BACTERIAL ECOLOGY

Snapshot of a superorganism

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URLs
Online Links:
KEGG
http://www.genome.jp/kegg/

COG
http://www.ncbi.nlm.nih.gov/Class/NAWBIS/Modules/Genomes2Other/genomes41.html

The human colon is the most densely populated ecosystem known, with an estimated 10^{11}–10^{12} microbial cells ml^{-1}. In the first metagenomic analysis of this complex microbial community, Steven Gill and colleagues analysed ~78 Mb of unique DNA sequences from faecal samples obtained from two healthy adults, and the results are reported in a recent issue of *Science*.

The composition of the microbiome has only recently started to be investigated in detail. However, other studies, including a comprehensive analysis of 13,335 16S rRNA gene sequences from the intestinal microflora of three healthy individuals in 2005, have indicated which species are abundant in the intestine. This has allowed the contributions of these species to human metabolism and physiology to be predicted from knowledge of their metabolic abilities combined with analysis of available genome-sequence data. Now, with their metagenomic approach, Gill *et al*. have been able to build on this early work and attempt an *in silico* reconstruction of the metabolic potential of the microbiome.

The predicted gene products from identified genes were mapped to metabolic categories in the Kyoto Encyclopedia of Genes and Genomes (KEGG) and Clusters of Orthologous Groups (COG) databases. The enrichment or under-representation in the microbiome was then calculated, relative to the human genome, all bacterial genomes in the databases or all archaeal genomes in the databases. Notable enrichments include enrichment for the key genes involved in methanogenesis, a reaction that is crucial for the removal of H_2 in the intestine but which can only be performed by methanogenic archaeal species, and enrichment for genes involved in carbohydrate fermentation, including the gene encoding butyrate kinase, which phosphorylates butyrate to generate butyryl coenzyme A, an important source of energy for human colonocytes. Additionally, genes involved in the 2-methyl-D-erythritol 4-phosphate (MEP) pathway were enriched. The MEP pathway generates deoxyxylulose 5-phosphate, a precursor of many vitamins, and isopentenyl pyrophosphate, a key intermediate in many metabolic pathways.

Gill *et al*. argue that we should consider ourselves: "superorganisms whose metabolism represents an amalgamation of microbial and human attributes". As our bodies contain ten times as many microbial cells as they do human cells, we are effectively one part human to ten parts microbe, and with this latest work the precise functional attributes of the microbial majority are now beginning to be decoded.

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ORIGINAL RESEARCH PAPER Gill, S. R. *et al.* Metagenomic analysis of the human distal gut microbiome. *Science* **312**, 1355–1359 (2006)
FURTHER READING Eckburg, P. B. *et al.* Diversity of the human intestinal microbial flora. *Science* **308**, 1635–1638 (2005)