HUMAN MICROBIOMA VARIABILITY: SAMPLING RELATED CHANGES

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The relation between gut microbiota and health is increasingly evident. Gut microbiota is crucial for the development of the immune system, in fact, animals raised under absolute sterile conditions (without colonizing microbiota) have a deficient intestinal immune system. The bidirectional interaction between microbiota and the host immune system begins at birth and both evolve throughout the life of the host.
Gut microbiota is influenced by several "strong factors", including host genetics, age, pregnancy, and some environmental factors such as diet, the type of birth, stress, and antibiotic intake. Notwithstanding the fact that several factors influence microbiota, it seems that microbiota composition remains relatively constant throughout our lives, although in old age species diversity seems to be lower. When microbiota is studied at levels below the phylum, a greater variation of microbiota between individuals is observed, and although it is known that microbiota of healthy individuals provides them a number of health benefits, it is not clear what would be the ideal composition of the "healthy microbiota."
Nowadays we have literature demonstrating that some "minor factors" during our lifestyle can also affect our microbiota. The gut microbiota regulates its cellular activity and behavior over 24-hour cycles known as the circadian clock or rhythm. Intestinal microbiota exhibits diurnal oscillations influenced by feeding rhythms, leading to time-specific compositional and functional profiles over the course of a day.
Jet lag can also induce changes in the gut microbiota composition, in particular Firmicutes are more abundant during jet lag. Domestic animals can also affect microbiota composition: household members share more of their microbiota than individuals from different households, with stronger effects of co-habitation on skin than oral and fecal microbiota.
Colonoscopy is strongly suggested after 50 years old. It has been demonstrated that the bowel lavage introduces an instant and substantial change to the intestinal microbiota. Recently we have demonstrated that one month after the colonoscopy, Firmicutes have been observed to be less abundant, while Proteobacteria abundance showed a significant increase if compared with samples collected before the colonoscopy.
Other than this external minor factors affecting the microbiota during our normal life, we need to take in account also that microbiota can have an intra-individual variability. Within the same subject, indeed, samples taken at closer time intervals were not necessarily more similar than samples obtained across longer sampling times.
Sampling, storage and delivery conditions of samples are also mandatory for a correct interpretation of the results.
In the next future, in order to avoid drawbacks and not optimal results the researchers should pay much more attention to the many factors affecting the microbiota composition. Strong exclusion/inclusion criteria should be then addressed before starting a study and any NGS analysis on human microbiota.