

Human populations are divided in three groups by their intestinal bacteria

The international MetaHIT consortium shows that human populations can be differentiated by their intestinal bacteria. The individuals can be grouped into three “enterotypes”, irrespective of their geographic origin, health or age. Enterotypes, which can be compared to blood types, are defined by characteristic populations of bacterial species and the functions that they encode. They open avenues for better understanding of human biology and for numerous applications in human health and nutrition. The results have been published in Nature online, dated April 20 (<http://www.nature.com/nature>).

MetaHIT consortium has published in March 2010 the first comprehensive catalog of human intestinal bacterial genes, dubbed our second genome¹. It was found that the gut bacteria encode 150 times as many genes as our own genome and that each individual harbors some 170 bacterial species out of a total of about 1000 that are predominant in the gut. Most of these species are common to many individuals, showing that we are all rather similar.

The current study has refined this view. A *tour de force* bioinformatic analysis at EMBL has shown that human populations are split into three groups by the particular combinations of bacterial species they harbor, independently of the geographic origin, health status (obesity or inflammatory bowel disease) or age. The groups can be compared to the blood types and are denoted enterotypes.

This new and unexpected facet of human biology has been shown with three different study populations. One included 39 individuals from three continents (Danish, French, Italians and Spaniards from Europe; Japanese and Americans), another comprised 85 Danes and the last 154 Americans. The same three enterotypes were observed with all.

In parallel, bacterial genes that can be used as biomarkers for the disease and age have also been found. This indicates that the bacterial communities from our gut not only divide human populations in large groups but can also signal a health status of an individual.

Enterotypes will impact human biology, which will have to account for their existence and effects. They will impact medicine and nutrition, by allowing to properly group individuals and determine their particular needs more efficiently. Furthermore, gut microbial populations appear to contain novel and promising biomarkers, which will impact detection and possibly prognostic of chronic diseases such as obesity and its complications (metabolic syndrome, diabetes and cardio-vascular pathologies). We foresee development of the personalized and preventative medicine and nutrition based on gut microbial populations, leading to the overall improvement of human health and well-being.

Reference: Arumugam et al., Enterotypes of the human gut microbiome.

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¹ Qin et al. Nature. 2010, **464**, 59-65.