## SÉMINAIRES ET CONFÉRENCES



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## "Studying the nasal epithelium to understand gene-environment interactions in asthma and allergic diseases"

Common diseases and complex traits, such as asthma and allergy-related traits, are influenced by both genetic and environmental factors and interactions between them (gene-environment interactions). That is, different genotypes may promote or prevent disease risk only in the presence of specific environmental exposures. Environmental exposures can also impact diseases through their direct effects on epigenetic marks, such as DNA methylation, and regulation of gene expression.

The respiratory epithelium is increasingly recognized in asthma, allergic and other airway inflammatory diseases as an immune and physical barrier that modulates the host's responses to environmental and microbial exposures. We hypothesized that studying the nasal epithelium would allow us to identify new gene-environment interactions associated with asthma and allergyrelated traits. We first revealed evidence of how early-life upper airway microbiota diversity leaves a lasting signature in DNA methylation patterns in nasal epithelial cells that influences the expression of genes and the development of allergic rhinitis in childhood. We then built a pipeline to select high-value DNA methylation sites (CpGs) from nasal epithelial cells in order to develop a custom array tailored to study asthma and allergic diseases. This pipeline also revealed signature features of functional and high-value CpGs currently missed by commonly used arrays. Finally, we identified gene-environment interactions at the most replicated asthma GWAS loci and suggest that gene expression during viral respiratory infection may modify asthma risk.

Lien zoom:

https://umontreal.zoom.us/j/86111888381?pwd=ei9MekZoUDZyelV0QTNsTFI4cGppZz09







Le lundi 11 avril 2022, 11h30



Invité de Pascale Legault