The microbiome from the Lyme disease principal reservoir host in southern Quebec (*Peromyscus leucopus*)

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Introduction

• *Peromyscus leucopus* is the principal reservoir for Lyme disease (Borreliosis) in North America.
• The species is expanding its northern range into southern Quebec causing the emergence of the illness in the region.
•Monitoring its health has become critical to determine its ability to colonize new territories.
•Studying its microbiome in particular can help estimating the pathogen pressure acting on the different populations.

Objectives

- To detect Borreliosis and other infections in mice using NGS methods.
- To determine the microbiome concordance level between different organs of a same individual.
- To investigate the geographic structure in the pathogenic bacterial presence.

Material and methods

• Sampling: 360 mice were captured in southern Quebec between summers 2011 and 2014.
•Bacterial screening was performed by sequencing the V5-V6 regions from the bacterial 16S rRNA from mouse livers, lungs and spleens, using a Miseq sequencing system (Illumina).

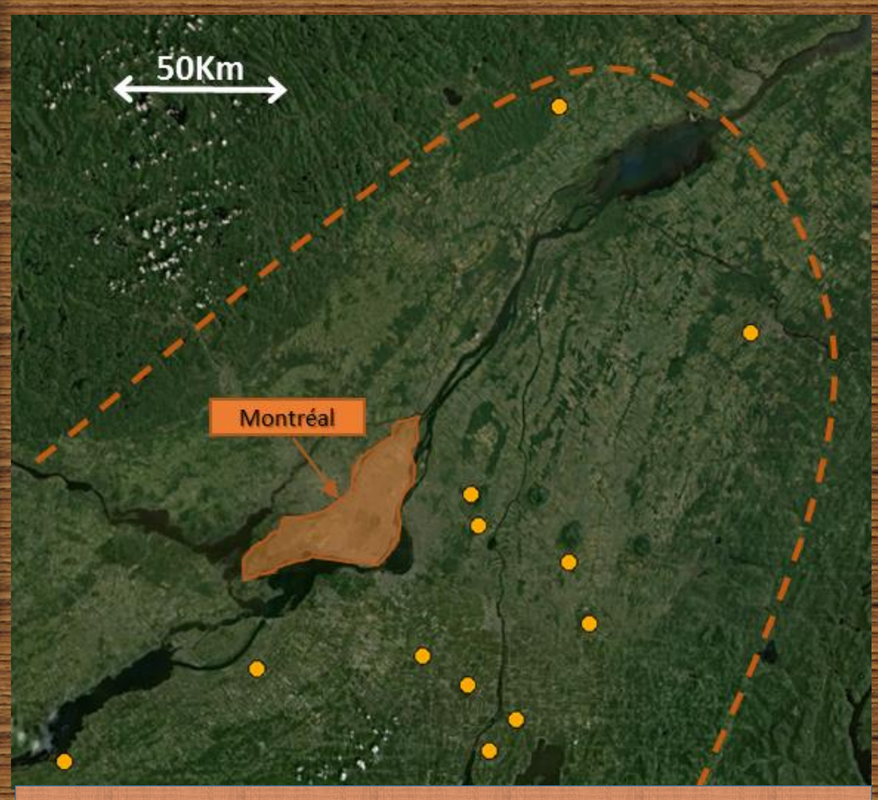

Fig. 1 : Sampling site map

Fig. 2 : *Peromyscus leucopus*

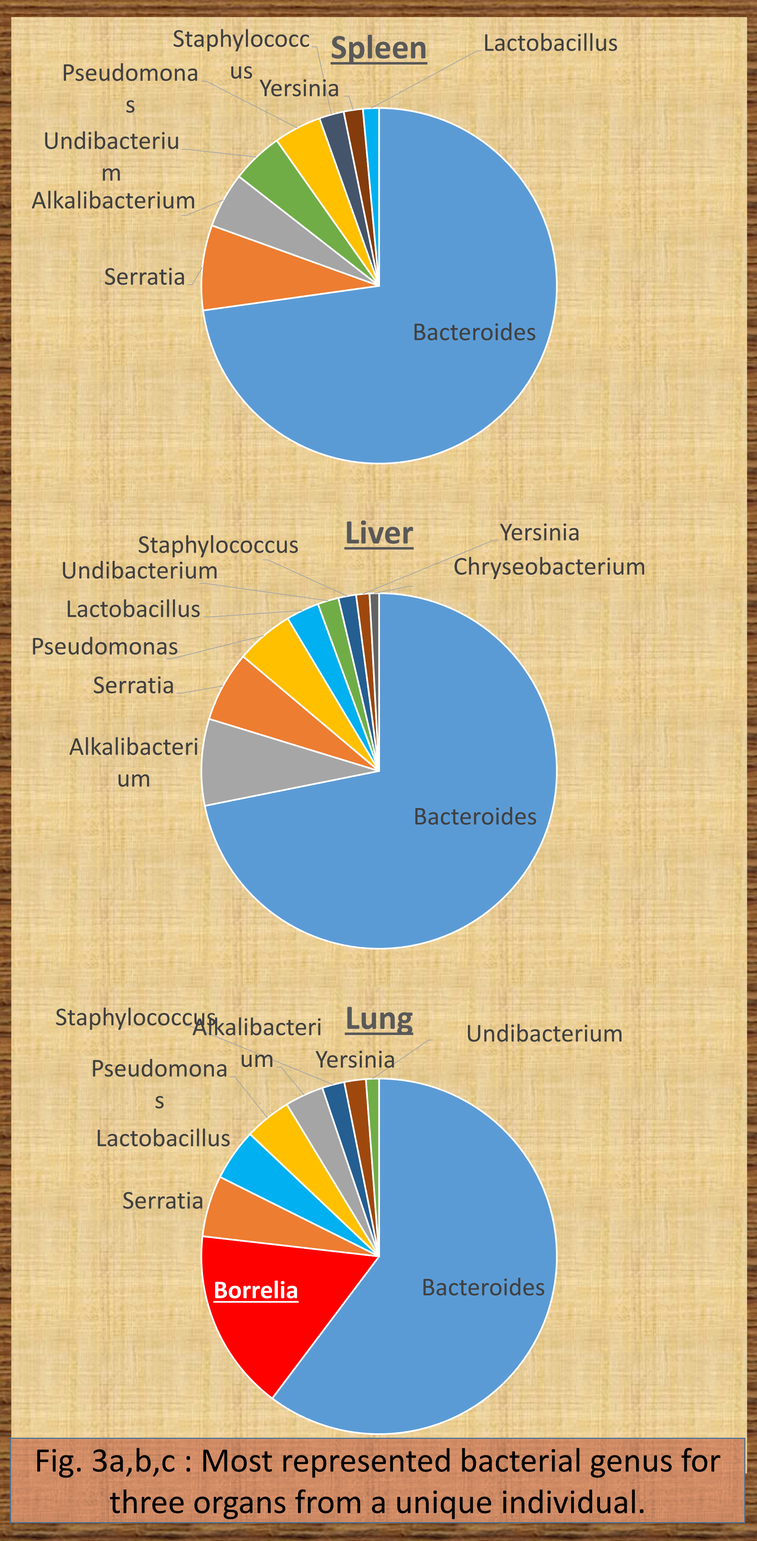

Fig. 3a,b,c : Most represented bacterial genus for three organs from a unique individual.

Preliminary results and discussion

- The microbiome of 213 mice has been succesfully determined.
- Excepted for *Borrelia*, microbiomes show consistent results between the three organs and among the liver triplicate in the studied sample.
- The liver and spleen screenings could not confirm the presence of *Borrelia* in the 3 mice known to be positive (using markers specifics to *Borrelia burgdorferi* on DNA extracted from heart tissues). However lung screening could detect it in 2 out of the 3 infected mice.
- Pathogen bacteria like *Bartonella, Yersinia* and *Ehrlichia* have been detected in several mice.

Perspectives

To Test two opposed theories (central-marginal and enemy release hypothesis) concerning the expansion of the species distribution range in southern Quebec.
➔ The present data will be associated with other parameters such as:

- Genetic diversity related to the immune system (MHC genes);
- Gastrointestinal helminth presence;
- Long term stress level;
- Body condition index;
- Spleen and testis size.

Funding: