

Georges MOUTON MD

INTESTINAL MICROFLORA IMPACT ON HEALTH

"The endogenous gastrointestinal microbial flora plays a fundamentally important role in health and disease" [1]. It is almost unbelievable that our intestinal microbial population exceeds our total number of cells by at least an order of magnitude (10^{14} compared to 10^{13}), representing a biomass not far from 2 kg [2]. The last estimations about the different species of gut microorganisms now exceed one thousand [3]. The global genome represented within all those species (called the microbiome) may contain more than one hundred times the number of genes in our human genome, i.e. 4000K versus 35K genes [4]. Major functions of the gut microflora concern salvage of energy from the nutrients, trophic effects on the intestinal epithelium and on the underlying immune system, and protection against invasion by aliens [5].

Anaerobic bacteria are strongly predominant, most common species belonging to the genus **Bacteroides** (putrefactive Gram-negative anaerobic rods), **Bifidobacterium** (fermentative Gram-positive anaerobic rods) and **Clostridium** (putrefactive Gram-positive anaerobic rods) [6, 7]. The global balance between putrefactive species (i.e. thriving on proteins and amino acids) and fermentative ones (i.e. thriving on carbohydrates and fibers) seems to be determinant for health. In most formula-fed infants, *Bacteroides* catch-up the normally dominant *Bifidobacterium* among breast-fed infants, due to the lower content in oligosaccharides of cow's milk compared to human milk [8]. Important changes in the intestinal microflora of the elderly also concern the same genus, but reversely as *Bifidobacterium* loses two orders of magnitude (from 10^9 to 10^7 cfu/g of feces) to the profit of putrefactive species [9].

Many years ago, during Skylab experiments with astronauts, stress appeared as being able to influence the balance of the intestinal microflora, once again in the favor of putrefactive species *Bacteroides thetaiotaomicron* [10]. The same tendency favoring the genus *Bacteroides* and other putrefactive genera has been identified in Crohn's disease [11], in ulcerative colitis [12] and in many allergic symptoms (where a link has been established with a significant overgrowth of *Bacteroides vulgatus*) [13].

As the complete genome of *Bacteroides thetaiotaomicron* has been recently characterized, we realize how this highly abundant obligate anaerobe found in the colonic microflora of adult humans is able to thrive either from dietary polysaccharides (using a phenomenal array of saccharolytic enzymes, despite its belonging to a supposedly putrefactive genus) or from host mucus polysaccharides according to nutrient availability [14]. Experiments with gnotobiotic murine models have demonstrated to what extent this single bacterial species could, by itself, increase host fat storage and total body fat content [15].

"There is a growing awareness of the importance of variation in the gut microbiota as a factor that influences human and animal health, and there is increasing recognition that poor gut health and dysbiosis are related to a wide range of non-infectious disease processes" [3]. Indeed, we now have to consider the "possibility that the rapidly rising incidence of insulin resistance (and related diseases) might be correlated with underlying dysbiosis" [3]. As *Bacteroides* represents one of the rare Gram-negative major genera within the gut microflora and even if this hypothesis appears more controversial, "the root of this medical problem could be related to the increase in antibiotic use since World War II" [3].

Among fermentative microorganisms, we shouldn't forget that minor quantities of several fungal species may exist physiologically in our gut microflora. The most frequently encountered is *Candida albicans*, which seems harmless if rare (10^2 or 10^3 cfu/g), but severely affecting the patient's well-being if much more abundant. Non *albicans* species of **Candida** and other genera such as **Geotrichum**, **Aspergillus** or **Saccharomyces** are detected more and more often, with the additional concern that they resist more frequently to conventional common antifungal therapies (such as fluconazole or itraconazole) [16].

Protozoan should not be considered as normal inhabitants of the human intestinal ecosystem. Still, their prevalence is increasing not only as exotic tropical amoebas, but especially through cosmopolitan amoebas such as *Iodamoeba bütschlii*, *Endolimax nana* and above all *Blastocystis hominis*, or through flagellates called *Dientamoeba fragilis* and especially *Giardia intestinalis*. They all can trigger highly variable complaints among hosts, from digestive troubles (diarrhea or bloating but also constipation or cramps) to fatigue, depression, headaches, joint pain and stiffness, lower backache, skin conditions...

1. Eckburg, P.B., et al., *Diversity of the human intestinal microbial flora*. Science, 2005. **308**(5728): p. 1635-8.
2. Xu, J. and J.I. Gordon, *Inaugural Article: Honor thy symbionts*. Proc Natl Acad Sci U S A, 2003. **100**(18): p. 10452-9.
3. Nicholson, J.K., E. Holmes, and I.D. Wilson, *Gut microorganisms, mammalian metabolism and personalized health care*. Nat Rev Microbiol, 2005. **3**(5): p. 431-8.
4. Backhed, F., et al., *Host-bacterial mutualism in the human intestine*. Science, 2005. **307**(5717): p. 1915-20.
5. Guarner, F. and J.R. Malagelada, *Gut flora in health and disease*. Lancet, 2003. **361**(9356): p. 512-9.
6. Mai, V., *Dietary modification of the intestinal microbiota*. Nutr Rev, 2004. **62**(6 Pt 1): p. 235-42.
7. Macfarlane, G.T. and S. Macfarlane, *Human colonic microbiota: ecology, physiology and metabolic potential of intestinal bacteria*. Scand J Gastroenterol Suppl, 1997. **222**: p. 3-9.
8. Harmsen, H.J., et al., *Analysis of intestinal flora development in breast-fed and formula-fed infants by using molecular identification and detection methods*. J Pediatr Gastroenterol Nutr, 2000. **30**(1): p. 61-7.
9. Hebuterne, X., *Gut changes attributed to ageing: effects on intestinal microflora*. Curr Opin Clin Nutr Metab Care, 2003. **6**(1): p. 49-54.
10. Holdeman, L.V., I.J. Good, and W.E. Moore, *Human fecal flora: variation in bacterial composition within individuals and a possible effect of emotional stress*. Appl Environ Microbiol, 1976. **31**(3): p. 359-75.
11. Linskens, R.K., et al., *The bacterial flora in inflammatory bowel disease: current insights in pathogenesis and the influence of antibiotics and probiotics*. Scand J Gastroenterol Suppl, 2001(234): p. 29-40.
12. Ishikawa, H., et al., *Randomized controlled trial of the effect of bifidobacteria-fermented milk on ulcerative colitis*. J Am Coll Nutr, 2003. **22**(1): p. 56-63.
13. Fukuda, S., et al., *Allergic symptoms and microflora in schoolchildren*. J Adolesc Health, 2004. **35**(2): p. 156-8.
14. Sonnenburg, J.L., et al., *Glycan foraging in vivo by an intestine-adapted bacterial symbiont*. Science, 2005. **307**(5717): p. 1955-9.
15. Backhed, F., et al., *The gut microbiota as an environmental factor that regulates fat storage*. Proc Natl Acad Sci U S A, 2004. **101**(44): p. 15718-23.
16. Zupanic-Krmek, D. and D. Nemet, *[Systemic fungal infections in immunocompromised patients]*. Acta Med Croatica, 2004. **58**(4): p. 251-61.