Pathobiome of the Lyme disease principal reservoir in southern Quebec (Peromyscus leucopus) A. André^{1,2}; A. Mouton¹; V. Millien²; J. Michaux¹ 1: GeCoLAB, Université de Liège, institut botanique ; Belgique 2: Redpath Museum, McGill University; Montréal; Canada

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.

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.

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).

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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	1	1	0	581
1970		165	186	/	25	45
1555	Negative	3	0	/	0	19
1595		37	0	1	72	8
1717		21	0	/	11	80
1719		5	0	1	0	2
1783		28	4	1	1	0
1792		22	19	/	6	477
1615		1	1	/	/	1
1835		1	1	/	/	1
1951		1	1	1	/	1
1957		2	1	/	/	1
1971		1	1	/	1	1
2009		2	/	/	/	1
1455		6*	/	1	1 -	1
1631		2*	1	1	/	/
	1630 1667 1710 1793 1954 1970 1555 1595 1595 1717 1719 1783 1783 1783 1792 1615 1835 1951 1951 1957 1971 2009 1455	1630 Positive 1667	1630 Positive 12 1667 44 1710 0 1793 227 1954 0 1970 165 1555 Negative 3 37 1717 21 1793 227 1954 0 1970 165 1555 Negative 3 37 1717 21 1719 5 1783 28 1792 22 1615 1 1835 1 1951 1 1957 2 1971 1 2009 2 1455 6*	1630 Positive 12 0 1667 44 10 1710 0 1 1793 227 49 1954 0 / 1970 165 186 1555 Negative 3 0 1595 37 0 1 1717 21 0 1 1718 28 4 1 1792 22 19 1 1615 1 / 1 1835 1 / 1 1951 1 / 1 1957 2 / 1 1957 2 / 1 1957 2 / 1 2009 2 / 1 1455 6* / 1	1630 Positive 12 0 0 1667 44 10 0 1710 0 1 0 1793 227 49 / 1954 0 / / 1970 165 186 / 1555 Negative 3 0 / 1595 377 0 / / 1717 21 0 / / 1717 21 0 / / 1717 21 0 / / 17183 28 4 / / 1792 22 19 / / 1615 1 / / / 1835 1 / / / 1951 1 / / / 1957 2 / / / 1971 1 / / /	1630 Positive 12 0 0 0 1667 44 10 0 0 1710 0 1 0 0 1793 227 49 / 0 1954 0 / / 0 1954 0 / 0 0 1970 165 186 / 25 1555 Negative 3 0 / 0 1595 377 0 / 72 1717 21 0 / 11 1792 28 4 / 1 1792 22 19 6 1 1615 1 / / / 1835 1 / / 1 1951 1 / / 1 1957 2 / / 1 1971 1 / / 1

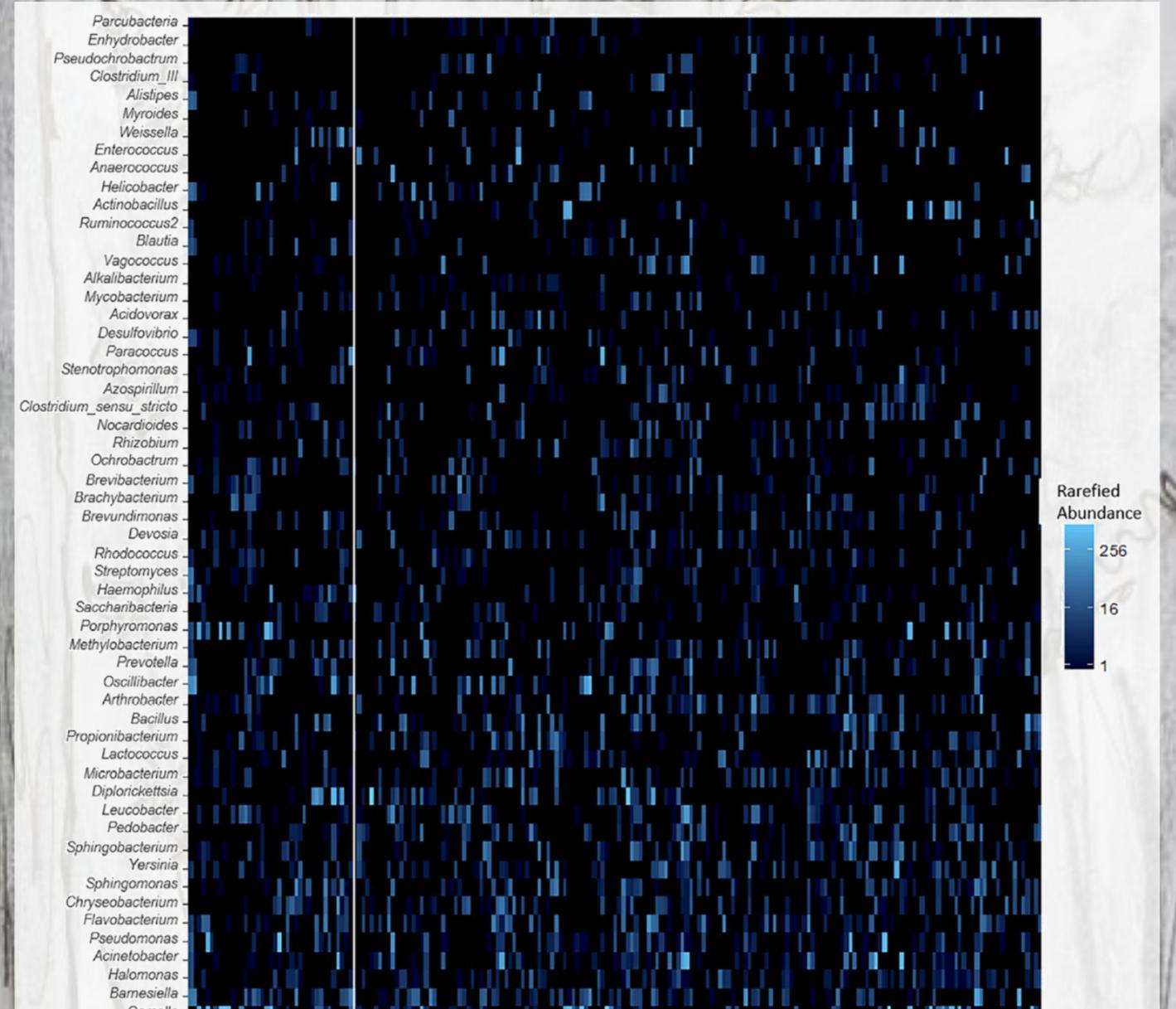
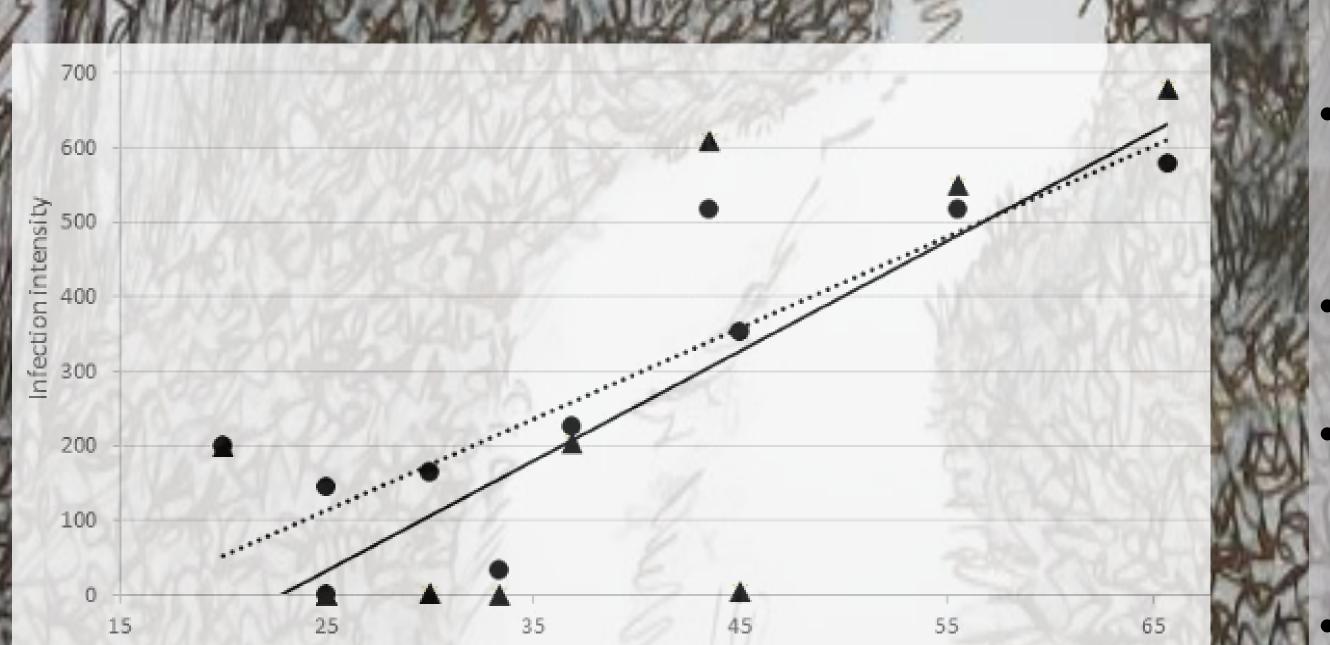


Fig. 1 : Borrelia sp. detection using PCR targeting twomarkers for B. burgdorferi, and rarefied number of Borrelia reads within livers (up to 3 replicates), spleens and lungs using NGS. (*) = number of reads before the rarefaction step but silenced after it. (/) = not tested



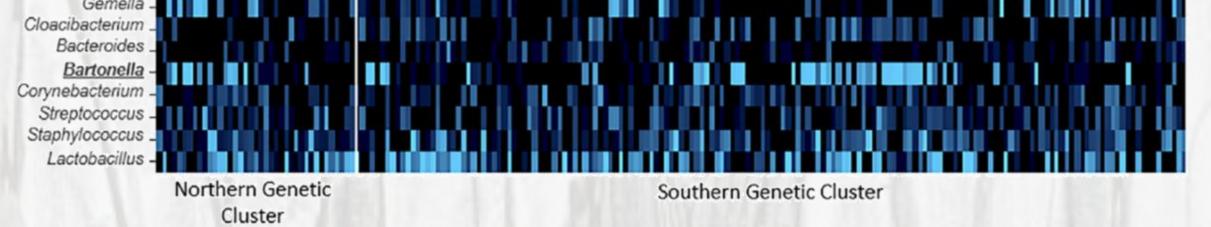


Fig. 3 : Heatmap representing the rarefied abundances from the most abundant genera in each sample. Genera are arranged in order of increasing prevalence from the top to the bottom. Samples on the x axis are ordered according to the genetic cluster they belong to.

Results

- The liver microbiome of 203 mice was succesfully 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

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Population prevalence (%)

Fig. 2 : Relation between the prevalence of Bartonella within each population and the mean (circles, dashed line; r²=0.73) and median (triangles, solid line; r² = 0.58) Bartonella infection intensities (number of Bartonella sp. sequences per infected mouse).

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.

McGill

Transpose the diagnostic method to humans?

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