Pathobiome of the Lyme disease principal reservoir in southern Quebec (*Peromyscus leucopus*)

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**Introduction**

- *Peromyscus leucopus* is the principal reservoir for the Lyme disease (*Borreliosis*) in North America.
- The species is expanding its northern range toward southern Quebec causing the emergence of the disease in the region.
- Two genetic clades of *Peromyscus* exist, separated by the St-Lawrence River.

**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 gene from mouse livers, lungs and spleens, using a Miseq sequencing system (Illumina).

**Objectives**

- Characterize the liver microbial community in *P. leucopus* individuals.
- Find the most appropriate organ for the detection of Borrelia between liver, lung and spleen.
- Explore infection patterns in *Bartonella* and *Borrelia* genera.
- Examine the effect of the host phylogeny on the liver microbiome.

**Results**

The liver microbiome of 203 mice was successfully determined. It is dominated by the Lactobacillus genus.

- 20 mice were diagnosed positive for *Borrelia* instead of 6 mice using the classical PCR method => better sensitivity of our method, especially using lungs as starting material (fig. 1).  
- First reported case of a wild mammal infected by Borrelia on the northern side of the St-Lawrence river.
- High prevalence of *Bartonella vinsonii arupensis* (>40%) detected across the studied region. Relation found between Bartonella prevalence and infection intensities among populations (Fig. 2). No effect of the host genotype on the liver microbiome. The two genetic clusters of mice separated by at least 2 Ma are characterized by the same microbiome (Fig. 3).

**Future perspectives**

- Establish a cartography of the Lyme disease risks based on vector and reservoir infection rates.
- Transpose the diagnostic method to humans?