

MICROBIOLOGIE, INFECTIOLOGIE ET IMMUNOLOGIE

CONFÉRENCE

Université 
de Montréal



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Xenobiotics and the active human gut microbiota: unintended effects revealed

The human gut is home to trillions of microbial cells, bacteriophages (viruses specific to bacteria), fungi, and eukaryotes; collectively referred to as the gut microbiota. Large-scale studies on this host-associated community using sequencing approaches have tremendously improved our understanding of how it modulates our health, identifying its central role in digestion, vitamin synthesis, xenobiotic metabolism, and shaping of the host immunity. However, these sequencing approaches cannot identify the active cells within the community or the impact of clinically relevant perturbations, such therapeutic drug exposure. Combining single-cell and metagenomics approaches to the study of the human gut microbiota, we identified its active subset and determined its response to a short exposure to a panel of therapeutic drugs. Our results demonstrate the power of moving beyond DNA-based measurements of microbial communities to better understand their physiology and metabolism, while highlighting their rapid response to perturbations.

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Pavillon Jean-Coutu, salle S1-131

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