

The globalization of intestinal microbiota

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Abstract Many microorganisms reside in human mucosa, specifically in the gut. There are many sources of the microorganisms that colonize our gut, and these sources are mainly environmental. Indeed, food is a major source of bacteria and viruses. Food also modifies the equilibrium of microorganisms in our gut, with vegetables favoring a wider diversity. The increasing role of industrial food in our alimentation is generating a globalization of our gut microbiota that may influence our health and aid the diffusion of clonal bacteria.

Humans are complex ecosystems and coexist with an extremely complex invisible population. With an estimated 10^{12} prokaryotes (bacteria and archaea) residing in the human body, human bodies contain 100 times more prokaryotic cells than human cells [1], with at least 150 times more prokaryotic genes than human genes [1]. The number of viruses present in the human body is also considerable [2]. Not surprisingly, digestive microbiota have been the subject of many recent studies that raise certain questions about their evolution [2, 3].

The role of the digestive microbiota is still largely unknown, but these organisms do contribute enzymes absent in humans for food digestion [4]. Interestingly, many of these enzymes are necessary for the digestion of vegetables. The composition of gut microbiota in animals and humans varies according to the type of food consumed; vegetarian animals and humans have more microbial

diversity than carnivores and omnivores. This microbial diversity is also associated with higher enzymatic diversity, which is likely necessary for plant digestion.

There exist incontestable links between gut microbiota and obesity, as shown by differences in the ratio between *Firmicutes* and *Bacteroidetes* populations in the gut. It is obvious that the manipulation of gut microbiota plays a part in weight gain in animals in which growth promoters (probiotics and antibiotics) have been studied [5]. Gut microbiota from mice with obesity and metabolic syndrome cause obesity when transplanted into normal mice [6]. In humans, preliminary data demonstrate that obese people have more *Lactobacillus* sp. [7, 8]. Because *Lactobacillus* is a bacterium often used as a probiotic in animals [5, 9, 10] and vancomycin, an antibiotic used in the form of Avoparcin as a growth promoter in animals, has a comparable effect in humans, we have tested if it and vancomycin prescribed in association with gentamycin to treat endocarditis is also associated with weight gain [11].

The composition of the intestinal microbiota plays a role in metabolism and, likely, in human health. The source of the microorganisms in the digestive tract has greatly changed in recent years. Historically, the microbial ecosystem of the digestive tract was specific for a geographic area, much as the flora and fauna of an ecosystem are geographically distinct. The visible differences of animals and plants in isolated geographical regions are associated with a comparable microbial diversity. For example, currently in Africa, the microbial composition is very different from that described in Europe or America. Globalization involves a mutualization of living beings. The relative homogeneity of the microbial composition of Europeans and Americans reflects this globalization, rather than a transcendent tendency of humans to select the same bacteria worldwide [1].

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The question being investigated is whether it is important to identify the source of the gut microorganisms. They are ingested with food, drinks, and in the course of physical contact and inter-human relationships. Children are initially colonized by the mother's milk, the contact with the breast, and, subsequently, their fingers [3]. Thereafter, food will upset this ecosystem. Industrial foodstuffs represent an important source of globalization for gut microorganisms that is specific to the current era. For example, fermented dairy products (e.g., yogurt, functional foods, and fermented cheese) can include 10^8 to 10^{10} bacteria, primarily *Lactobacillus* sp. or *Bifidobacterium* sp. These strains, which are often patented, are then distributed worldwide, resulting in the globalization of digestive bacterial strains.

It should be noted that this globalization of food has been involved in a series of pandemics, such as epidemics of *Escherichia coli* contamination in chicken products causing urinary infections in humans [12]. Indeed, epidemics that occur in the farm industry have the potential to cause millions of infections via food consumption.

There is a comparable problem with viruses. The source of the new hepatitis virus subtype (hepatitis E) in developed countries seems to be the mutualization of pig livers in sausages, consumed uncooked, which was involved in a true epidemic in Europe. In France, the "figatelli" (i.e., pork liver sausages) are a vector [13]. In addition, the initial work of Forest Rohwer showed that the human digestive tract includes a huge number of plant viruses [2]. Concerning the source of these viruses, we recently found that Tabasco products were contaminated at a very high level with the mild pepper virus. We showed that there is a statistical link between the presence of this virus at high load (in the feces, the virus is alive and cultivable) and clinical signs of fever, pruritis, and abdominal pain [14]. In this work, we showed that industrial products had a higher rate of contamination than local products due to the mutualization of microorganisms. These elements demonstrate that we are experiencing globalization of the microbial population of our digestive tracts due to industrialized products that homogenize the microorganisms which we ingest.

However, it is necessary to understand that globalization is only occurring in those who live in the global village and consume industrial products. Humans, who have marginal contact with this type of evolution, particularly those living in rural areas, present microbial populations that remain specific to their geographic area.

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