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Gastro Congress 2018: Gut Microbiota: An epochal revolution - Giovanni Gasbarrini - Catholic University of Rome

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Few data exist on differences in gut microbiota composition among principal gastrointestinal diseases. We evaluated the differences in gut microbiota composition among uncomplicated diverticular disease (DD), IBS and IBD patients. DD, IBS and IBD patients along with healthy controls (CT) were enrolled in our Italian GI outpatient clinic. Stool samples were collected. Microbiota composition was evaluated through a metagenomic gene-targeted approach. GI pathology represented a continuous spectrum of diseases where IBD displayed one extreme while healthy controls displayed the other. Among Phyla, Biplot PC2/PC3 and dendrogram plot showed major differences in samples from IBS and IBD. DD resembled species CT composition, but not for Bacteroides fragilis. In IBS, Dialyser spp and then Faecal bacterium parasitize were the most representative species.

UC showed a reduced concentration of Clostridium difficile and an increase of Bacteroides fragilis. In CD, Parabacteroides distensions was the most represented, while Faecal bacterium parasitize and Bacteroides fragilis were significantly reduced. Each disorder has its definite overall microbial signature, which produces a clear differentiation from the others. On the other side, shared alterations constitute the "core dysbiosis" of GI diseases. The assessment of these microbial markers represents a parameter that may complete the diagnostic assessment.

Human influences on the planet's atmosphere, hydrosphere and biosphere are of such magnitude as to justify naming a new geological epoch, the Anthropocene. Different starting dates and phases have been proposed for this epoch, depending on the criteria used. Recent advances in microbial genomics and ecology show that human perturbations to microbial populations correspond closely to the proposed phases of the Anthropocene: the 'paleo Anthropocene' which began with the rise of agriculture; the industrial revolution, from the late 1700s; and the 'Great Acceleration' from the 1950s to the present day.

As the Anthropocene unfolds, environmental instability will trigger episodes of directional natural selection in microbial populations, adding to contemporary effects that already include changes to the human microbiome; intense selection for antimicrobial resistance; alterations to microbial carbon and nitrogen cycles; accelerated dispersal of microorganisms and disease agents; and selection for altered pH and temperature tolerance. Microbial evolution is currently keeping pace with the environmental changes wrought by humanity. It remains to be seen whether organisms with longer generation times, smaller populations and larger sizes can do the same. The microorganisms associated with humans are notably diverse, varying between individuals, between body sites and over development. By adulthood, there are ten times more microbial cells in a human body than there are human cells. This diverse community of microorganisms is known as the human microbiome and can be analyzed in a manner similar to more conventional ecosystems, by examining colonization, climax communities, and perturbations by disturbance or invasion. Questions can be asked about how the human microbiome might have changed over evolutionary time, how human activities might alter colonization and community development, and the role of the microbiome in health and disease.

On a very general level, the human microbiome has changed in parallel with phases of the Anthropocene. Oral microbiota from fossilized dental calculus shows a marked change in bacterial diversity and composition during the transition from a huntergatherer lifestyle toward a greater consumption of cereals during the Neolithic. A second major shift is apparent around the start of the industrial revolution, coinciding with increased availability of processed flour and sugar.

Analyses of gut bacteria preserved in coprolites show that ancient human microbiomes were similar to those from modern rural communities, and that diet dramatically affects microbiome composition. For instance, the increased availability of simple carbohydrates in the Neolithic selected for altered microbiome components. Such 'Neolithic' microbiomes still dominate the gut flora of communities with high fibre, polysaccharide rich diets whereas shifting to a modern, high protein and animal fat diet causes a corresponding shift in microbiome composition.

Dietary influences on gut microbiomes are also evident at higher taxonomic levels, since mammalian gut flora cluster according to diet, not phylogeny, and herbivore microbiomes can be clearly distinguished from those of carnivores and omnivores. Acquisition of the microbiome begins at birth when the neonate is first exposed to both maternal and environmental bacteria. Delivery mode affects this early colonization, since Csection babies harbour different microbiomes compared to vaginal delivery.