Heidelberg, 4 March 2010** – The thousands of bacteria, fungi and other microbes that live in our gut are essential contributors to our good health. They break down toxins, manufacture some vitamins and essential amino acids, and form a barrier against invaders. A study published today in *Nature* shows that, at 3.3 million, microbial genes in our gut outnumber previous estimates for the whole of the human body. Scientists at the European Molecular Biology Laboratory (EMBL) in Heidelberg, Germany, working within the European project MetaHIT and in collaboration with colleagues at the Beijing Genomics Institute at Shenzhen, China, established a reference gene set for the human gut microbiome – a catalogue of the microbe genes present in the human gut. Their work proves that high-throughput techniques can be used to sequence environmental samples, and brings us closer to an understanding of how to maintain the microbial balance that keeps us healthy.

“Knowing which combination of genes is necessary for the right balance of microbes to thrive within our gut may allow us to use stool samples, which are non-invasive, as a measure of health,” says Peer Bork, whose group at EMBL took part in the analysis. “One day, we may even be able to treat certain health problems simply by eating a yoghurt with the right bacteria in it.”

This catalogue of the microbial genes harboured by the human gut will also be useful as a reference for future studies aiming to investigate the connections between bacterial genetic make-up and particular diseases or aspects of people’s lifestyles, such as diet.

To gain a comprehensive picture of the microbial genes present

in the human gut, Bork and colleagues turned to the emerging field of metagenomics, in which researchers take samples from the environment they wish to study and sequence all the genetic material contained therein. They were the first to employ a high-throughput method called Illumina sequencing to metagenomics, dispelling previous doubts over the feasibility of using this method for such studies.

From a bacterium’s point of view, the human gut is not the best place to set up home, with low pH and little oxygen or light. Thus, bacteria have had to evolve means of surviving in this challenging environment, which this study now begins to unveil. The scientists identified the genes that each individual bacterium needs to survive in the human gut, as well as those that have to be present for the community to thrive, but not necessarily in all individuals, since if one species produces a necessary compound, others may not have to. This could explain another of the scientists’ findings, namely that the gut microbiomes of individual humans are more similar than previously thought: there appears to be a common set of genes which are present in different humans, probably because they ensure that crucial functions are carried out. In the future, the scientists would like to investigate whether the same or different species of bacteria contribute those genes in different humans.

The research was conducted within the European project MetaHIT, coordinated by Dusko Ehrlich at the Institut National de la Recherche Agronomique, in France, with genetic sequencing carried out by Jun Wang’s team at the Beijing Genomics Institute at Shenzhen, China. ●

### Source Article

Qin et al. A human gut microbial gene catalog established by deep metagenomic sequencing. *Nature*, 4 March 2010.

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