

Update on the Human Microbiome projects

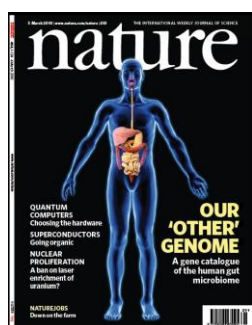
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Humans live in association with a large number of microorganisms, which affect our health and well-being. Most reside in the intestine, where their numbers exceed 10-fold the number of our cells. The intestinal micro-organisms are thought to have an important role in health and disease, but are still poorly characterized. To understand and exploit the impact of the gut microbes on human health and wellbeing it is necessary to decipher the content, diversity and functioning of the gut microbial community. This is being attempted by several large projects, such as the Human Microbiome Project of the NIH and the MetaHIT project of the European Commission.

MetaHIT, (<http://www.metahit.eu>) has as a first objective creation of a catalog of the microbial genes from our intestinal tract, thus laying foundations for characterization of the gut microbial community. Next, it aims to explore associations between microbial genes and human phenotypes. For that, it develops, on the one hand, molecular tools for profiling of the intestinal microbial genes that are harbored by any individual and on the other a bio-informatics resource to organize and interpret heterogeneous information, including sequencing data and clinical metadata. Finally, MetaHIT develops approaches to detect and analyze functional interactions of microbes and the human host, focusing on the role of target genes in the microbial cell and the effect of gene products on the human host.

We have established an extensive catalog of the gut microbial genes, based on the Illumina metagenomic sequencing. The catalog contains 3.3 million nonredundant microbial genes, derived from 576.7 Gb sequence of the DNA prepared from faecal samples of 124 individuals of the European origin. The sequencing and the assembly was carried out BGI Shen Zhen, one of the MetaHIT partners. The gene set is more than 150 times larger than the human gene complement, contains an overwhelming majority of the prevalent microbial genes present in the cohort and likely includes a large proportion of the prevalent human intestinal microbial genes. The gene pool is largely shared among individuals of the cohort. Over 99% of the genes are bacterial, suggesting that the entire cohort harbors between 1000 and 1150 prevalent bacterial species and each individual at least 160 such species, which are also largely shared. We define and describe the minimal gut metagenome and the minimal gut bacterial genome in terms of functions encoded by the gene set.



Qin, J. et al. A human gut microbial gene catalogue established by metagenomic sequencing. *Nature* 464, 59-65 (2110).