Abstract Form

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Title of presentation
Gut microbiota structure and functions: Scientific state of the art.

1. Brief description/abstract for the content of the presentation. 150 words maximum
Introduction / Objectives / Methodology / Results / Conclusion

The complexity of the human intestinal microbiota has recently been revealed, thanks to the metagenomic approach. Indeed, it allowed rapid advancement in characterizing the genetic and genomic diversity of our microbiome. Exhaustive sequencing of the gut microbiome of hundreds of healthy individuals, but also of patients suffering from various pathologies demonstrated the importance of a symbiosis between the microbiota and its host. Dysbiosis of this ecosystem is associated with several diseases, revealing bacterial species as signatures of the patient’s condition. An innovative functional metagenomic approach has been implemented allowing identifying bacterial genes and metabolites involved in this cross talk. The cutting-edge characterization of our other genomes remains a crucial step in the full understanding of human biology.

2. Please give two to three key references which can be used to inform future work:
3. Please identify up to three specific outcomes that dietitians and participants will take away to inform their future practice.

- The human gut microbiota is composed of about 39 trillion microorganisms, thus as many microorganisms as human cells.
- It is a key organ interacting with food and cells and protecting against pathogens.
- Dysbiosis has been observed in several diseases including obesity and diabetes, and its role in the pathogenicity is now recognized.