

# Chemical and biomolecular studies on the intestinal microbiome: the pluriennial experience of the Joint International Unit “MicroMeNu” between the CNR and Université Laval

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The microbiomes are complex ecosystems constituted of different types of microorganisms (bacteria, archaea, yeasts and viruses, as well as, in some cases, unicellular prokaryotes, which together form different *microbiota*), as well as their genes, proteins and metabolites, through which these microorganisms communicate with their typical environments. The microbiota composition in different kingdoms, phyla and taxa depends on the surrounding environment and its changes and, in the case of animal microbiomes, on the genetics of the host. In animals, all exposed parts of the body (and, as suggested by recent evidence, internal organs too) conserve their specific microbiomes.

The gut microbiome is the best studied of the animal microbiomes, and is defined as the system of trillions of microorganisms belonging to thousands of species that populate the intestine of animals (the gut microbiota), together with their molecular components. The taxonomic composition of the gut microbiome is regulated by both innate and external factors, in a way that two different individuals will never have the exact same taxonomic profile, especially at the genus or species level. The host microbiomes, and in particular the gut microbiome, are deeply involved in the regulation or, instead, when they are pathologically altered, dysregulation of almost all physiological functions. They do so by producing, often following the processing of different nutrients, small chemical signals, such as short chain fatty acids, various tryptophan metabolites, secondary bile acids and endocannabinoid-like molecules, among others, which can enter the host circulation or affect its enteric nervous system. However, still relatively little is known about most of the chemicals produced by the microbiomes.

The Joint International Research Unit on Chemical and Biomolecular Studies on the Microbiome and its Impact on Metabolic Health and Nutrition (JIRU-MicroMeNu), between the CNR and Université Laval in Quebec City, Canada, aims at investigating the known, or yet to be discovered, small chemicals produced by, among others, the gut microbiome and understand the molecular mechanisms underlying their biological activity in various physiopathological conditions. The JIRU-MicroMeNu was founded in 2016, and started its activities in 2017. It exploits the unique infrastructures and expertise for microbiome research present at Université Laval and the exceptional expertise in small molecule chemistry, pharmacology and formulation present in some CNR institutes.

I will briefly describe the activities and some of the most important scientific results achieved in biomedical research within the framework of the JIRU-MicroMeNu (see references below) and thanks to the collaboration between the CNR and Université Laval.

## Keywords:

Lipids, short chain fatty acids, endocannabinoidome, inflammation, obesity.

## References:

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## Thematic Areas:

- ✓ Frontiers in Microbiome Research
- ✓ Microbiome: from Research to Clinics

## Infrastructures:

Metabolomics analytical infrastructures at ICB-CNR (Shimadzu IT-TOF, Orbitrap Q-exactive, triple-quad LC-MS-MS; 300 and 500 MHz NMR). Germ-free mouse colony (CRIUCPQ, Université Laval), metabolomics (Orbitrap Fusion, T-TOF ion mobility LC-MS-MS; Bruker-Rapiflex for MALDI- imaging on tissue, at INAF and CRIUCPQ), microbiology (P2 laboratories, bacterial single cell sorting and culture, MALDI-TOF bacterial identification, at INAF) and in vitro fermentation (M-SHIME, at INAF) platforms at Université Laval.