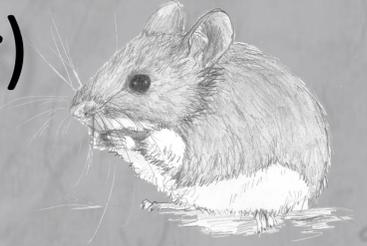


Pathobiome of the Lyme disease principal reservoir in southern Quebec (*Peromyscus leucopus*)

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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).

Sample	Classic PCR	Liver1	Liver2	Liver3	Spleen	Lung
1630	Positive	12	0	0	0	952
1667		44	10	0	0	971
1710		0	1	0	0	98
1793		227	49	/	0	403
1954		0	/	/	0	581
1970		165	186	/	25	45
1555	Negative	3	0	/	0	19
1595		37	0	/	72	8
1717		21	0	/	11	80
1719		5	0	/	0	2
1783		28	4	/	1	0
1792		22	19	/	6	477
1615		1	/	/	/	/
1835		1	/	/	/	/
1951		1	/	/	/	/
1957		2	/	/	/	/
1971		1	/	/	/	/
2009		2	/	/	/	/
1455		6*	/	/	/	/
1631		2*	/	/	/	/

Fig. 1 : *Borrelia* sp. detection using PCR targeting twomarkers for *B. burgdorferi*, and rarefied number of *Borrelia* reads within livers (up to 3 replicates), spleens and lungs using NGS.
(*) = number of reads before the rarefaction step but silenced after it. (/) = not tested

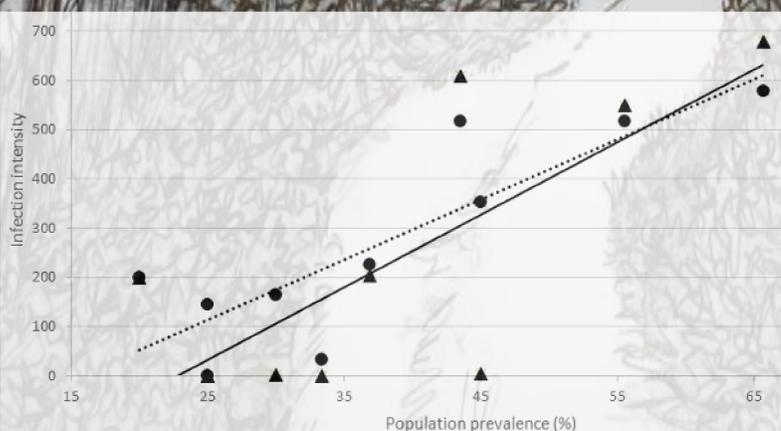


Fig. 2 : Relation between the prevalence of *Bartonella* within each population and the mean (circles, dashed line; $r^2=0.73$) and median (triangles, solid line; $r^2 = 0.58$) *Bartonella* infection intensities (number of *Bartonella* sp. sequences per infected mouse).

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.

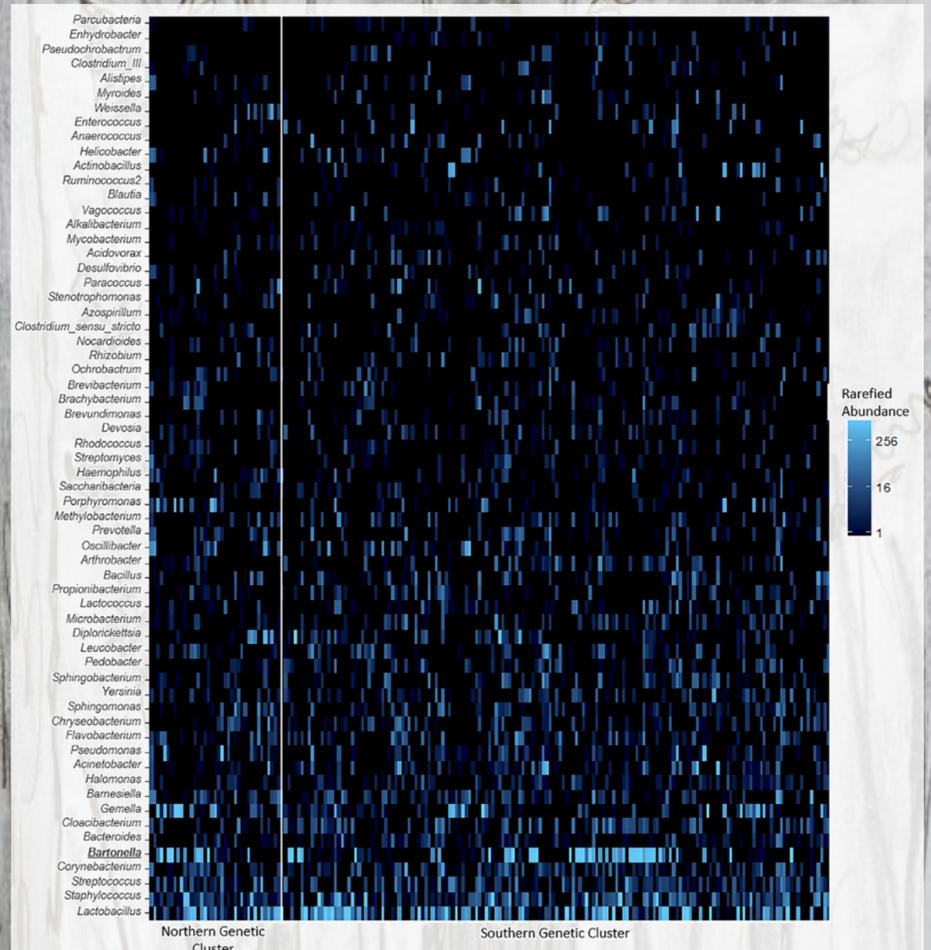


Fig. 3 : Heatmap representing the rarefied abundances from the most abundant genera in each sample. Genera are arranged in order of increasing prevalence from the top to the bottom. Samples on the x axis are ordered according to the genetic cluster they belong to.

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 sensibility 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?