



Microbiomes: human and environment

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We are surrounded by microorganisms. Since Anton Van Leeuwenhoek described bacteria and life in a drop of water in 1675, we have been fascinated by these living beings. Use of microorganisms by humans is ancient: we were making bread, wine, beer and fermented milk before yeasts and bacteria were known. Elie Metchnikoff (1845–1916) advocated the use of fermented milk containing lactic bacteria to prolong human life. However, bacteria around us were for a long time regarded as either harmful or innocuous, with a few exceptions. One of the most outstanding, I think, is the book by H. G. Wells (1866–1944) “*The War of the Worlds*”. In this book, Martians come to Earth to take over our planet, using weapons impossible to defeat. Then, one by one the Martians died, simply because they were not adapted to the Earth microbiota. Martians were defeated by the smallest inhabitants of our World. It is tempting to think that Wells knew the words of Louis Pasteur (1822–1895): “Messieurs, ce sont les microbes qui auront le dernier mot”. Microbes have increasingly been in the spotlight, and that was the subject of Symposium 11 of the 20th IUPAB Congress. In this symposium, we discussed the human microbiota in health and disease, the environmental microbiota to which humans are exposed, methods to determine the identity and interactions of these microbes and how the movement of some of these beings is regulated.

Professor Lars Engstrand (Karolinska Institutet, Sweden) remarked that 99% of our genes come from microbes distributed in several sites in the human body. However, 80% of this microbiota is still unknown. He presented data obtained by his laboratory in cooperation with clinicians, scientists, lab core, bioinformatics and biostatistics partners. The group is interested on the effects of microbiota in cancer, gastroenterology, women’s health and its consequences to newborn health. The first question addressed was “what

is a normal microbiota”? Analysis of upper and lower gut contents from 1000 healthy volunteers over time revealed a vast diversity of microbes which varied between volunteers and even in the same individual over time. However, use of antibiotics or flares in individuals suffering from inflammatory bowel disease decreased microbiota diversity. Women’s vaginal microbiota also varied among individuals: while some women had a large stable vaginal Lactobacilli population, others had a greater variety of microorganisms, which changed during the menstrual cycle. Prof. Engstrand professed a strong conviction that treatment to cancer will be improved once knowledge of the microbiota is advanced, and microbial products may be paramount in the stimulation of the immune system to fight cancer in association with therapy. Dr. Giorgio Trinchieri (NCI, NIH, USA, keynote lecture 3) also addressed this issue.

Hence, humans carry enormous amounts of microorganisms, but are also exposed to microorganisms from the environment, including those shed by other humans. Dr. Emmanuel Dias-Neto (AC Camargo Cancer Center, Brazil) presented data on characterization of microbiota present in urban environments exposed to large numbers of people, such as subways in several locations in the world. Thousands of microorganisms were identified, and they were differed according to geography and climate, and surface from which they were collected. Interestingly, the density of antibiotic resistance genes found was higher near hospitals and could be correlated with the use of antibiotics in different countries. He also discussed future projects, such as how a massive event such as the Olympic Games, which attracted people from all over the world to Rio and Tokyo would impact the urban microbiota. They are also studying the microbiota present on landmark monuments around the world. Importantly, they use these tools to detect the presence of Sars-Cov-2 in hospitals in Brazil.

Detection of microbes in living organisms and in the environment is dependent on careful sampling, sequencing, and bioinformatics analysis. Prof. João Carlos Setubal (USP, Brazil) talked about the field of microbiomics. He focused on shotgun metagenomics, in which all DNA from

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samples are sequenced. He explored the technique called metagenome-assembled genomes (MAGs) and very convincingly defended that this is a powerful tool for identifying microorganisms, genes and the products they code, and other information about microbial communities. He sustains that the main caveats of the method are quality control of MAGs and standardization, a point also stressed by Dr. Engstrand. He introduced two new concepts: SMAGs, which can be assigned to a known species, and HMAGs (hypothetical MAGs). He proceeded to show that the confidence in the biological reality of a SMAG is revealed when it matches genomes from isolates, using an elegant example of composts obtained from the zoo in São Paulo and oil palm compost from Malaysia. HMAGs are also judged by the same criteria, except that they are not from a known species. He made a strong point towards the reliability of MAGs and HMAGs, which would shed light onto the “microbial dark matter”, that is, the enormous number of microbial species that are unknown, and let alone sequenced.

Finally, two young scientists presented their work. Microbiota not only interact with humans, but with each other. Mr. Jumpei Yamagishi (University of Tokyo, Japan) studied the leakage of metabolites in isolated microbial cells and leakage and exchange of metabolites between members of microbiota using an elegant mathematical model that considers diffusion, increase in concentration and other variables, such as the deviation of substrates from one pathway to the other due to secretion or leakage of metabolites. Dr. Ivan Rosa e Silva, on the other hand, presented data on the regulation of cilia formation, which is present both in animals and microorganisms, underscoring the similarities of some structures throughout evolution.

The advancement of knowledge in this field has been exponential, and each day we find a new link between our microbial companions and our physiology and response to pathology. Hopefully, in the near future, we will be able to manipulate our commensals to promote health and prevent diseases.

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Declarations

Conflict of interest The author declares no competing interests.

Further reading

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