

Cataloguing 10 million human gut microbial genes

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Over the past several years, research on bacteria in the digestive tract (gut microbiome) has confirmed the major role they play in our health. An international consortium, in which INRA participates, has developed the most complete database of microbial genes ever created. The catalogue features nearly ten million genes and will constitute a reference for all research on gut bacteria.

Research on the [gut](#) microbiome (all of the bacteria in the digestive tract) has multiplied over the past several years, helped in great part by new sequencing technologies. The gut microbiome, which scientists have labelled a "new organ" that is composed of tens of trillions of bacteria – ten times as many as the number of cells in the human body – is directly linked to the immune system and brain. It is a major player in [chronic illnesses](#) such as obesity and Type 2 diabetes. However, research in the field depends on access to reference gene databases (or catalogues), which is particularly important when identifying the functions of microbial genes. Few and far between, existing catalogues were created using samples from a limited number of people and geographical origins.

INRA researchers, as part of the MetaHIT international consortium, put together a catalogue of microbial genes that regroups pre-existing catalogues (European, American and Chinese) and enhanced it with new sequences. Apart from being an unparalleled resource, the analyses done for the catalogue showed that it contains the broadest collection of [microbial genes](#) – and by extension, their functions – present in the global population. With ten million genes, this new catalogue presents

the most impressive array of human intestinal [bacteria](#) in the world.

Most of the genes (around six million) are shared by just 1% of the population, making them quite rare. While there is substantial data today regarding the most common genes, future research will focus on determining the importance and role of these rare genes.

Thanks to this catalogue, the most clinically significant genes can be described, most notably those related to illnesses such as Type 2 diabetes, cirrhosis of the liver, cardiovascular diseases and some cancers. It will also provide a more complete picture of imbalances in the [gut microbiome](#) (dysbiosis), particularly those caused by medication.

More information: Junhua Li et al. "An integrated catalog of reference genes in the human gut microbiome." *Nature Biotechnology*, 6 juillet 2014. [DOI: 10.1038/nbt.2942](https://doi.org/10.1038/nbt.2942)

The catalogue may be freely accessed at: meta.genomics.cn/

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