

# Pathobiome diversity and co-infection patterns in a community of rodents

Jessica Abbate, Maxime Galan, Yannick Chaval, Cécile Gotteland, Maria Razzauti, Tarja Sironen, Liina Voutilainen, Heikki Henttonen, Patrick Gasqui, Jean-François Cosson, Nathalie Charbonnel

AGENCE NATIONALE DE LA RECHERCHE  
**ANR**

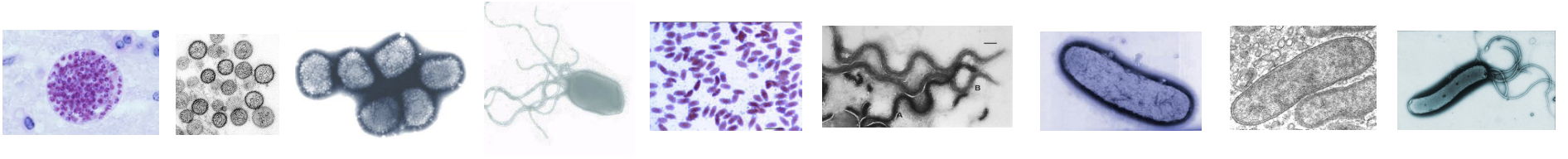
Pathobiome Paris, June 24, 2015

[jessie.abbate@gmail.com](mailto:jessie.abbate@gmail.com)

**CBGP**

INRA - Montpellier

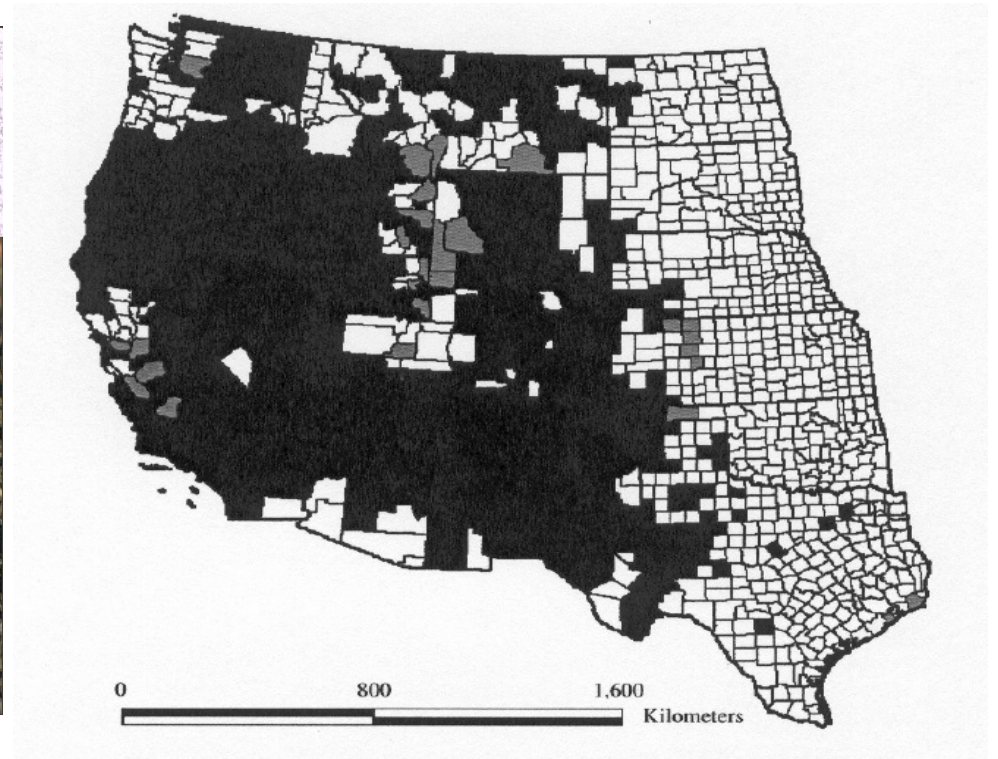
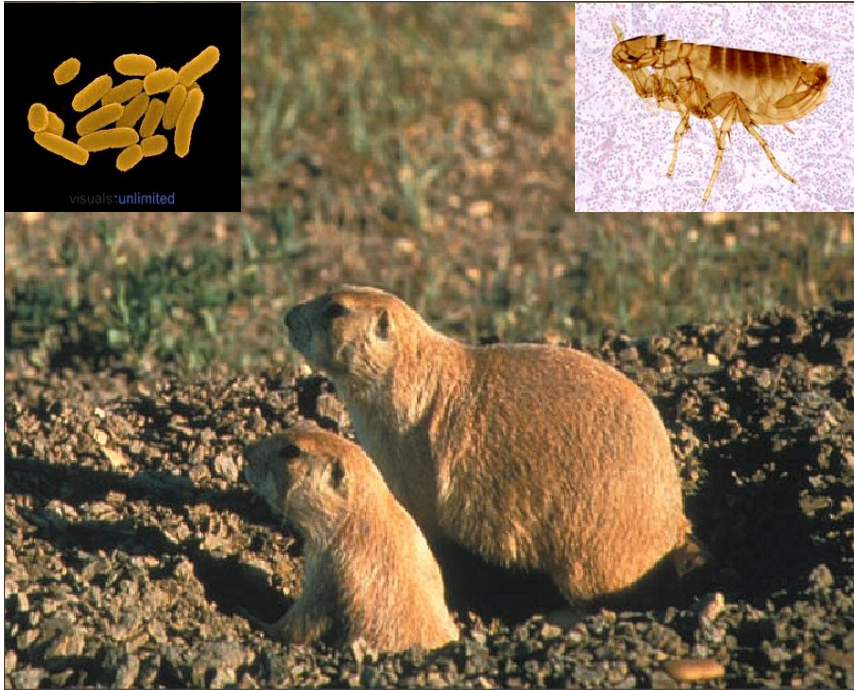




# Background



# DETERMINANTS of DISEASE DISTRIBUTION in NATURE



Example:

Sylvatic Plague in small mammals limited to west of the 100th Meridian

Antolin et al. 2002; Strapp et al. 2004

# DETERMINANTS of DISEASE DISTRIBUTION in NATURE

Natural History & Population Dynamics

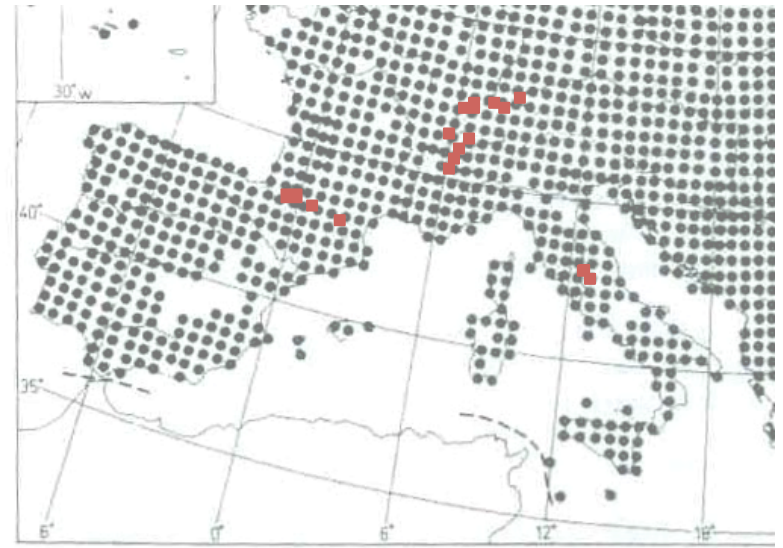
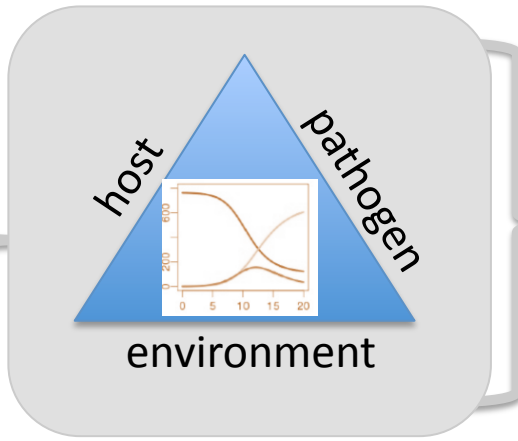
Geographic Distribution & Evolutionary History

Host – Pathogen Genetics

Phenotype & Life-History Traits

Environmental Variables

Ecological Interactions

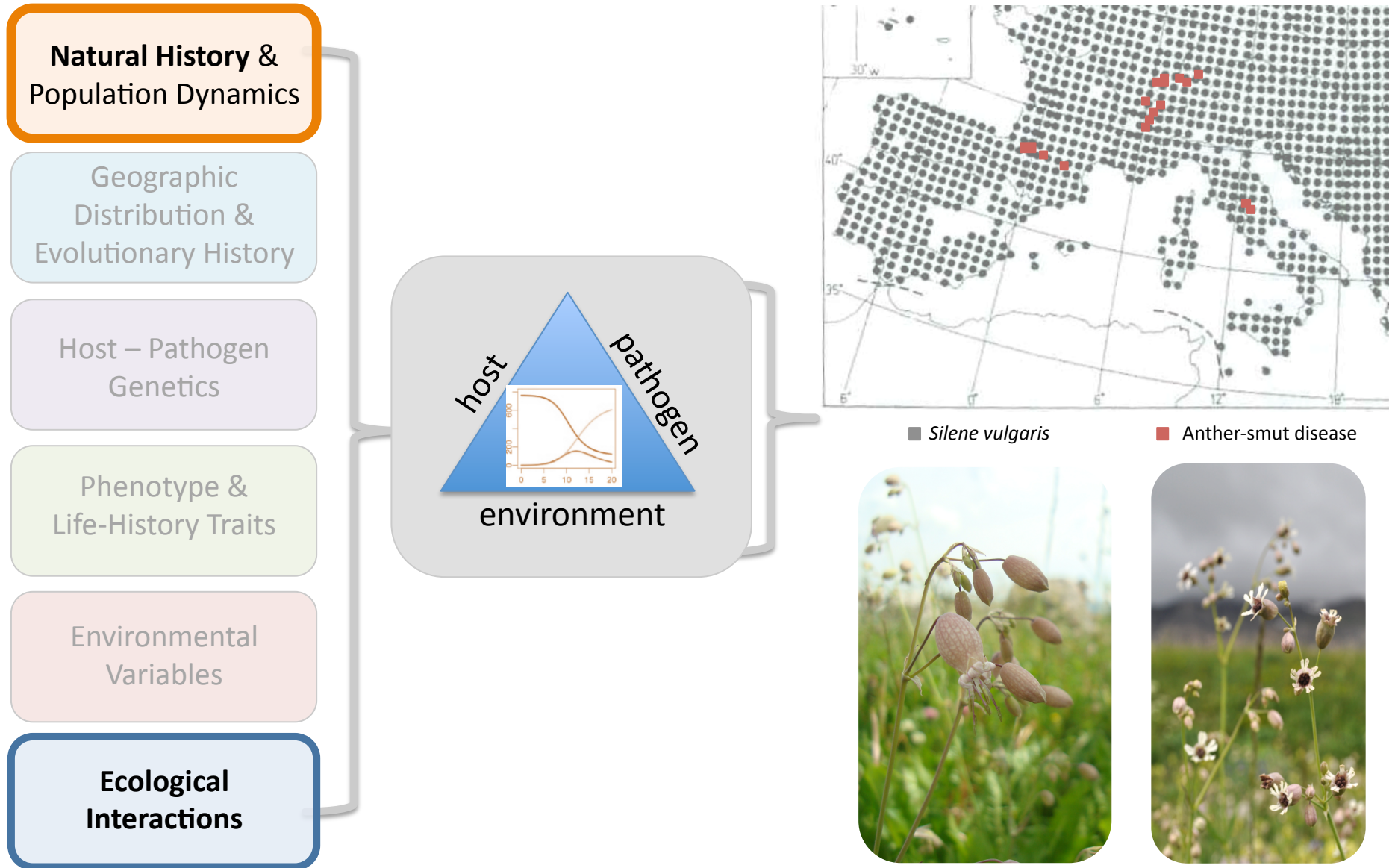


■ *Silene vulgaris*      ■ Anther-smut disease



Abbate & Antonovics 2014 *Oikos*

# DETERMINANTS of DISEASE DISTRIBUTION in NATURE



Abbate & Antonovics 2014 *Oikos*

# DETERMINANTS of DISEASE DISTRIBUTION in NATURE

Natural History & Population Dynamics

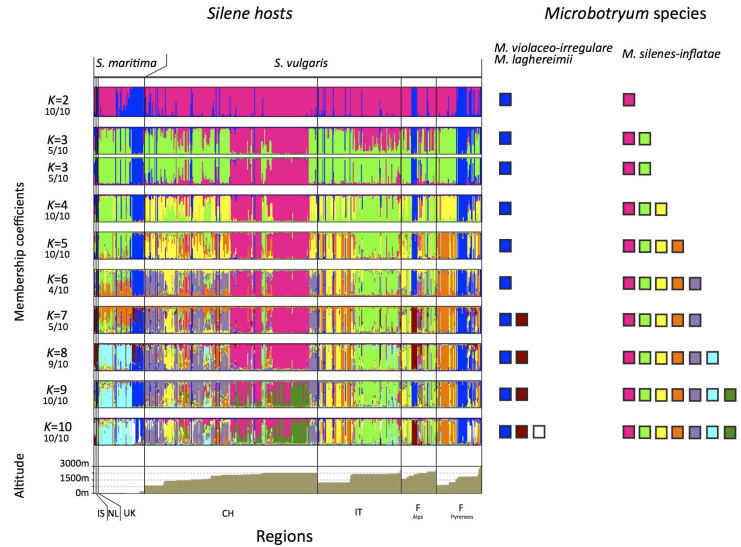
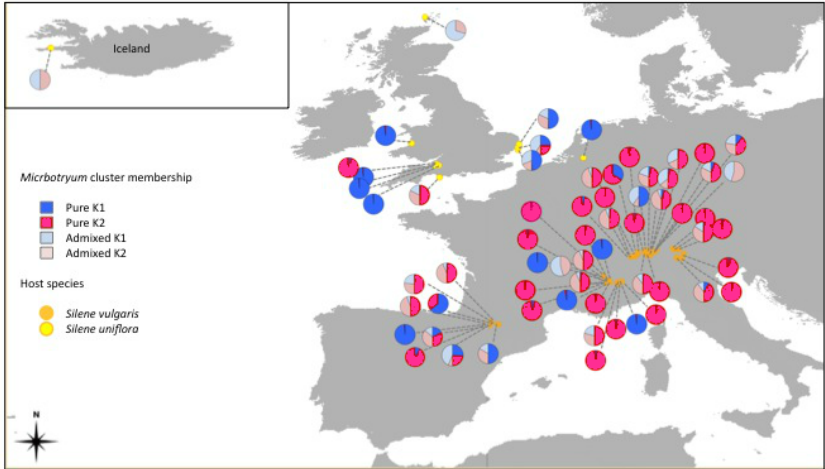
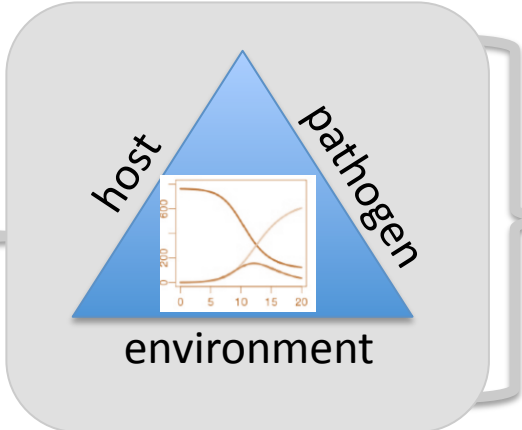
Geographic Distribution & Evolutionary History

Host – Pathogen Genetics

Phenotype & Life-History Traits

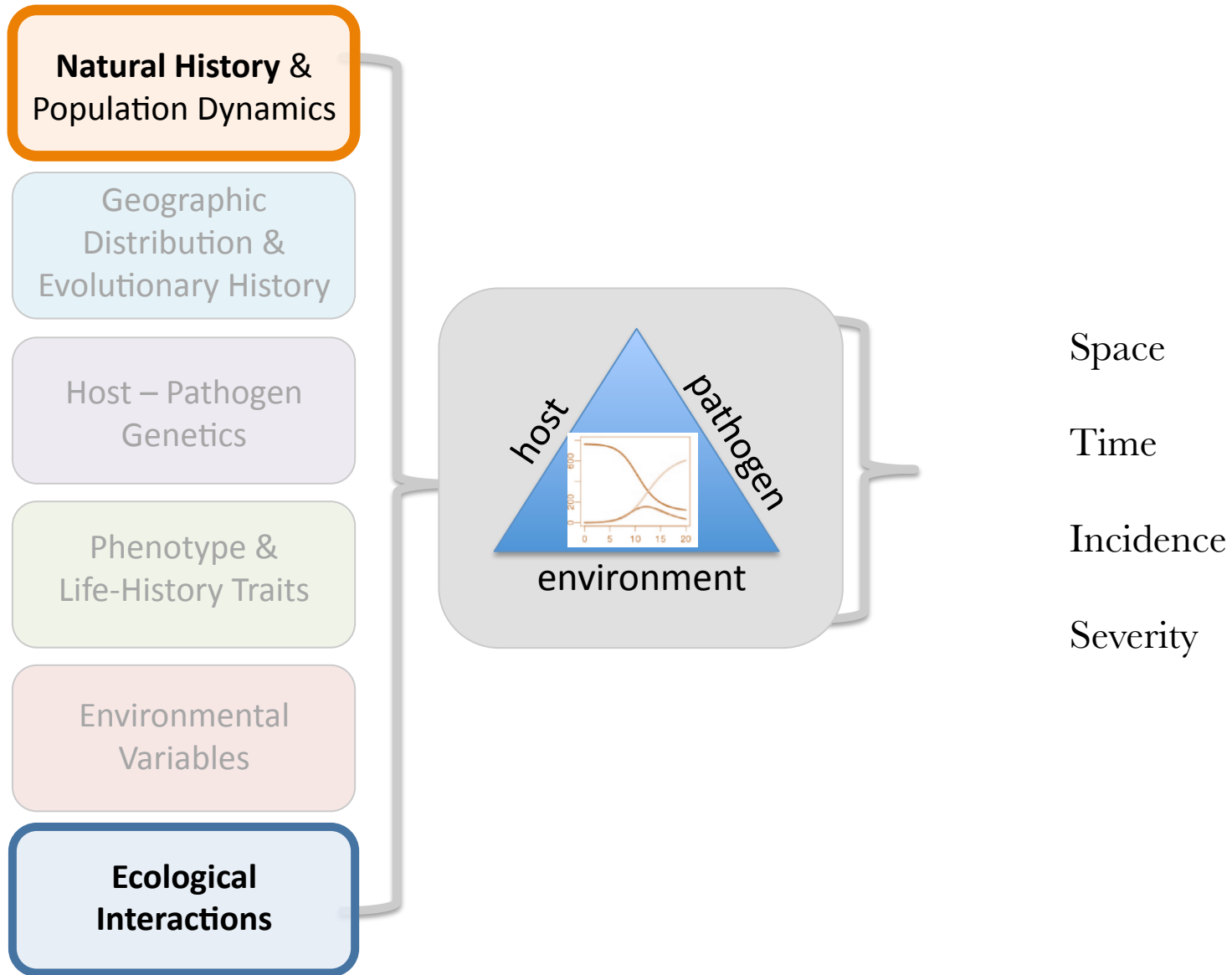
Environmental Variables

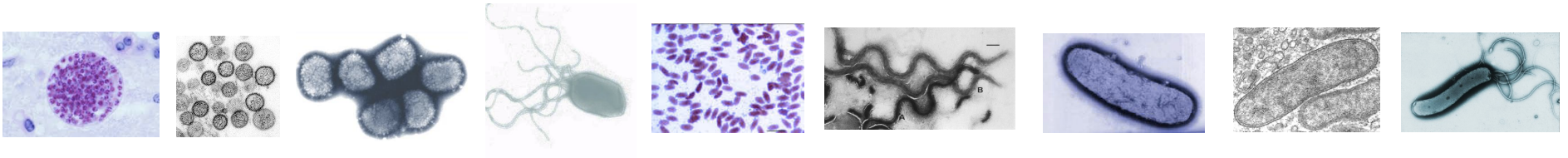
Ecological Interactions



Gladieux, Abbate, Giraud, et al. *in prep*

# DETERMINANTS of DISEASE DISTRIBUTION in NATURE





# The study

Pathobiome diversity and co-infection patterns in a community of rodents





## Rodent blood infections



# Pathobiome diversity (natural history)

&

## co-infection patterns

**Natural History &  
Population Dynamics**

Geographic  
Distribution &  
Evolutionary History

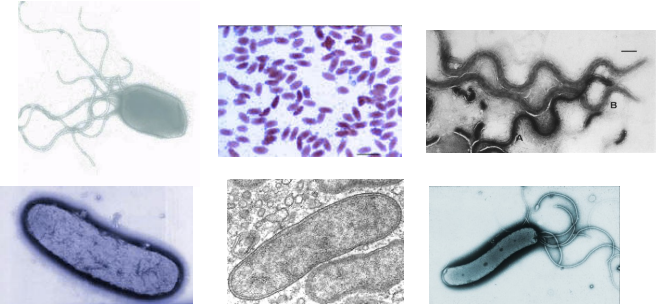
Host – Pathogen  
Genetics

Phenotype &  
Life-History Traits

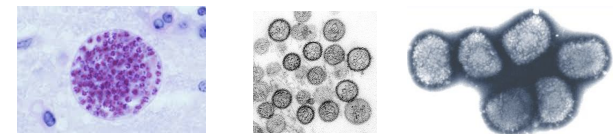
Environmental  
Variables

**Ecological  
Interactions**

- Splenic microbiota (16S MiSeq)



- Viral and protozoan seropositivity



- Nematodes & Ectoparasites

**Natural History & Population Dynamics**

Geographic Distribution & Evolutionary History

Host – Pathogen Genetics

Phenotype & Life-History Traits

Environmental Variables

**Ecological Interactions**

**Cricetidae**



*Microtus agrestis*  
(field vole)



*Microtus arvalis*  
(common vole)



*Microtus subterraneus*  
(European pine vole,  
Common pine vole)



*Myodes glareolus*  
(bank vole)



*Arvicola scherman*  
(Montane water vole)

**Muridae**

*Apodemus sylvaticus*  
(wood mouse)



*Apodemus flavicollis*  
(yellow tailed  
mouse)



*Rattus norvegicus*  
(brown rat)



**Natural History &  
Population Dynamics**

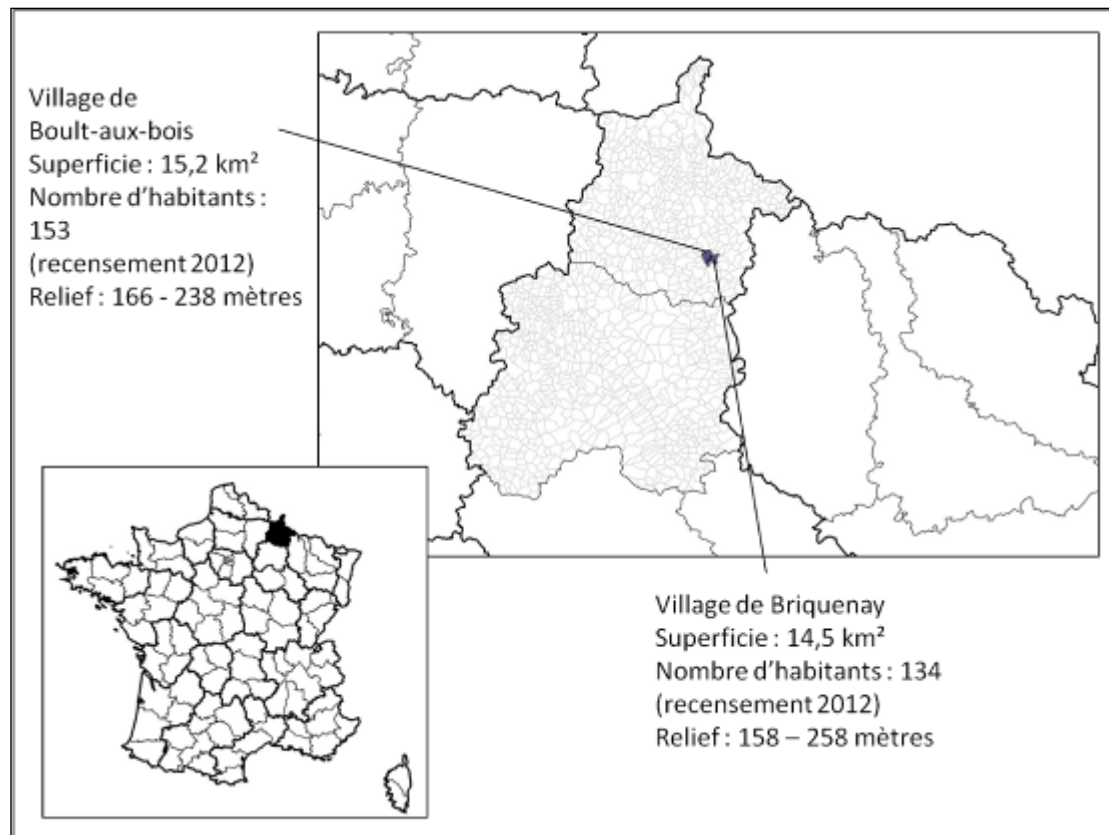
Geographic  
Distribution &  
Evolutionary History

Host – Pathogen  
Genetics

Phenotype &  
Life-History Traits

Environmental  
Variables

**Ecological  
Interactions**



**Figure 7 : Localisation et identité des deux sites d'études**

**Natural History & Population Dynamics**

Geographic Distribution & Evolutionary History

Host – Pathogen Genetics

Phenotype & Life-History Traits

Environmental Variables

**Ecological Interactions**



Forestiers



Prairiaux



Anthropisés



## Natural History & Population Dynamics

Geographic Distribution & Evolutionary History

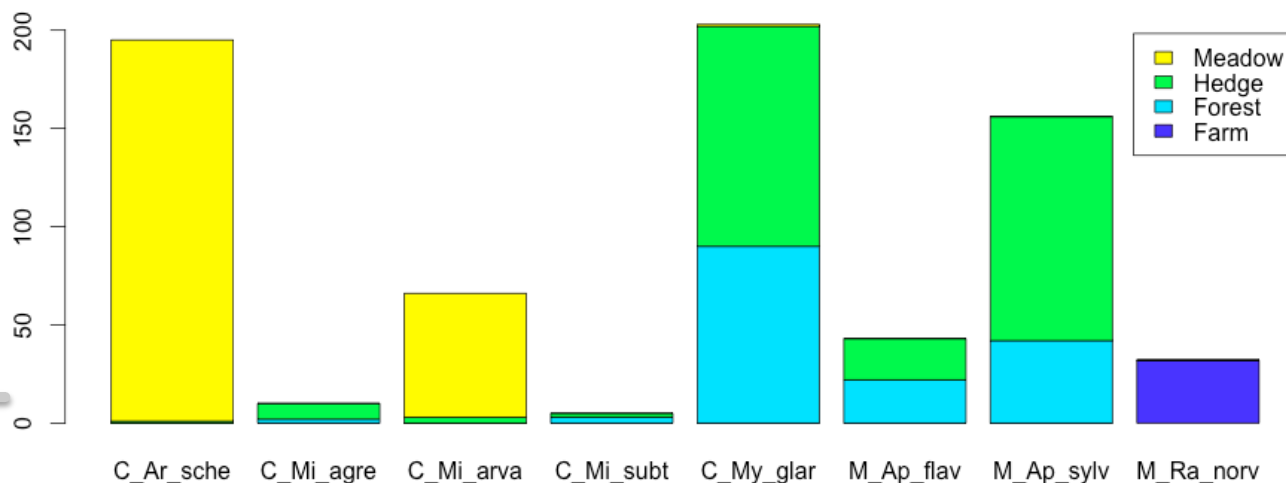
Host – Pathogen Genetics

Phenotype & Life-History Traits

Environmental Variables

## Ecological Interactions

N=710



**Natural History & Population Dynamics**

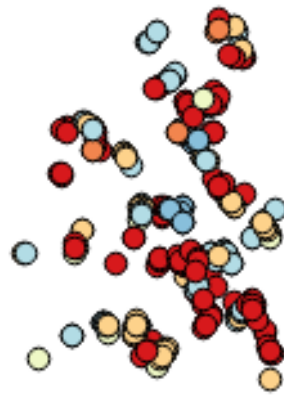
Geographic Distribution & Evolutionary History

Host – Pathogen Genetics

Phenotype & Life-History Traits

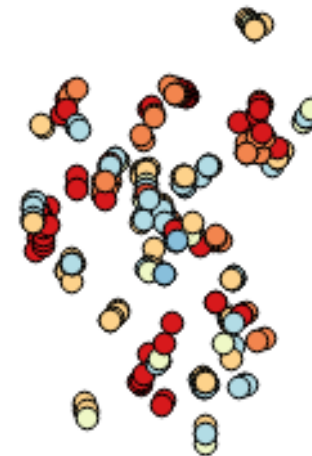
Environmental Variables

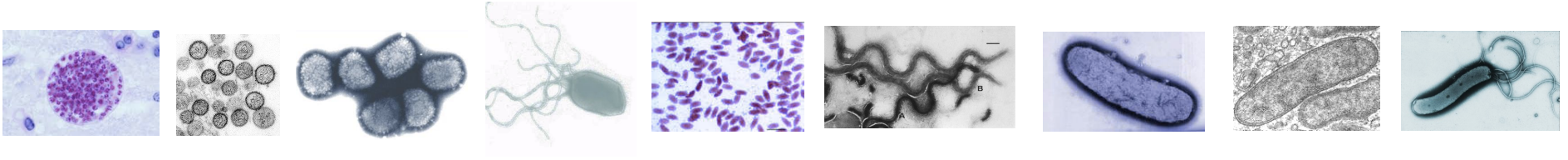
**Ecological Interactions**



**hosts**

- C\_Ar\_sche
- C\_Mi\_agre
- C\_Mi\_arva
- C\_Mi\_subt
- C\_My\_glar
- M\_Ap\_flav
- M\_Ap\_sylv
- M\_Ra\_norv





# Pathobiome Diversity (natural history)



# Pathobiome diversity (natural history)

Natural History &  
Population Dynamics

Geographic  
Distribution &  
Evolutionary History

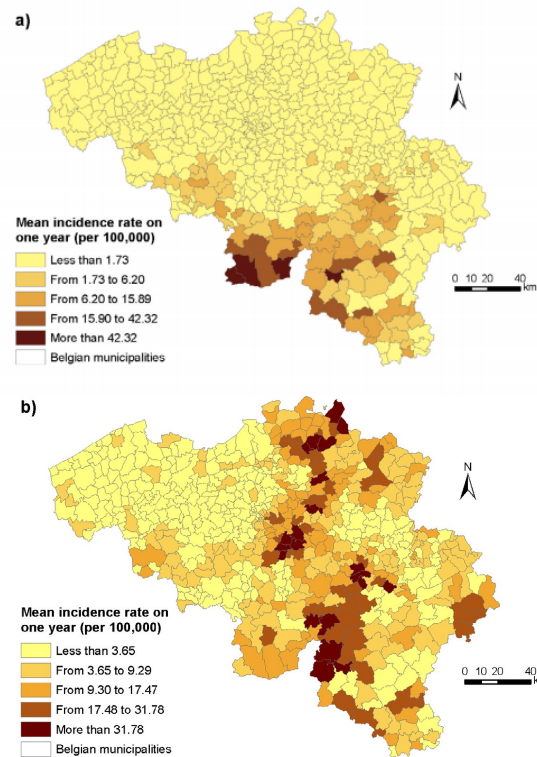
Host – Pathogen  
Genetics

Phenotype &  
Life-History Traits

Environmental  
Variables

Ecological  
Interactions

Determinants of the geographic distribution of Puumala virus and Lyme borreliosis infections in Belgium





# Pathobiome diversity (natural history)

Natural History &  
Population Dynamics

Geographic  
Distribution &  
Evolutionary History

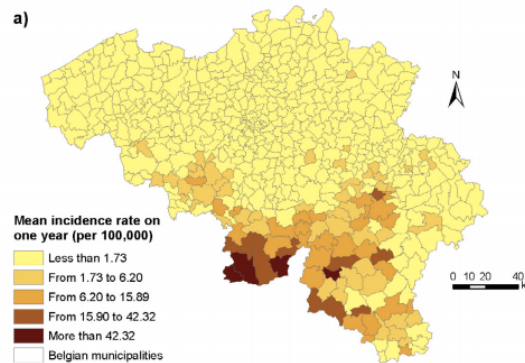
Host – Pathogen  
Genetics

Phenotype &  
Life-History Traits

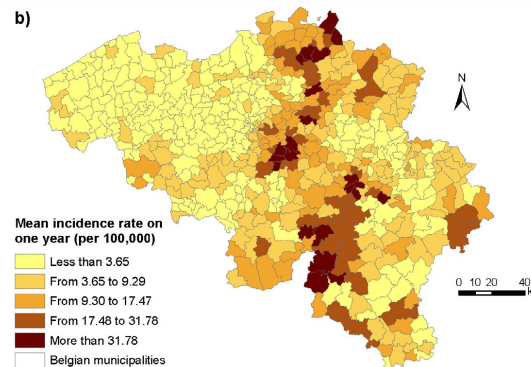
Environmental  
Variables

Ecological  
Interactions

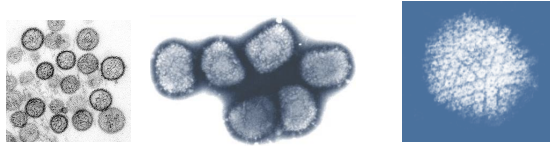
Determinants of the geographic distribution of Puumala virus and Lyme borreliosis infections in Belgium



*Myodes glareolus*  
(bank vole)



*Ixodes ricinus*



## Viruses (N=675)

- Cowpox Virus (OPXV)

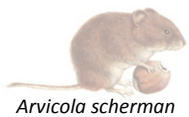
32.9% prev.

- Hantaviruses  
(PUUV, TULV)

2.4% prev.

- Lymphocytic  
Choriomeningitis Virus  
(LCMV)

3.2% (2/62) *M. arvalis*



*Arvicola scherman*



*Miodes agrestis*



*M. arvalis*



*M. subterraneus*



*Myodes glareolus*



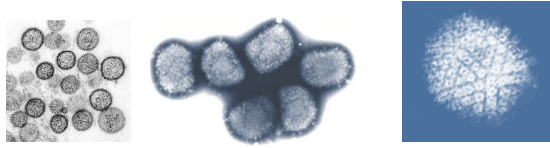
*Apo. flavicolus*



*Apo. sylvaticus*



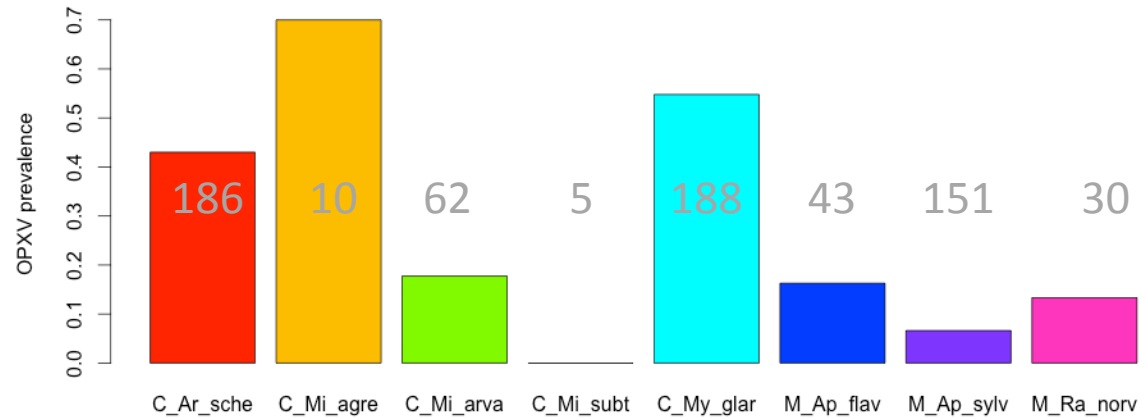
*Rattus norvegicus*



## Viruses (N=675)

- Cowpox Virus (OPXV)

32.9% prev.



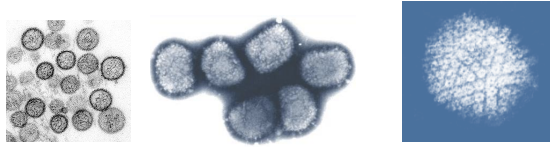
- Hantaviruses  
(PUUV, TULV)

2.4% prev.

- Lymphocytic  
Choriomeningitis Virus  
(LCMV)

3.2% (2/62) *M. arvalis*

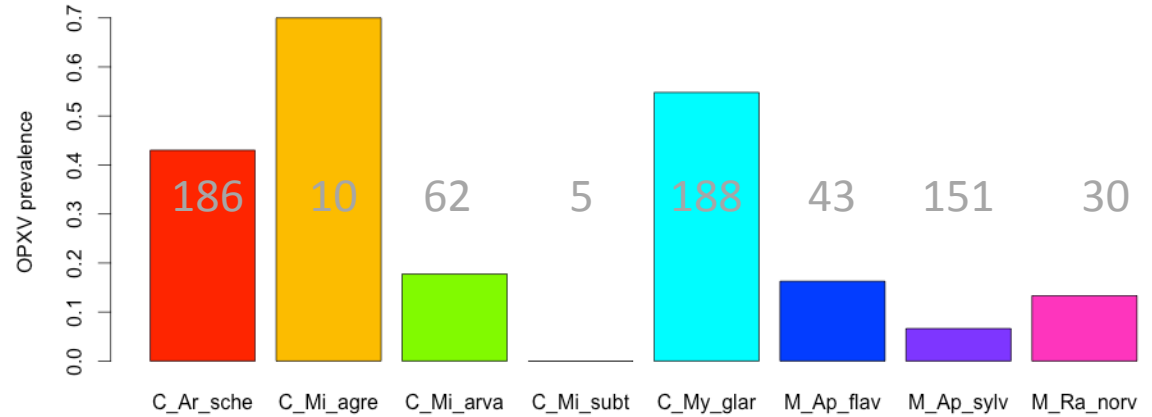




## Viruses (N=675)

- Cowpox Virus (OPXV)

32.9% prev.



- Hantaviruses (PUUV, TULV)

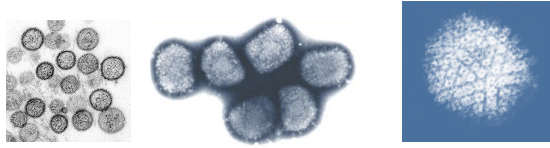
2.4% prev.



- Lymphocytic Choriomeningitis Virus (LCMV)

3.2% (2/62) *M. arvalis*

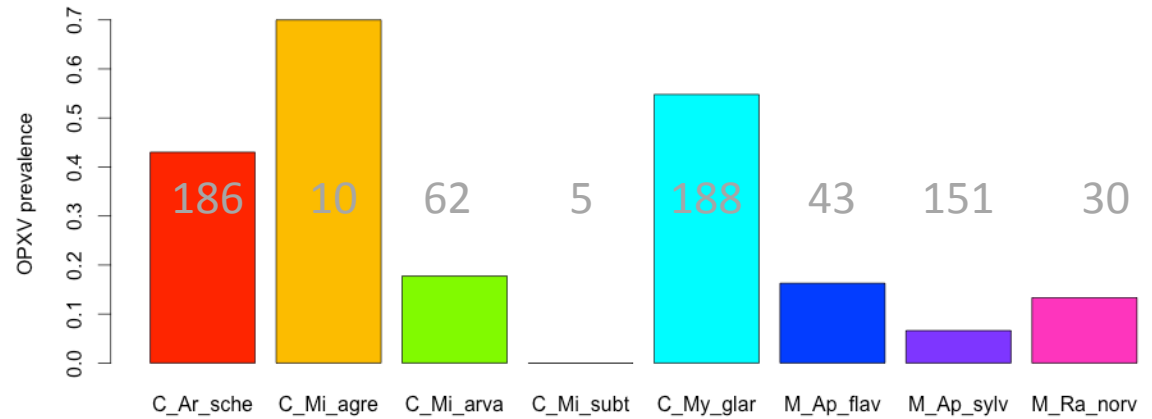




## Viruses (N=675)

- Cowpox Virus (OPXV)

32.9% prev.



- Hantaviruses (PUUV, TULV)

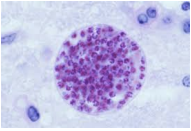
2.4% prev.



- Lymphocytic Choriomeningitis Virus (LCMV)

3.2% (2/62) *M. arvalis*





Protazoa(n)

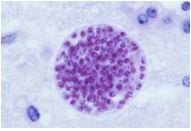
- *Toxoplasma gondii* antibodies (N=685)

7.2% prev.

- *Toxoplasma* or other eukaryotic (*Coccidian*) undefined OTU (N=315)  
(16S - MiSeq)

4.1% prev.

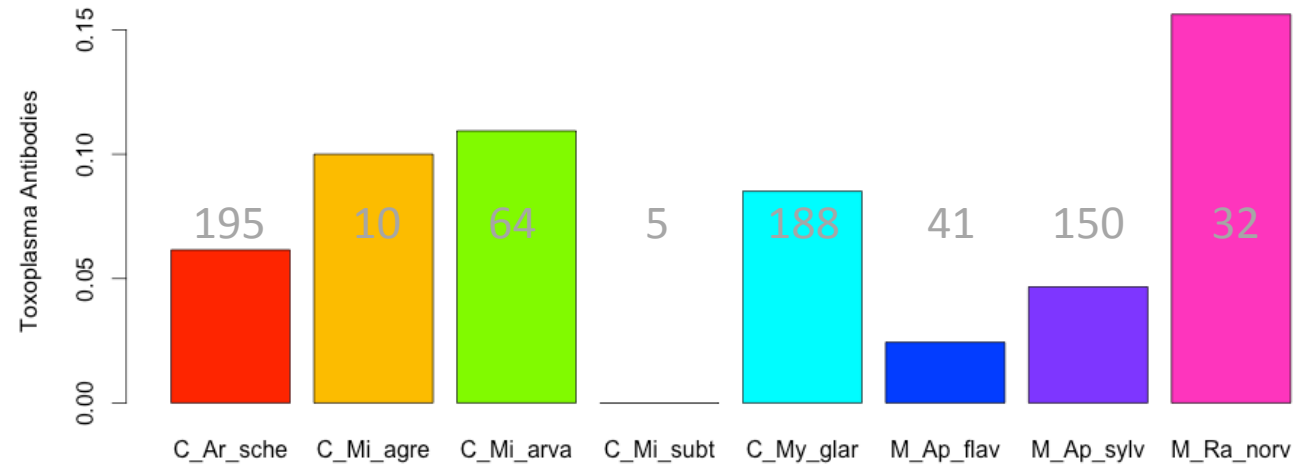




## Protazoa(n)

- Toxoplasma gondii* antibodies (N=685)

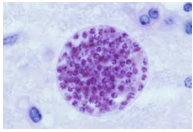
7.2% prev.



- Toxoplasma* or other eukaryotic (*Coccidian*) undefined OTU (N=315)  
(16S - MiSeq)

4.1% prev.

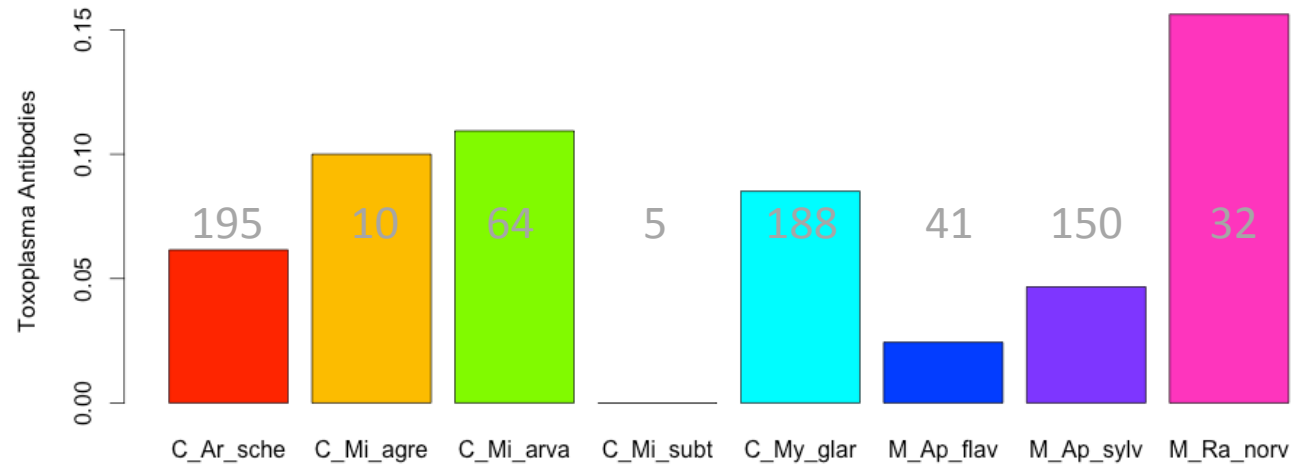




## Protazoa(n)

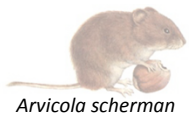
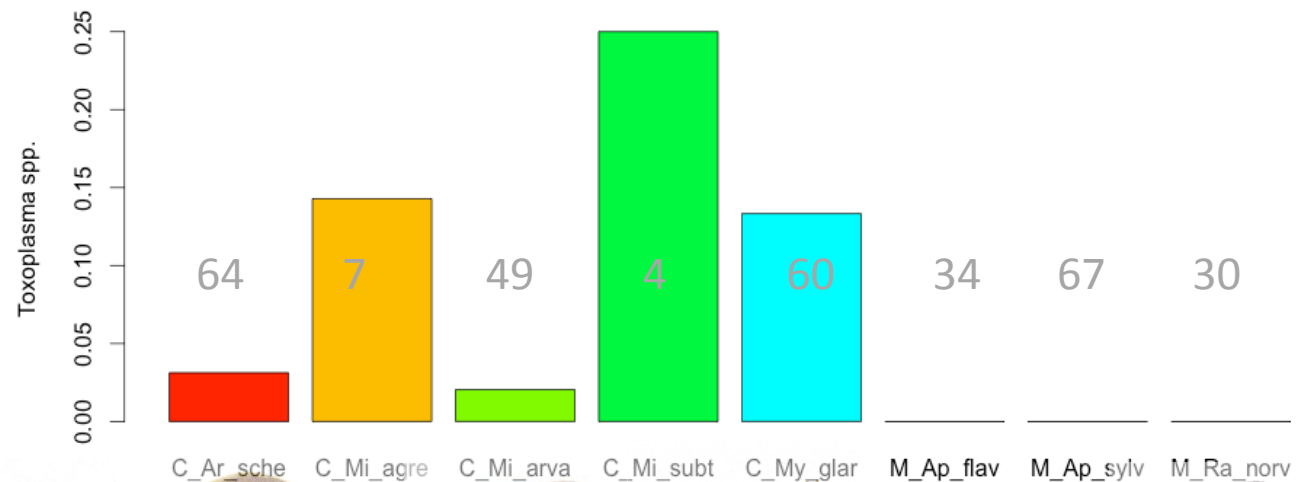
- Toxoplasma gondii* antibodies (N=685)

7.2% prev.

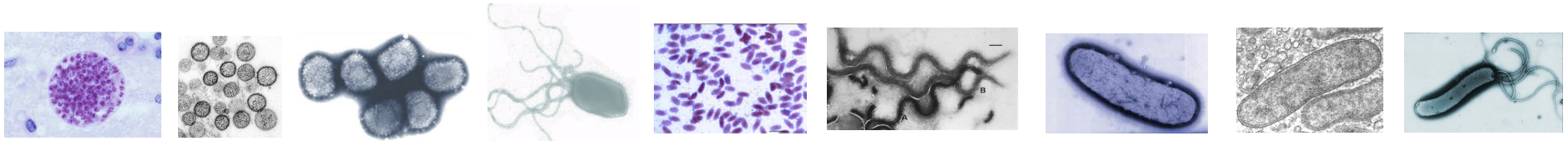


- Toxoplasma* or other eukaryotic (*Coccidian*) undefined OTU (N=315)  
(16S - MiSeq)

4.1% prev.





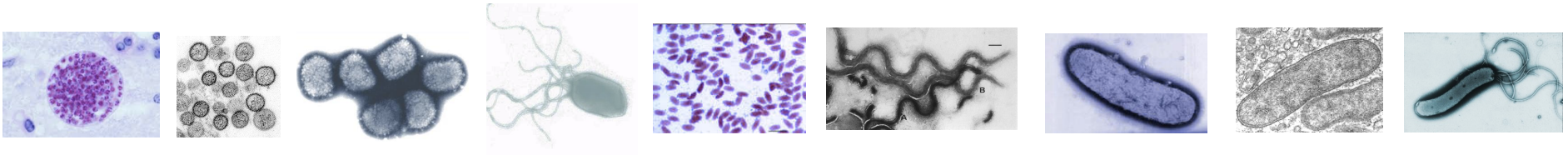


## Bacteria MiSeq (N=315)

- 954 OTUs >50 reads ; 591 prev > 0
- 184 OTUs >500 reads ; 146 with prev >0
- 31 pathogenic OTUs (15 species minimum)

- Bartonella (3 OTUs) 78.4%
- Mycoplasma (12 OTUs) 45.7%
- Helicobacter (2 OTUs) 14.0%
- Opportunists (9 OTU) 9.8%
- Yersinia (1 OTU) 5.4%
- Rickettsia (1 OTU) 2.5%
- Cand. Neoehrlichia
- Orientia
- Borrelia (3 OTUs) 1.2% (4 indiv.)
- Brevinema (1 OTU) 0.9% (3 indiv.)
- Rickettsiella
- Acrobacter
- Leptospira
- Spiroplasma (1 OTU) 0.6% (2 indiv.)
- Fusobacterium
- Neisseria 0.3% (1 indiv.)





## Bacteria MiSeq (N=315)

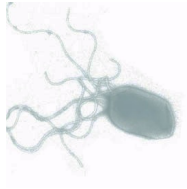
- 954 OTUs >50 reads ; 591 prev > 0
- 184 OTUs >500 reads ; 146 with prev >0

• <i>Bartonella</i> (3 OTUs)	78.4%	
• <i>Mycoplasma</i> (12 OTUs)	45.7%	
• <i>Helicobacter</i> (2 OTUs)	14.0%	
• Opportunists (9 OTU)	9.8%	
• <i>Yersinia</i> (1 OTU)	5.4%	
• <i>Rickettsia</i> (1 OTU)	2.5%	
• <i>Cand. Neoehrlichia</i>		
• <i>Orientia</i>		
• <i>Borrelia</i> (3 OTUs)	1.2%	(4 indiv.)
• <i>Brevinema</i> (1 OTU)	0.9%	(3 indiv.)
• <i>Rickettsiella</i>		
• <i>Acrobacter</i>		
• <i>Leptospira</i>		
• <i>Spiroplasma</i> (1 OTU)	0.6%	(2 indiv.)
• <i>Fusobacterium</i>		
• <i>Neisseria</i>	0.3%	(1 indiv.)

True Presence/Absence

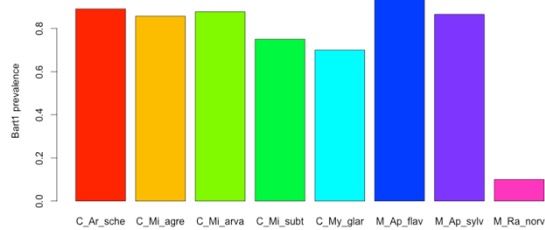
“Rare” species



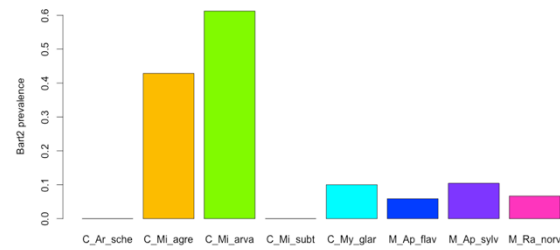


## Bartonella species : *Bartonella grahamii*, *B. doshiae*

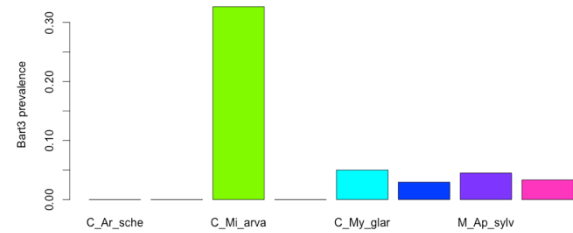
### Bartonella OTU 1 (100)



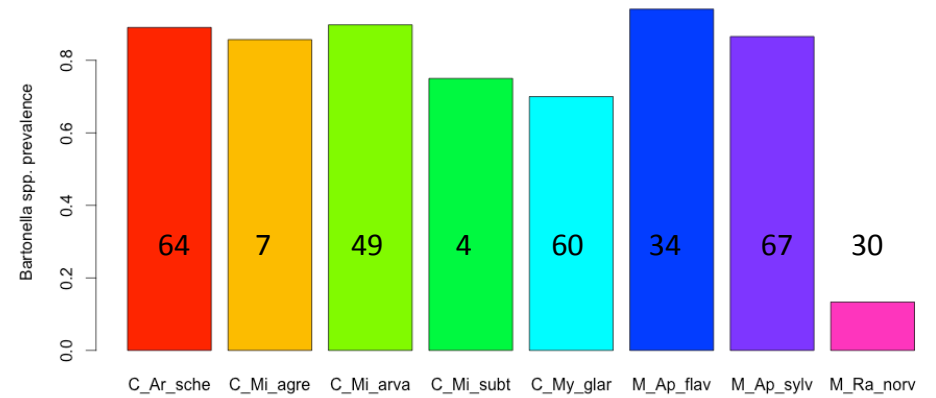
### Bartonella OTU 2 (92)



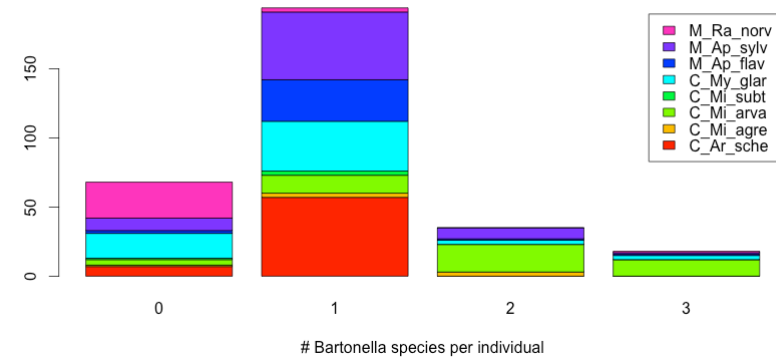
### Bartonella OTU 3 (74)



### Overall Bartnolla spp. prevalence



### Co-infection



*Arvicola scherman*

*Miodes agrestis*

*M. arvalis*

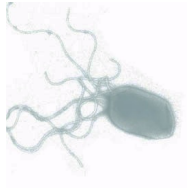
*M. subterraneus*

*Myodes glareolus*

*Apo. flavicolus*

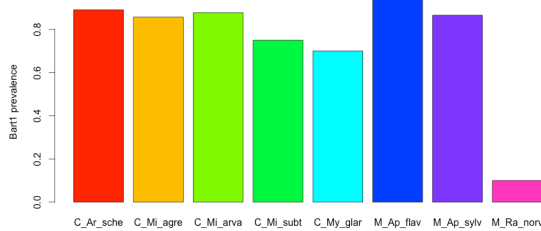
*Apo. Sylvaticus*

*Rattus norvegicus*

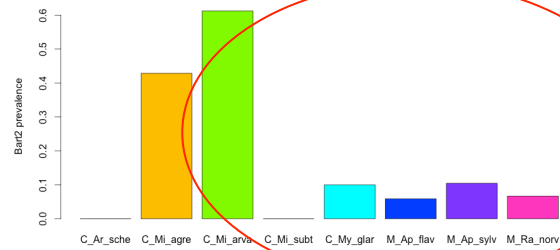


## Bartonella species : *Bartonella grahamii*, *B. doshiae*

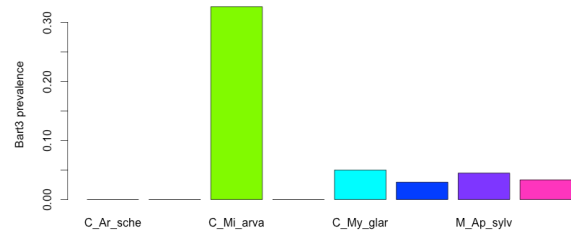
### Bartonella OTU 1 (100)



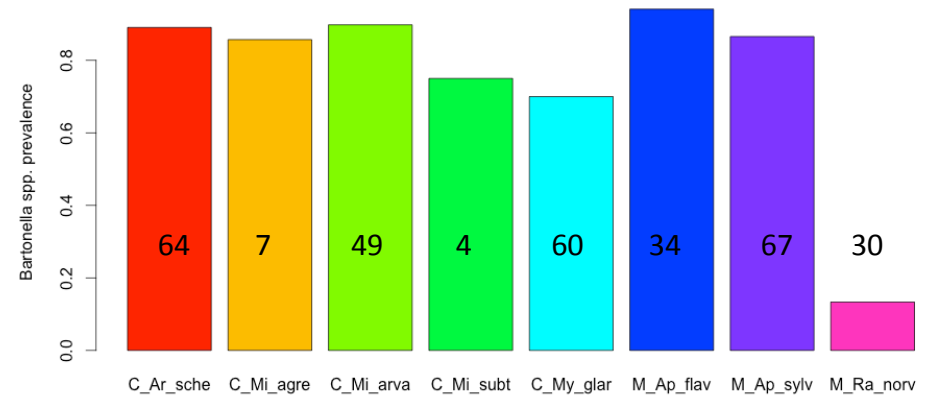
### Bartonella OTU 2 (92)



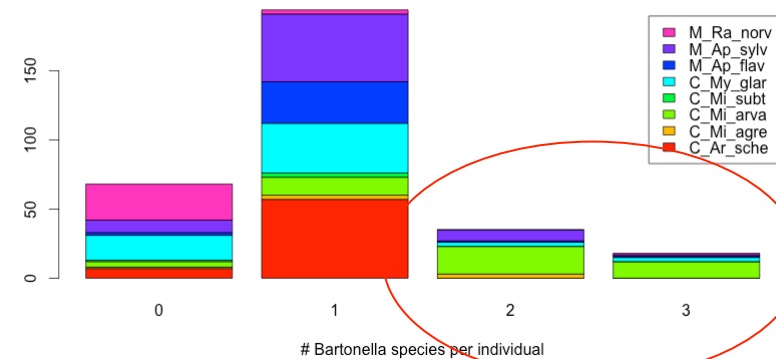
### Bartonella OTU 3 (74)

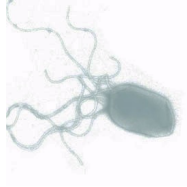


### Overall *Bartnolla* spp. prevalence



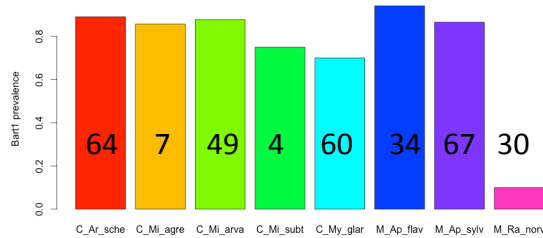
### Co-infection



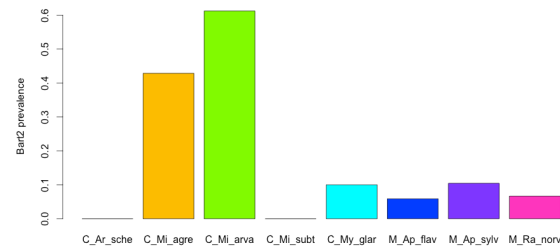


## Bartonella species : *Bartonella grahamii*, *B. doshiae*

### Bartonella OTU 1 (100)



### Bartonella OTU 2 (92)



## To be or not to be associated: power study of four statistical modeling approaches to identify parasite associations in cross-sectional studies

**Elise Vaumourin<sup>1,2\*</sup>, Gwenaël Vourc'h<sup>1</sup>, Sandra Telfer<sup>3</sup>, Xavier Lambin<sup>3</sup>, Dialdin Salih<sup>4</sup>, Ulrike Seitzer<sup>5</sup>, Serge Morand<sup>6,7</sup>, Nathalie Charbonnel<sup>8</sup>, Muriel Vayssier-Taussat<sup>2</sup> and Patrick Gasqui<sup>1</sup>**

<sup>1</sup> INRA, UR346 Epidémiologie Animale, Saint Genès Champanelle, France

<sup>2</sup> INRA-Anses-ENVA, USC BIPAR, Maisons-Alfort, France

<sup>3</sup> School of Biological Sciences, University of Aberdeen, Aberdeen, UK

<sup>4</sup> Department of Ticks and Tick-borne Diseases, Veterinary Research Institute, Khartoum, Sudan

<sup>5</sup> Division of Veterinary-Infection Biology and Immunology, Research Center Borstel, Borstel, Germany

<sup>6</sup> Institut des Sciences de l'Evolution (CNRS /IRD / UM2), University of Montpellier 2, Montpellier, France

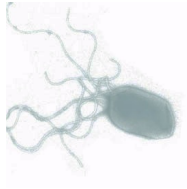
<sup>7</sup> Animal et Gestion Intégrée des Risques, CIRAD, Montpellier, France

<sup>8</sup> INRA, UMR CBGP (INRA / IRD / CIRAD / Montpellier SupAgro), Montpellier, France

*Vaumourin et al. 2014*

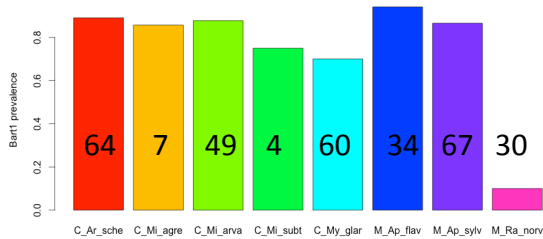
Association Screening Index



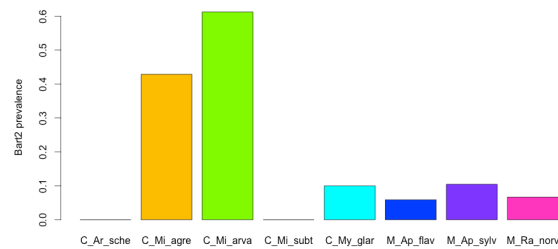


*Bartonella* species : *Bartonella grahamii*, *B. doshiae*

*Bartonella* OTU 1 (100)

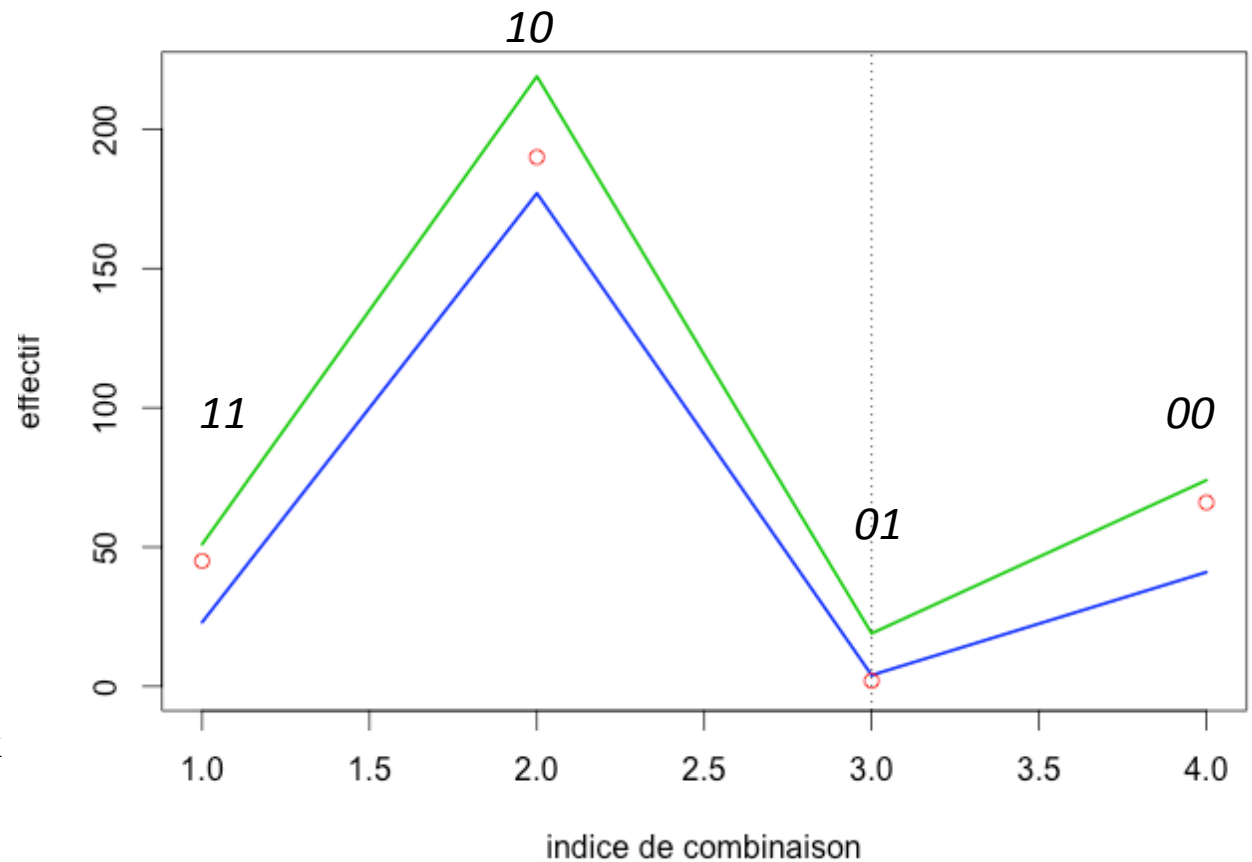


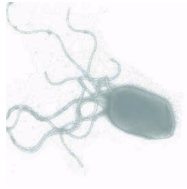
*Bartonella* OTU 2 (92)



Vaumourin et al. 2014  
Association Screening Index

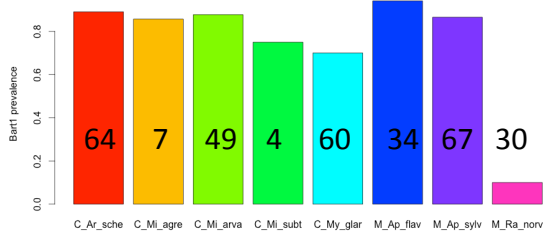
Association Obs - +  
01 2 4 19 p = 1 0.0020



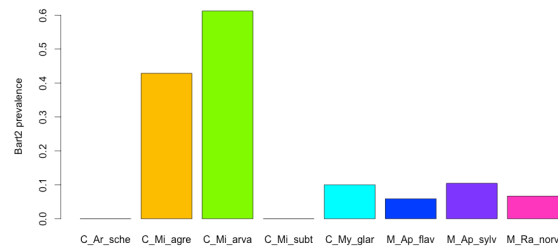


*Bartonella* species : *Bartonella grahamii*, *B. doshiae*

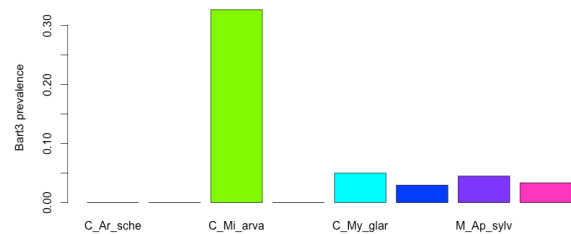
***Bartonella* OTU 1 (100)**



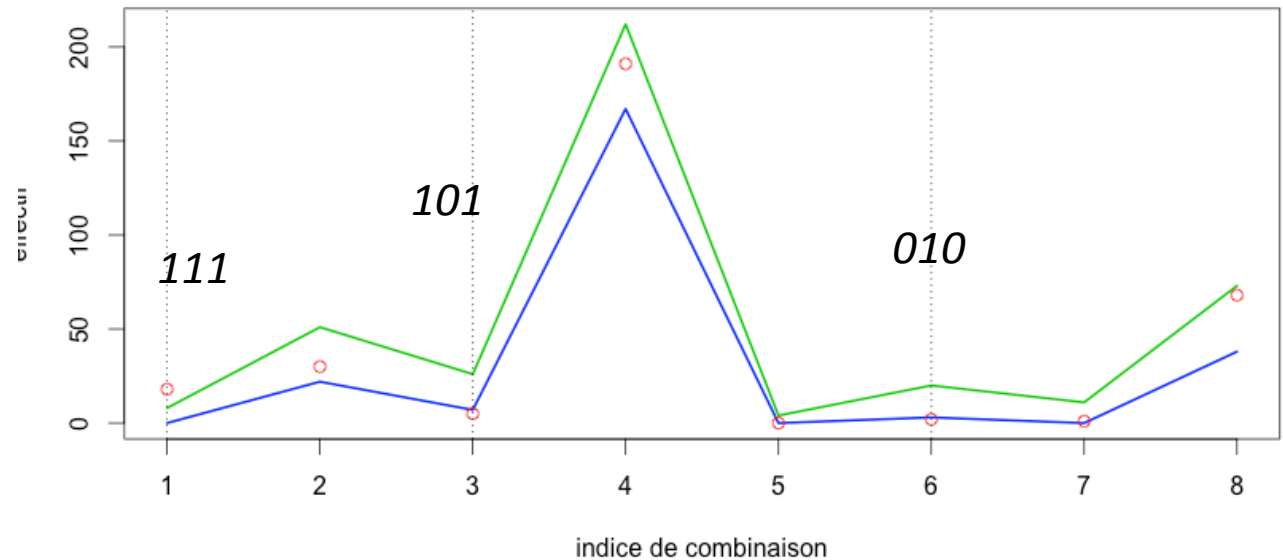
***Bartonella* OTU 2 (92)**



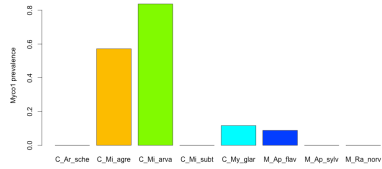
***Bartonella* OTU 3 (74)**



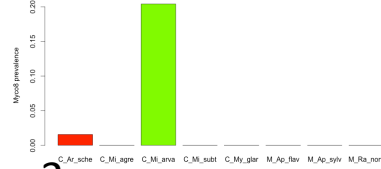
Association	Obs	-	+	p-value
111	18	0	8	p = 0.0000
101	5	7	26	p = 0.0020
010	2	3	20	p = 0.0036
001	1	1	0	p = 0.2152



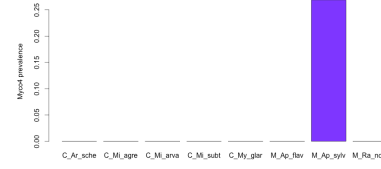
# 1 (99% Ixodes ticks)



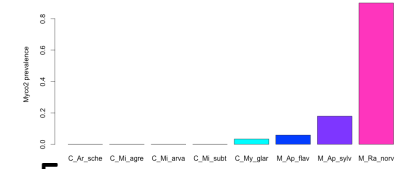
# 8 (95% bat)



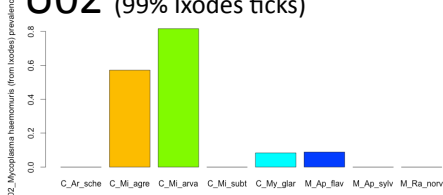
# 4 (99% mouse/ M.haemofelis)



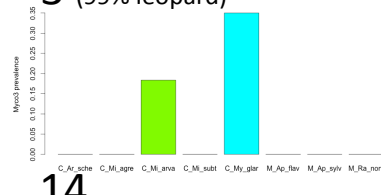
# 2 (99% rat)



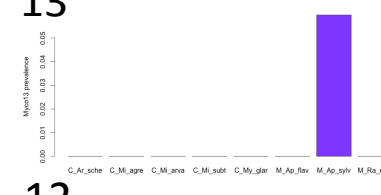
# U02 (99% Ixodes ticks)



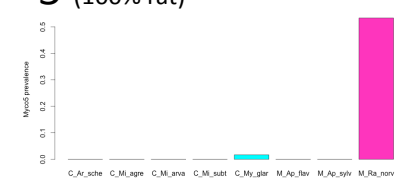
# 3 (99% leopard)



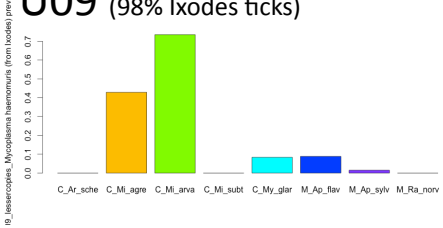
# 13



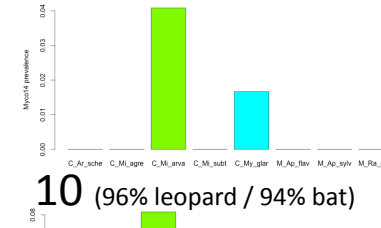
# 5 (100% rat)



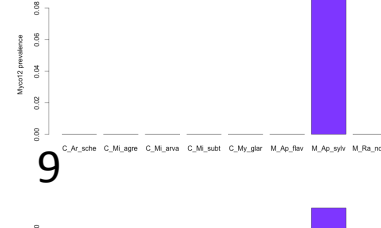
# U09 (98% Ixodes ticks)



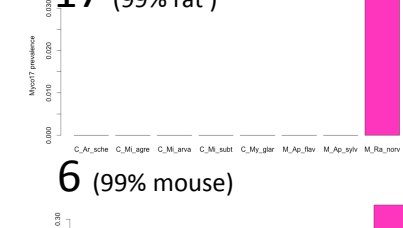
# 14



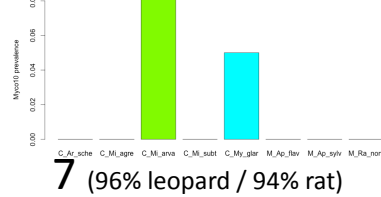
# 12



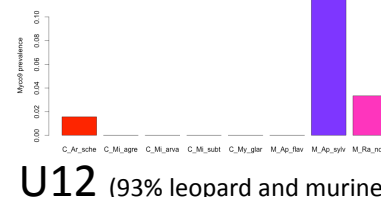
# 17 (99% rat)



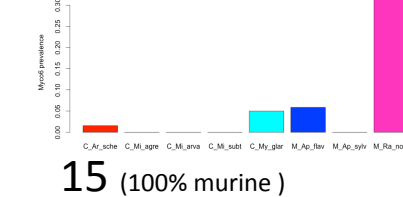
# 10 (96% leopard / 94% bat)



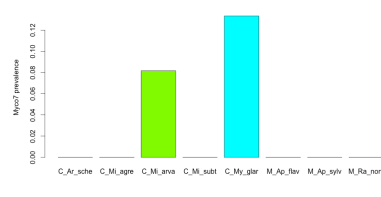
# 9



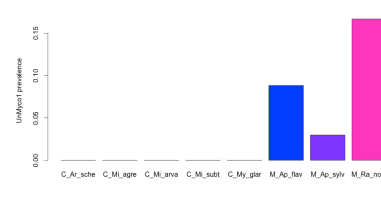
# 6 (99% mouse)



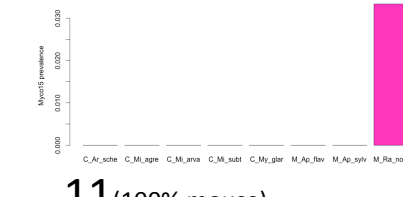
# 7 (96% leopard / 94% rat)



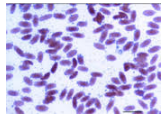
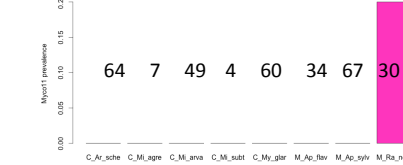
# U12 (93% leopard and murine)



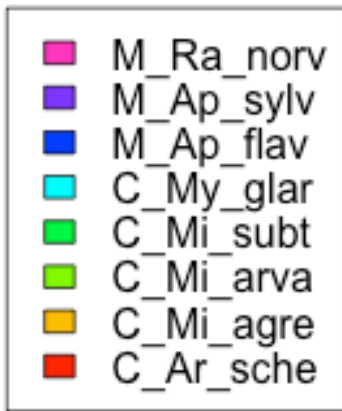
# 15 (100% murine)



# 11 (100% mouse)

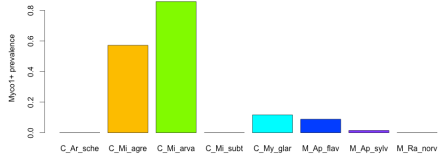


19+ independent *Mycoplasma* OTUs

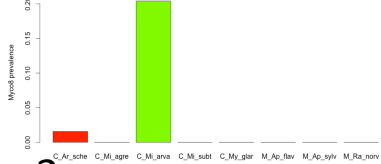




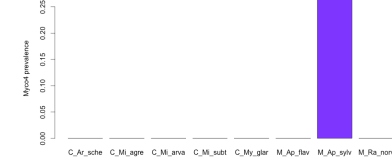
1+ (99% Ixodes ticks)



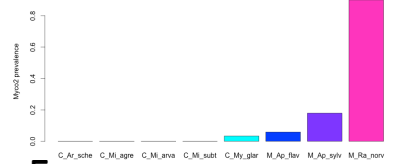
8 (95% bat)



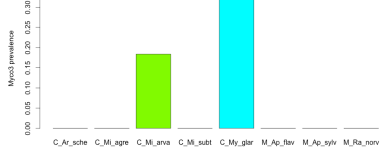
4+ (99% mouse/ M.haemofelis)



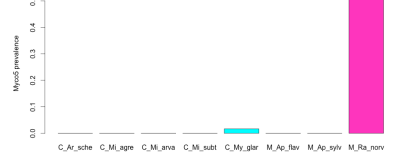
2 (99% rat)



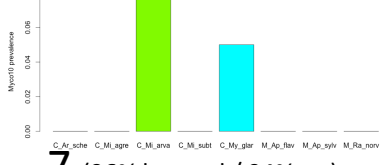
3 (99% leopard)



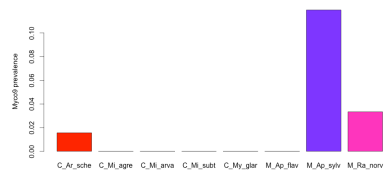
5 (100% rat)



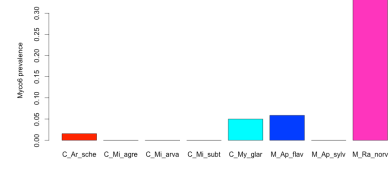
10 (96% leopard / 94% bat)



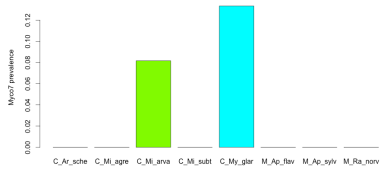
9



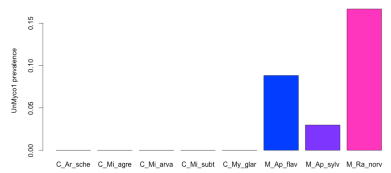
6 (99% mouse)



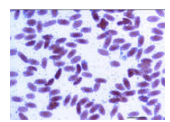
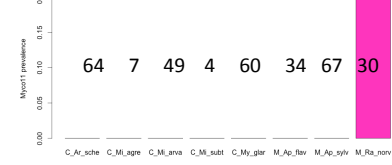
7 (96% leopard / 94% rat)



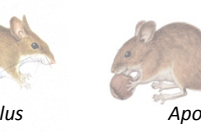
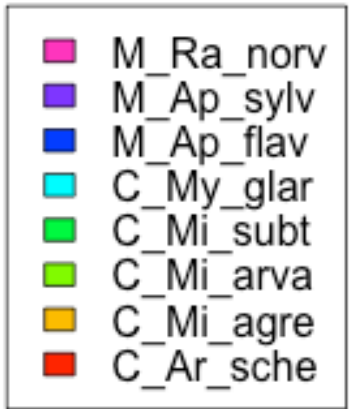
U12 (93% leopard and murine)



11 (100% mouse)



Most likely ~12 Mycoplasma spp.



Arvicola scherman

Miodes agrestis

M. arvalis

M. subterraneus

Myodes glareolus

Apo. flavicolus

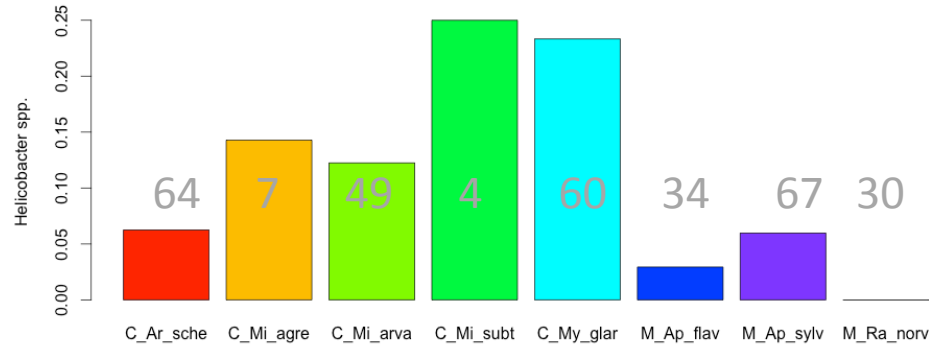
Apo. Sylvaticus

Rattus norvegicus

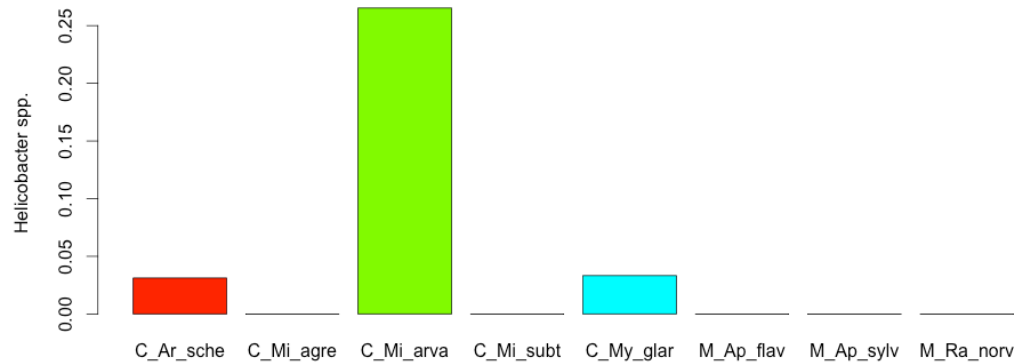


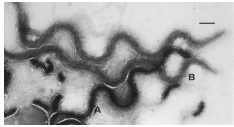
*Helicobacter* species : *H.suncus* + *H. trogontum* isolated from shrews and other mammals with chronic gastritis

*Helicobacter* OTU 1(100)



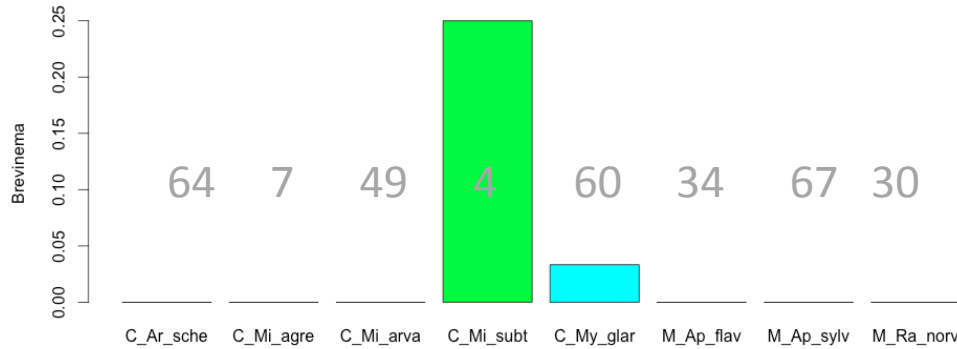
*Helicobacter* OTU 2 (100)





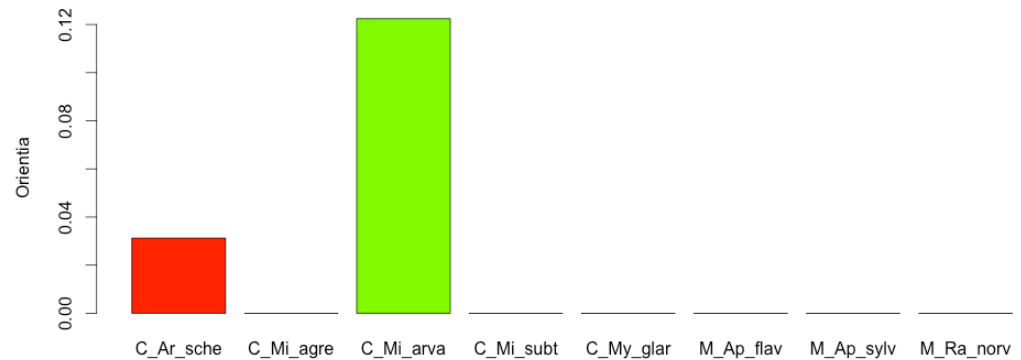
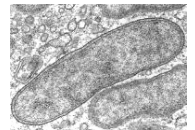
### Brevinema (100)

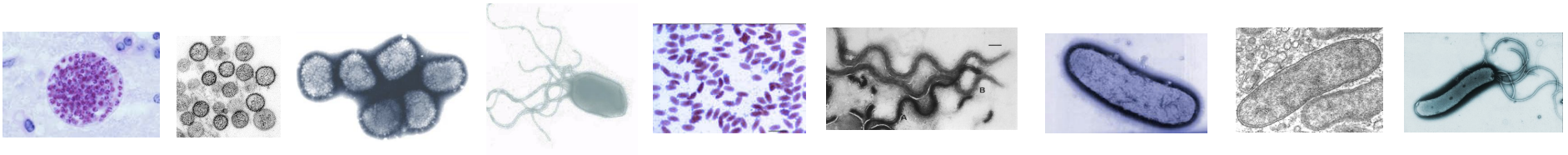
97% homology to *B. andersonii* spirochaete of short-tailed shrew (*Blarina brevicauda*) & white-footed mouse (*P. leucopus*) in N. America



### Orientia (100)

100% homology to rickettsial *O. tsutsugamushi* causing zoonotic scrub typhus; here, found only among meadow voles





**3 viruses (historical)**

**2? protazoa**

**15-31 bacteria species**

**✓ Host species is the main determinant of among - individual presence for any one parasite.**



# Co-infection Patterns

Natural History & Population Dynamics

Geographic Distribution & Evolutionary History

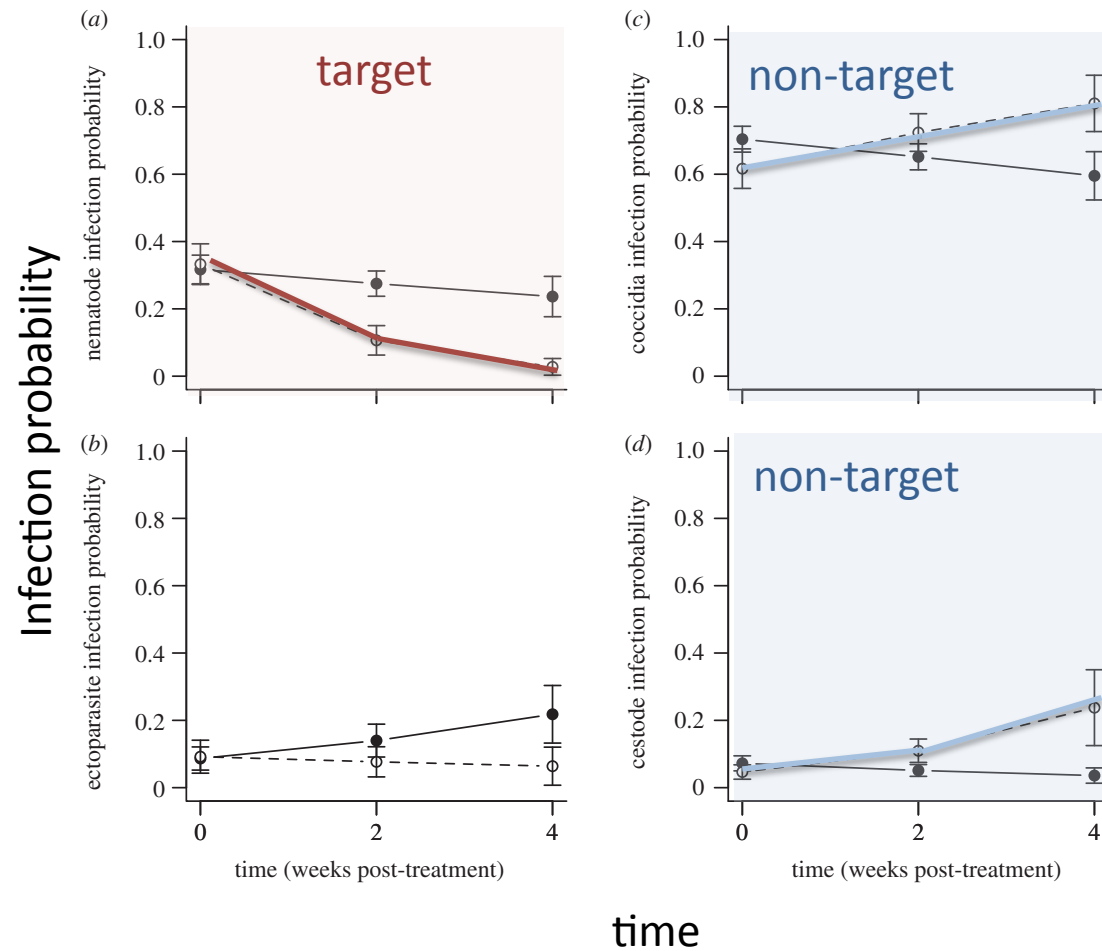
Host – Pathogen Genetics

Phenotype & Life-History Traits

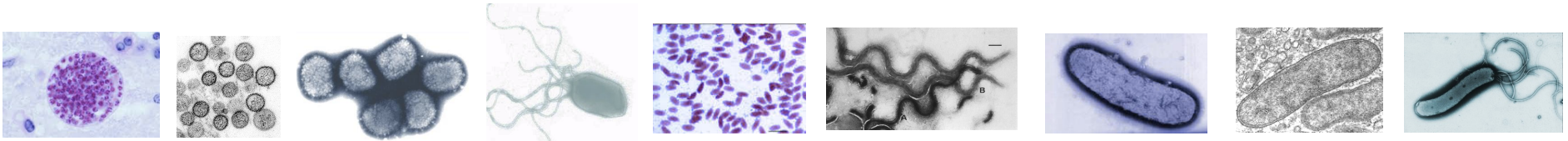
Environmental Variables

**Ecological Interactions**

Parasite removal experiment demonstrates competitive exclusion between gut parasites of *Peromyscus* spp. in the United States



Pedersen & Antonovics 2013 *Biol Letters*



## Co-infection Patterns

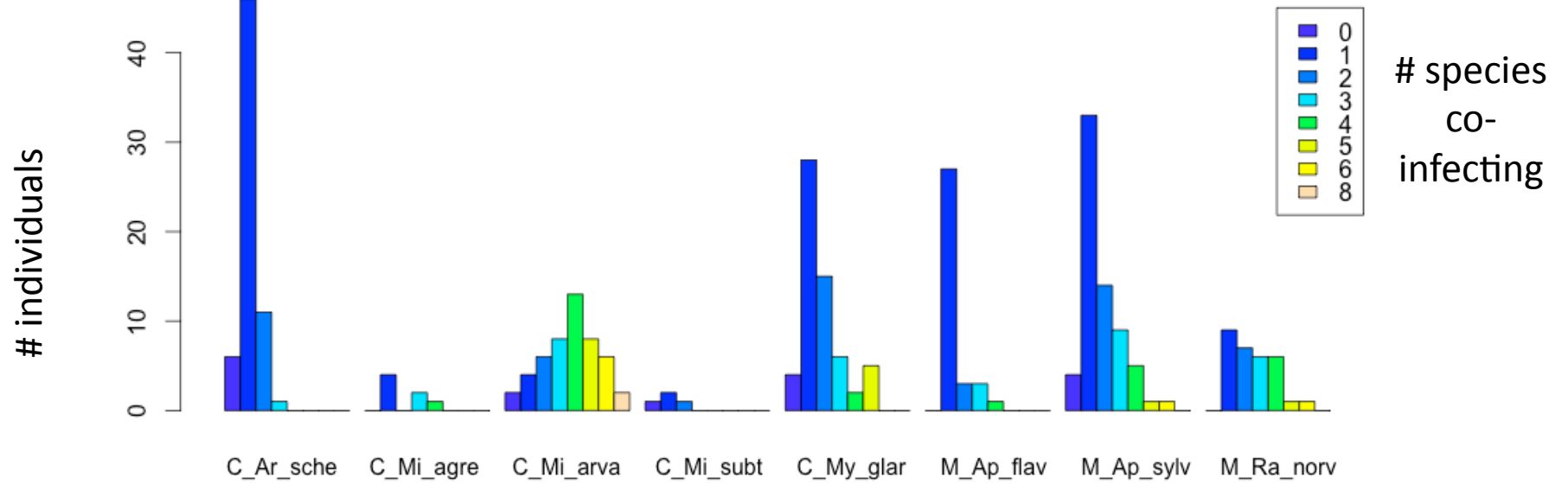
**Do co-infections occur?**

**What determines co-infection rates?**

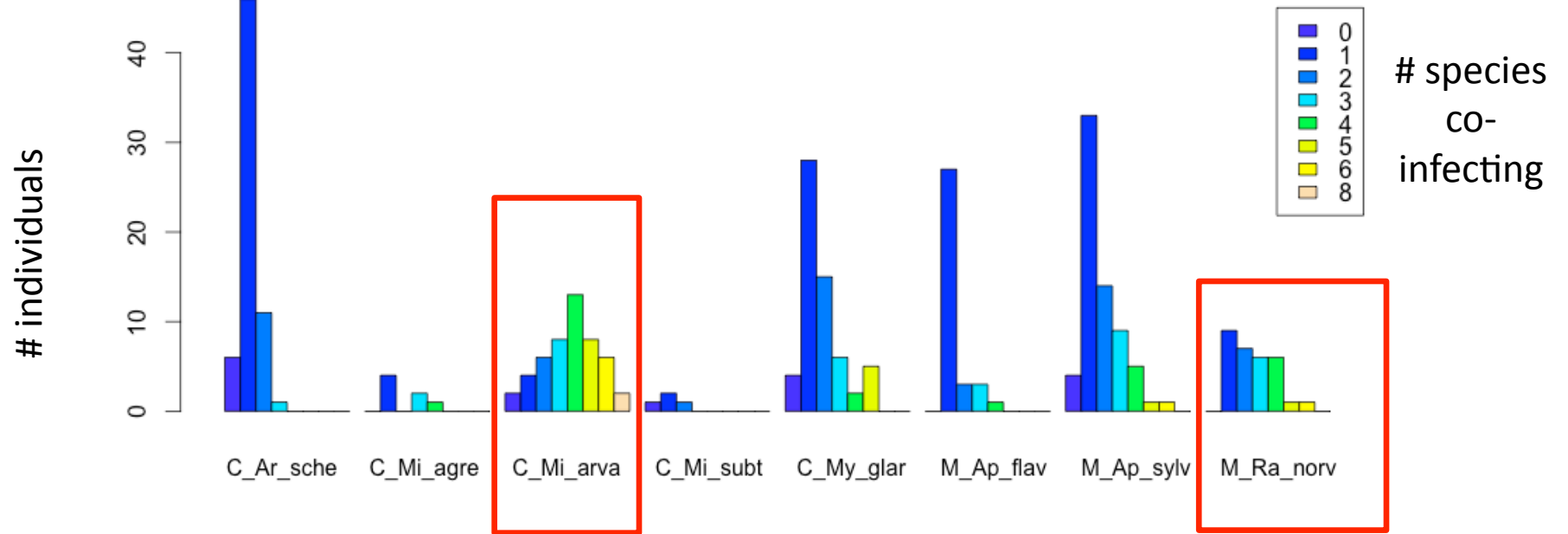
**Are there associations (+ & -) between parasites (or a history thereof)?**



### Number of Bacteria Species per Individual

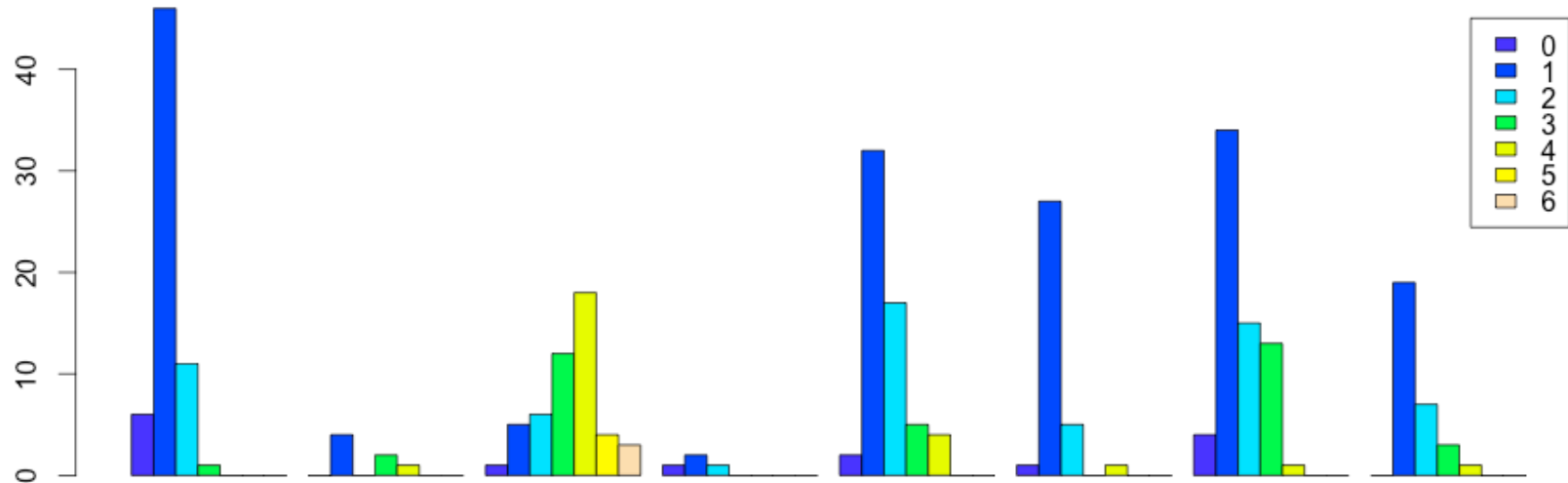


Number of Bacteria Species per Individual

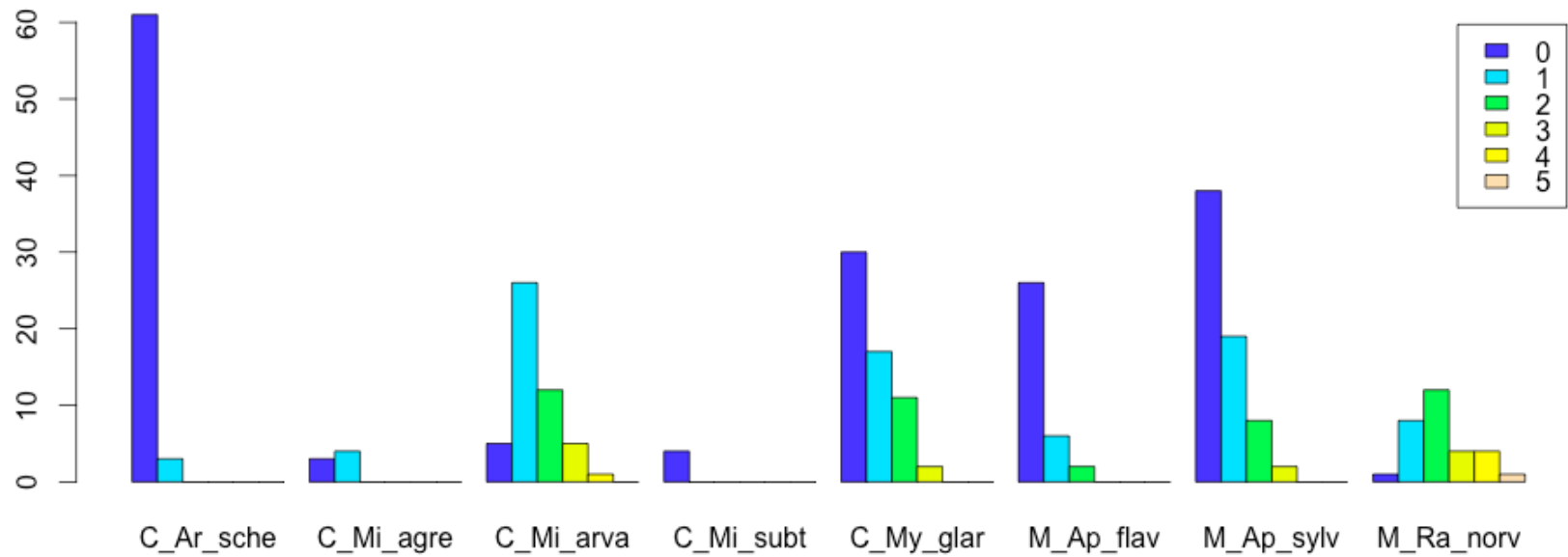




## Number of Bacteria Species (indep. of Mycobacteria) per Individual



## Number of Mycobacterium Species per Individual



*Arvicola scherman*



*Miodes agrestis*



*M. arvalis*



*M. subterraneus*



*Myodes glareolus*



*Apo. flavicolus*

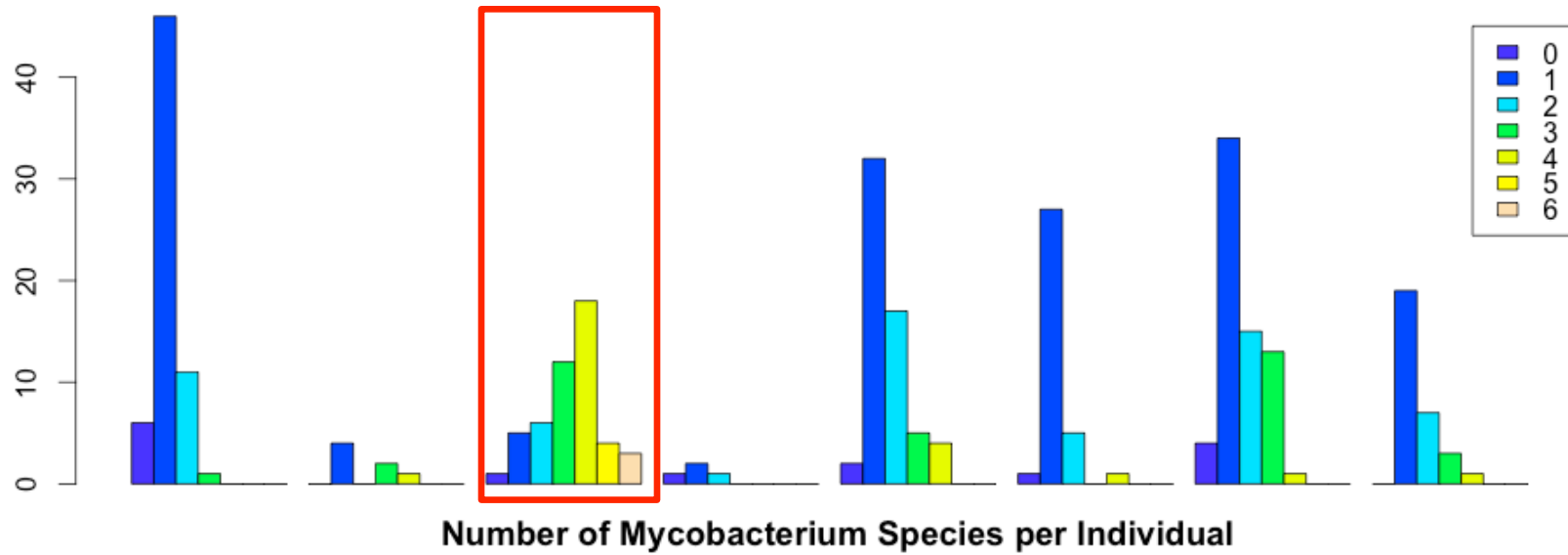


*Apo. sylvaticus*

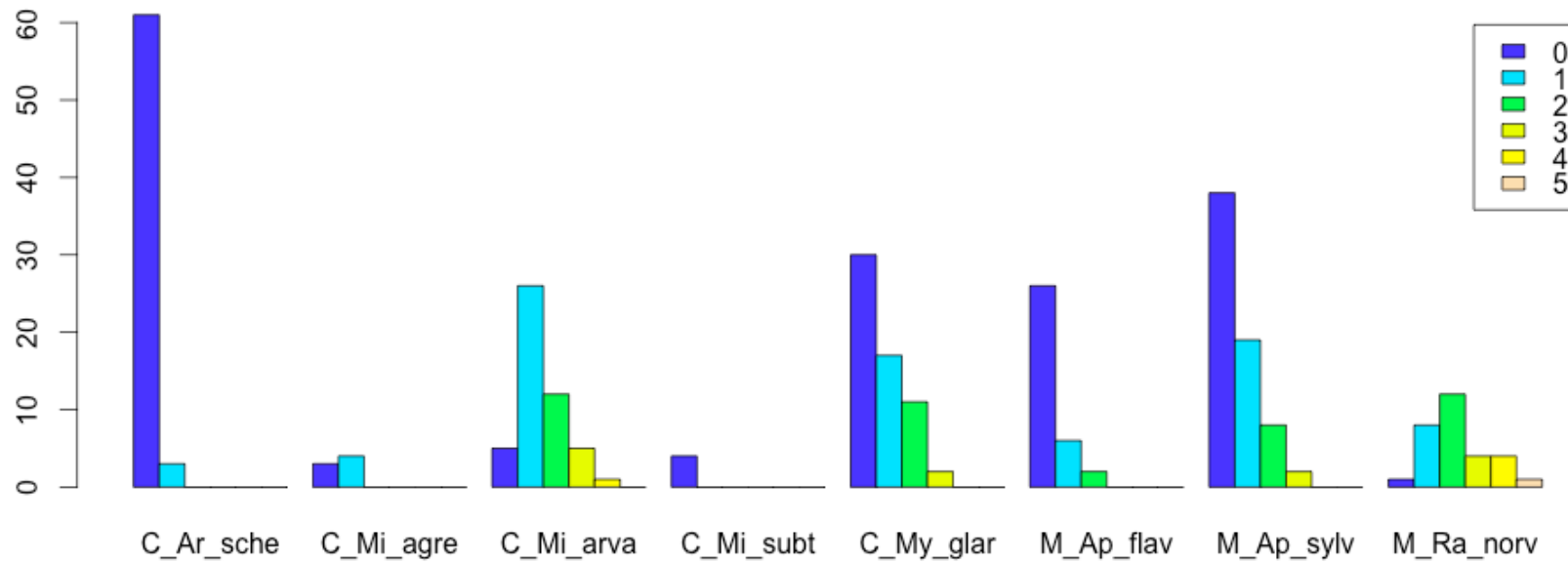


*Rattus norvegicus*

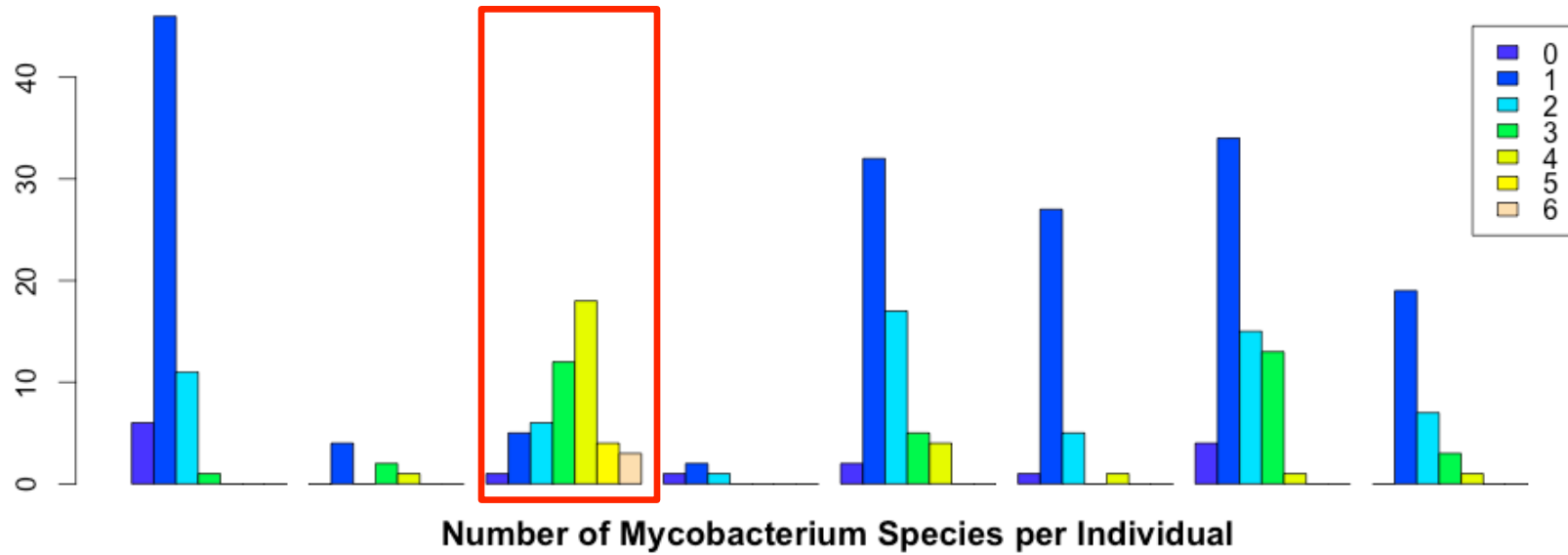
## Number of Bacteria Species (indep. of Mycobacteria) per Individual



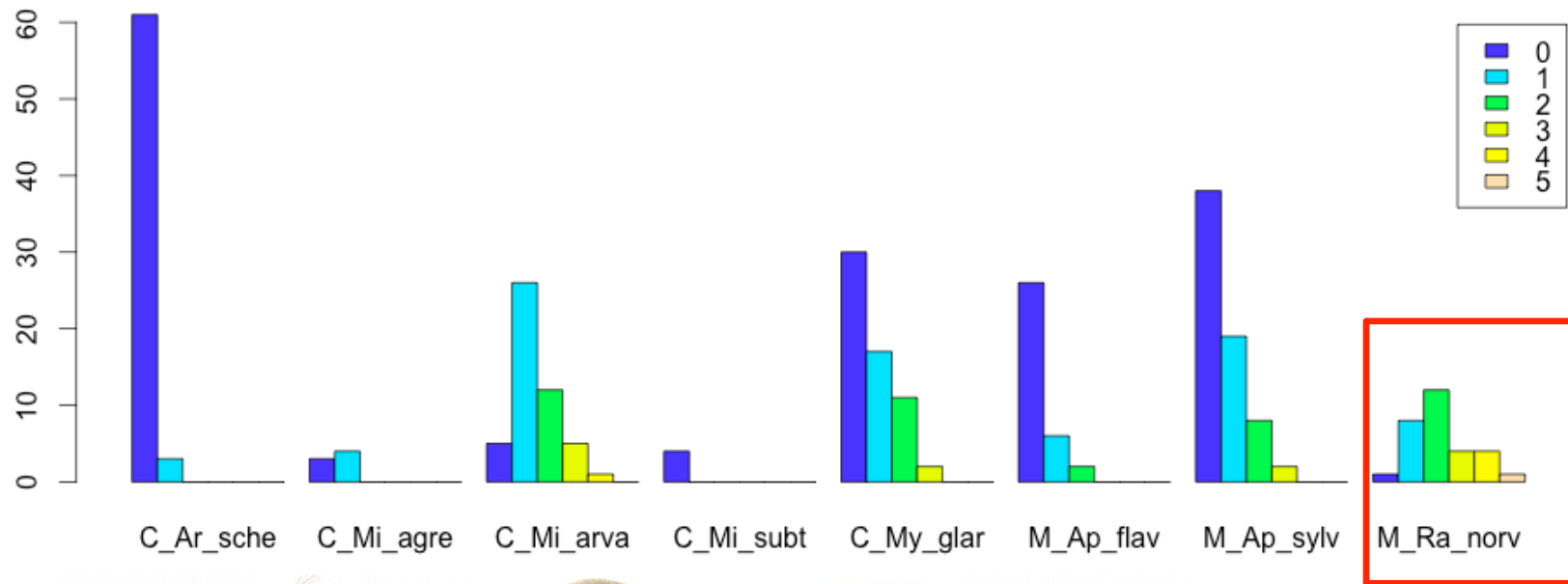
## Number of Mycobacterium Species per Individual



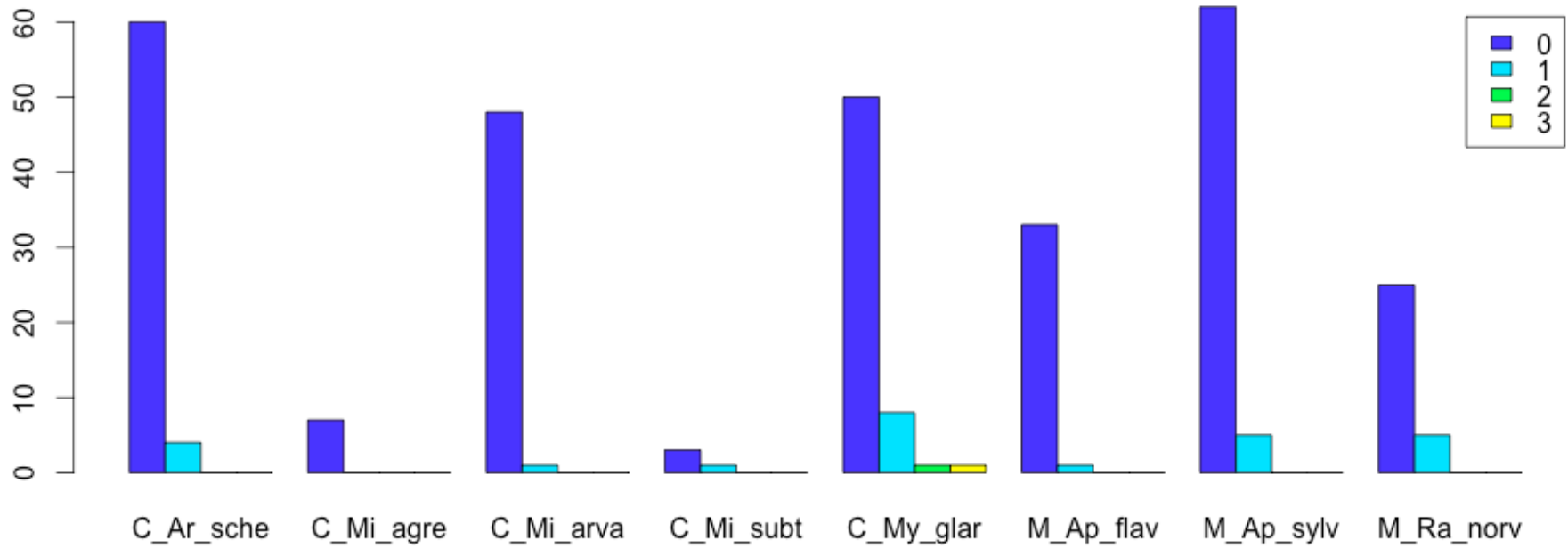
## Number of Bacteria Species (indep. of Mycobacteria) per Individual



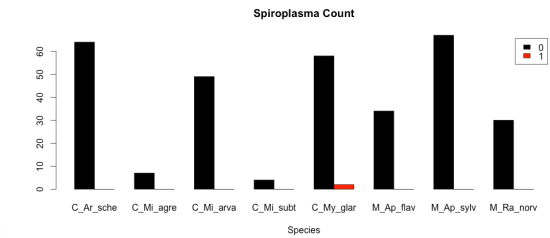
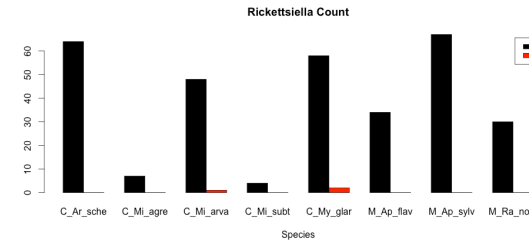
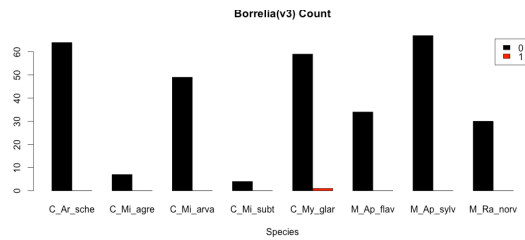
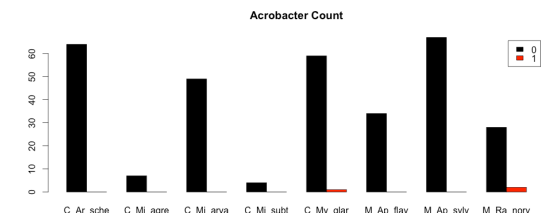
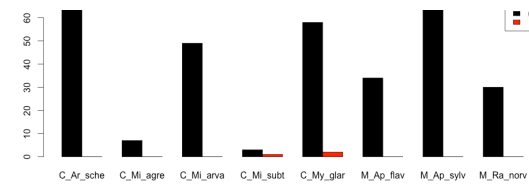
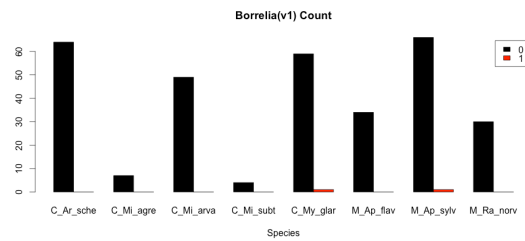
## Number of Mycobacterium Species per Individual



## Number of Rare Bacteria Species (indep. of Mycobacteria) per Individual



### Species



*Arvicola scherman*

*Miodes agrestis*

*M. arvalis*

*M. subterraneus*

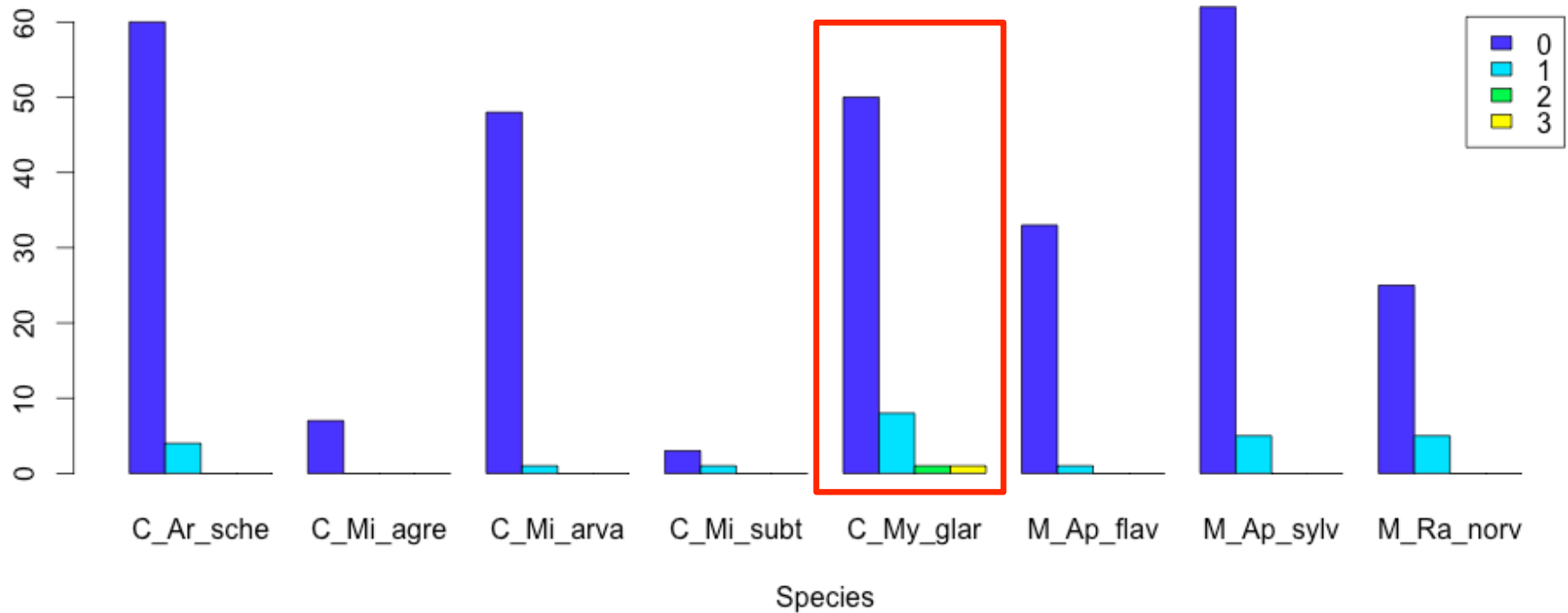
*Myodes glareolus*

*Apo. flavicolus*

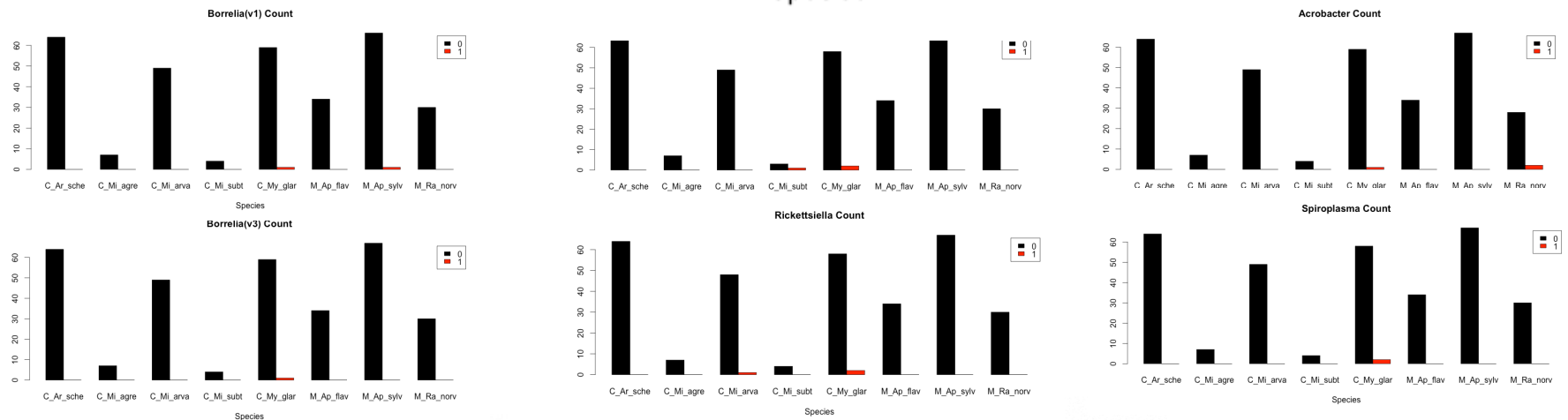
*Apo. sylvaticus*

*Rattus norvegicus*

## Number of Rare Bacteria Species (indep. of Mycobacteria) per Individual



### Species



*Arvicola scherman*



*Miodes agrestis*



*M. arvalis*



*M. subterraneus*



*Myodes glareolus*



*Apo. flavicolus*



*Apo. sylvaticus*

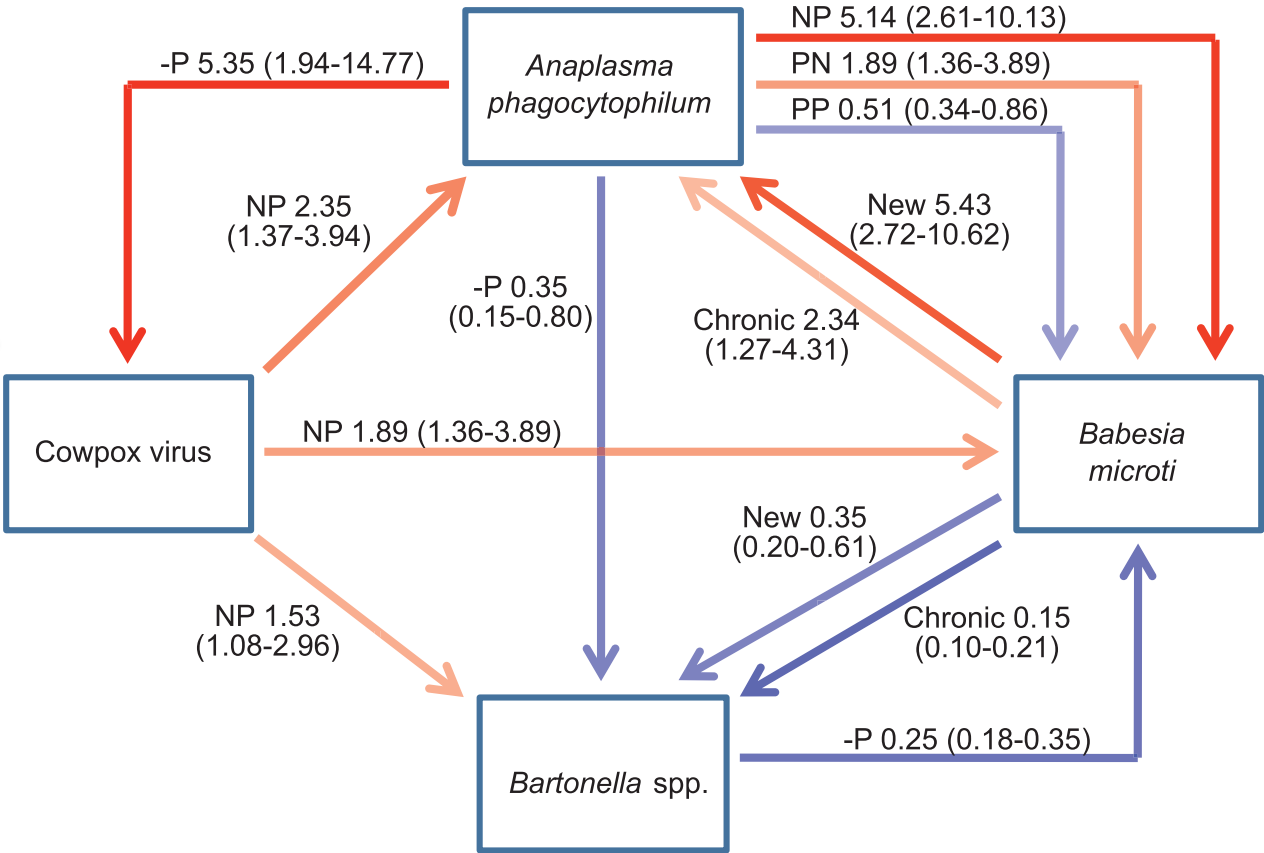


*Rattus norvegicus*

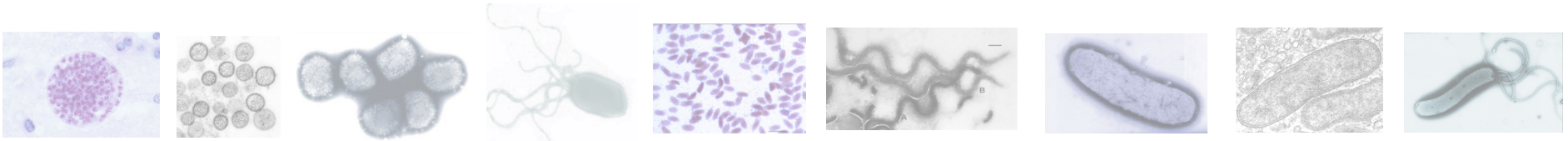
# Co-infection Patterns

Cowpox (OPXV) weakly facilitates bacterial infections in 5981 *Microtus agrestis* of a UK forest

- Natural History & Population Dynamics
- Geographic Distribution & Evolutionary History
- Host – Pathogen Genetics
- Phenotype & Life-History Traits
- Environmental Variables
- Ecological Interactions**



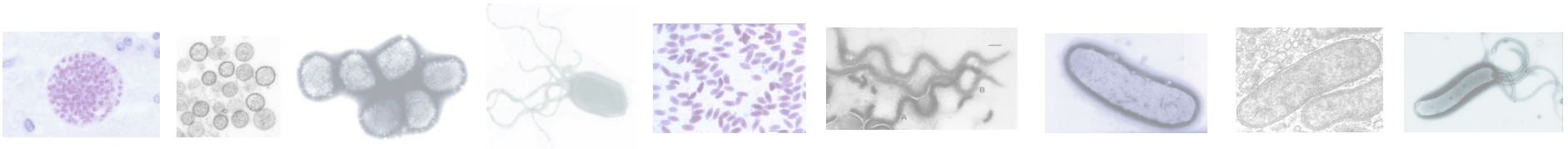
Telfer et al. 2010 *Science*



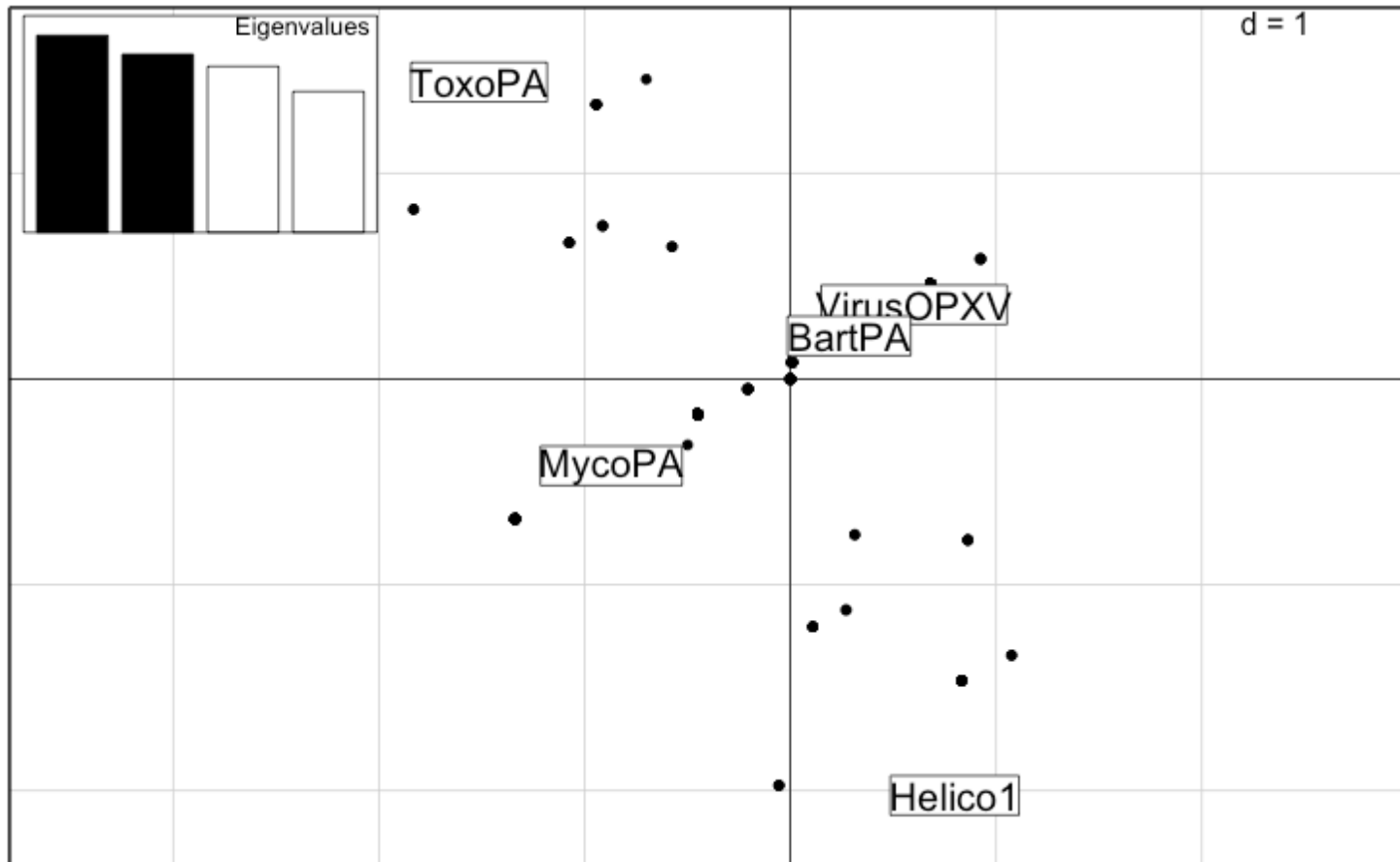
An example from our data:

Cowpox Virus (OPXV)	33%
Bartonella (any)	78%
Mycoplasma (any)	46%
Helicobacter (1)	10%
Toxo History (Abs)	7%

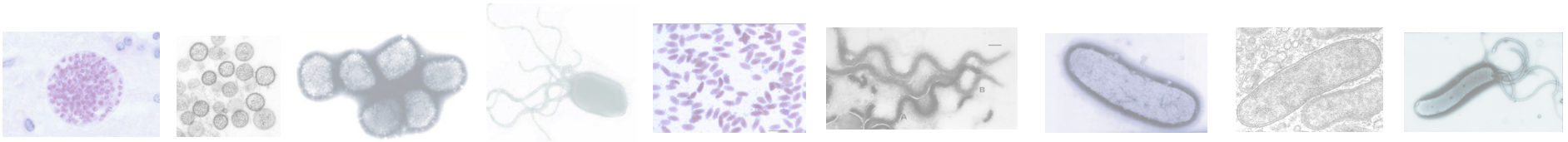




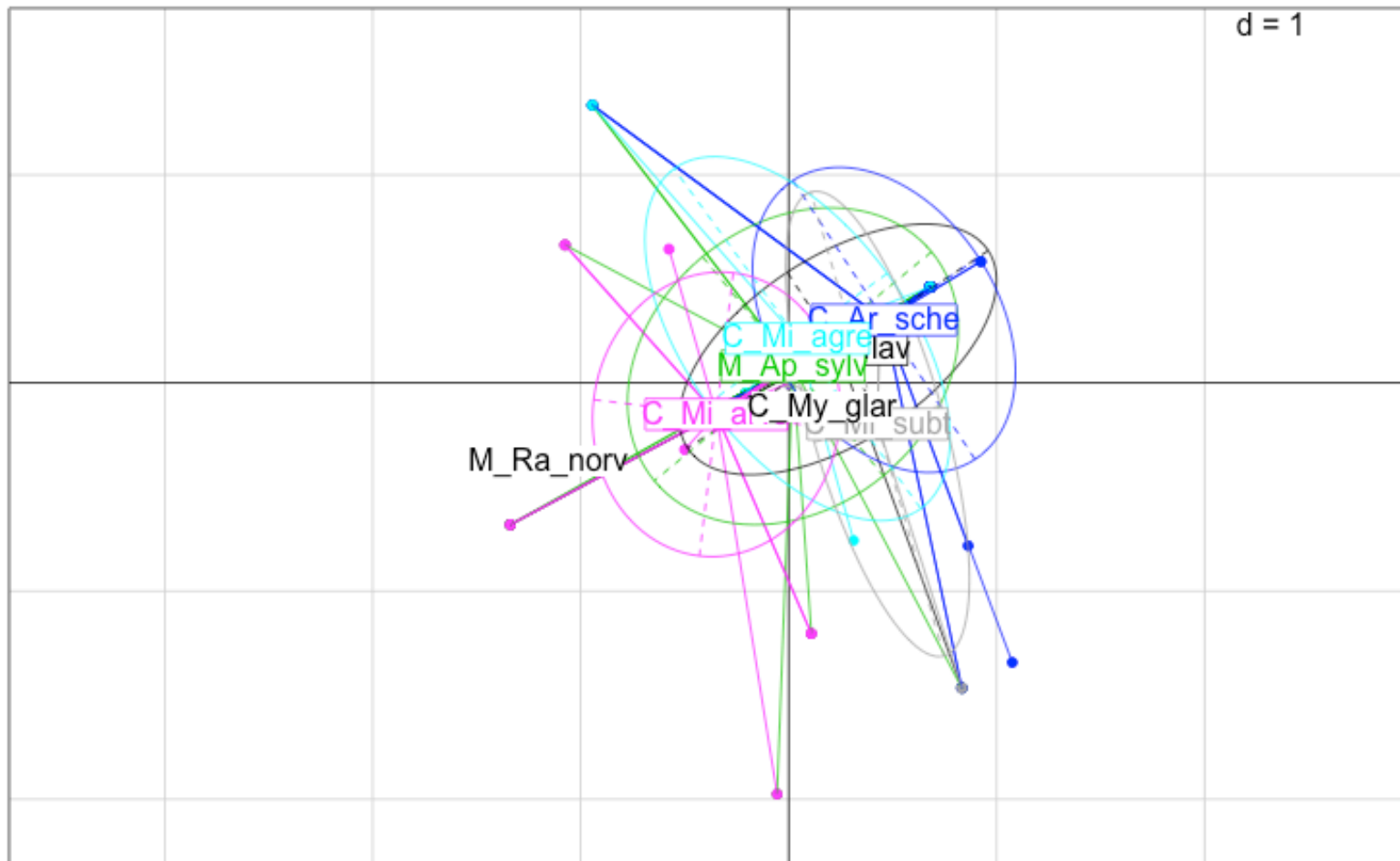
## Factor Correspondence Analysis (AFC)

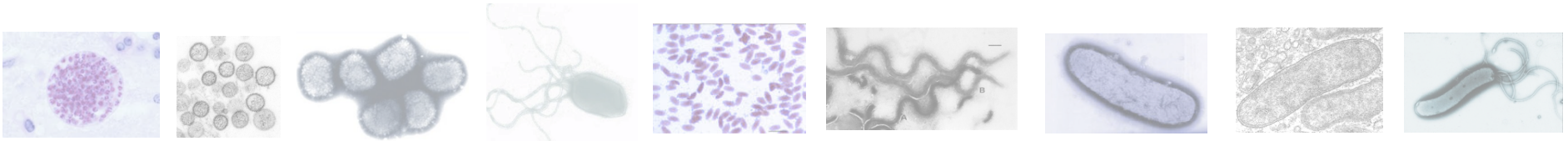




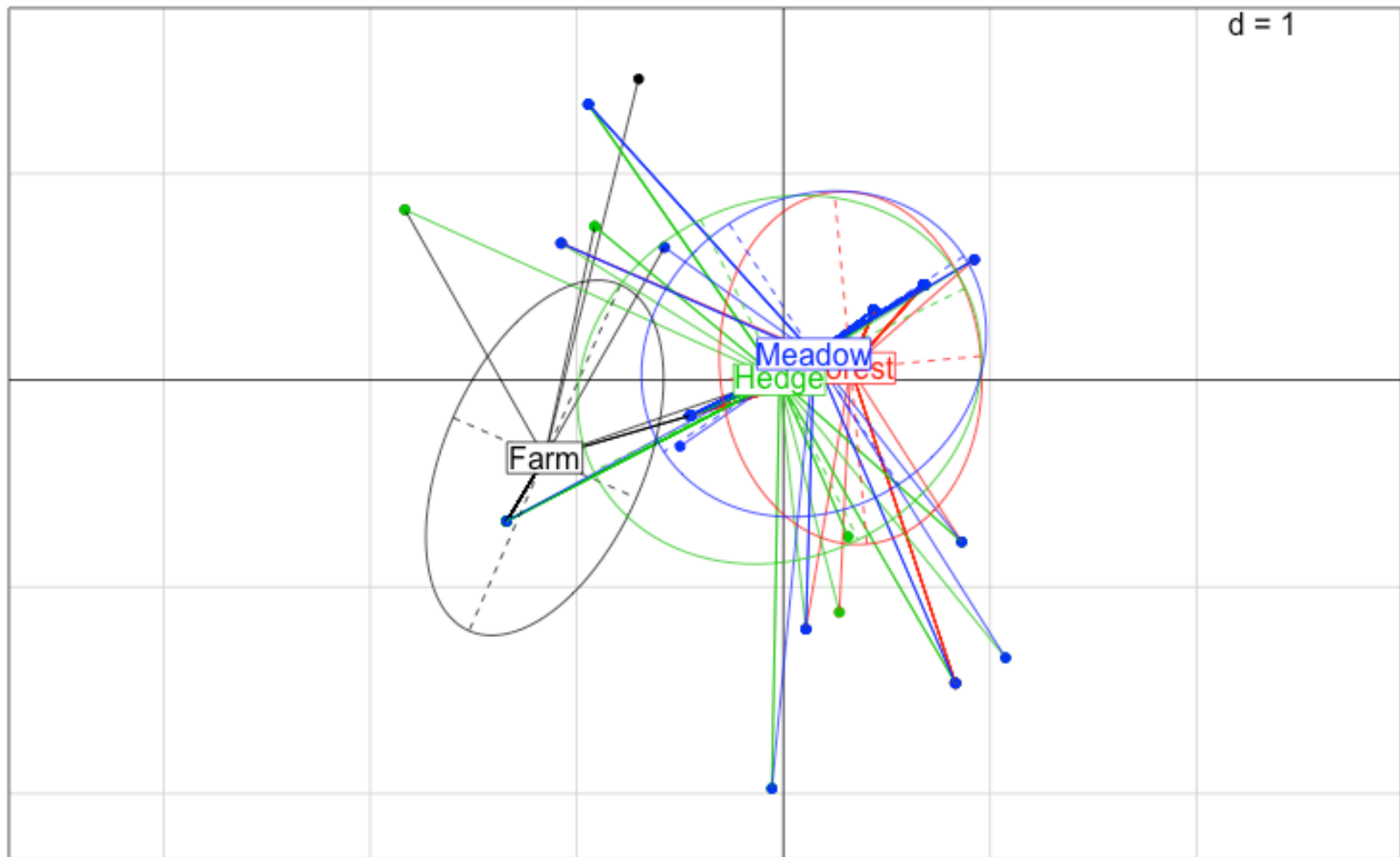


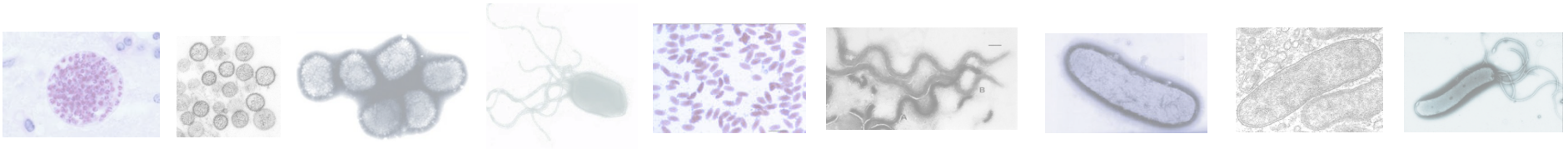
## Multiple Correspondence Analysis (MCA)



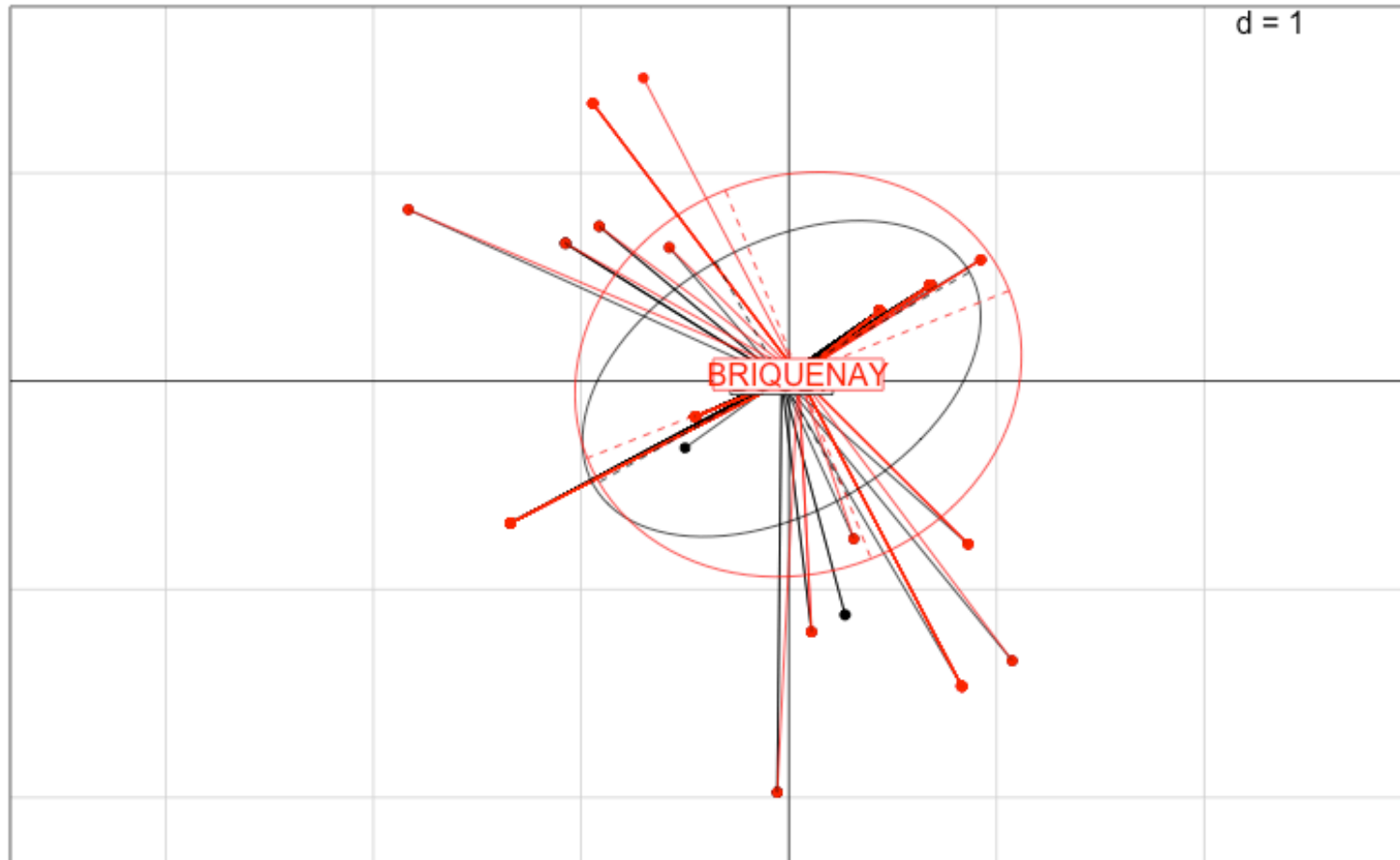


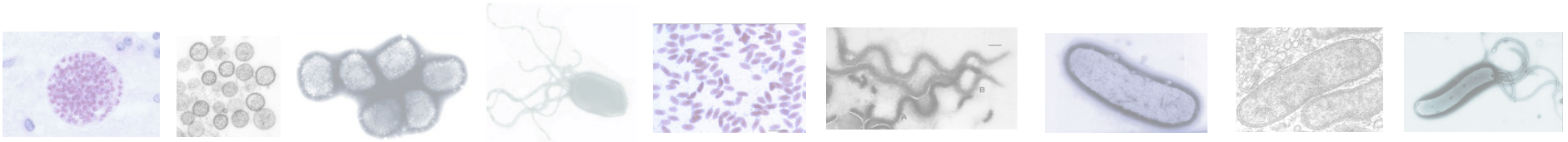
## Multiple Correspondence Analysis (MCA)



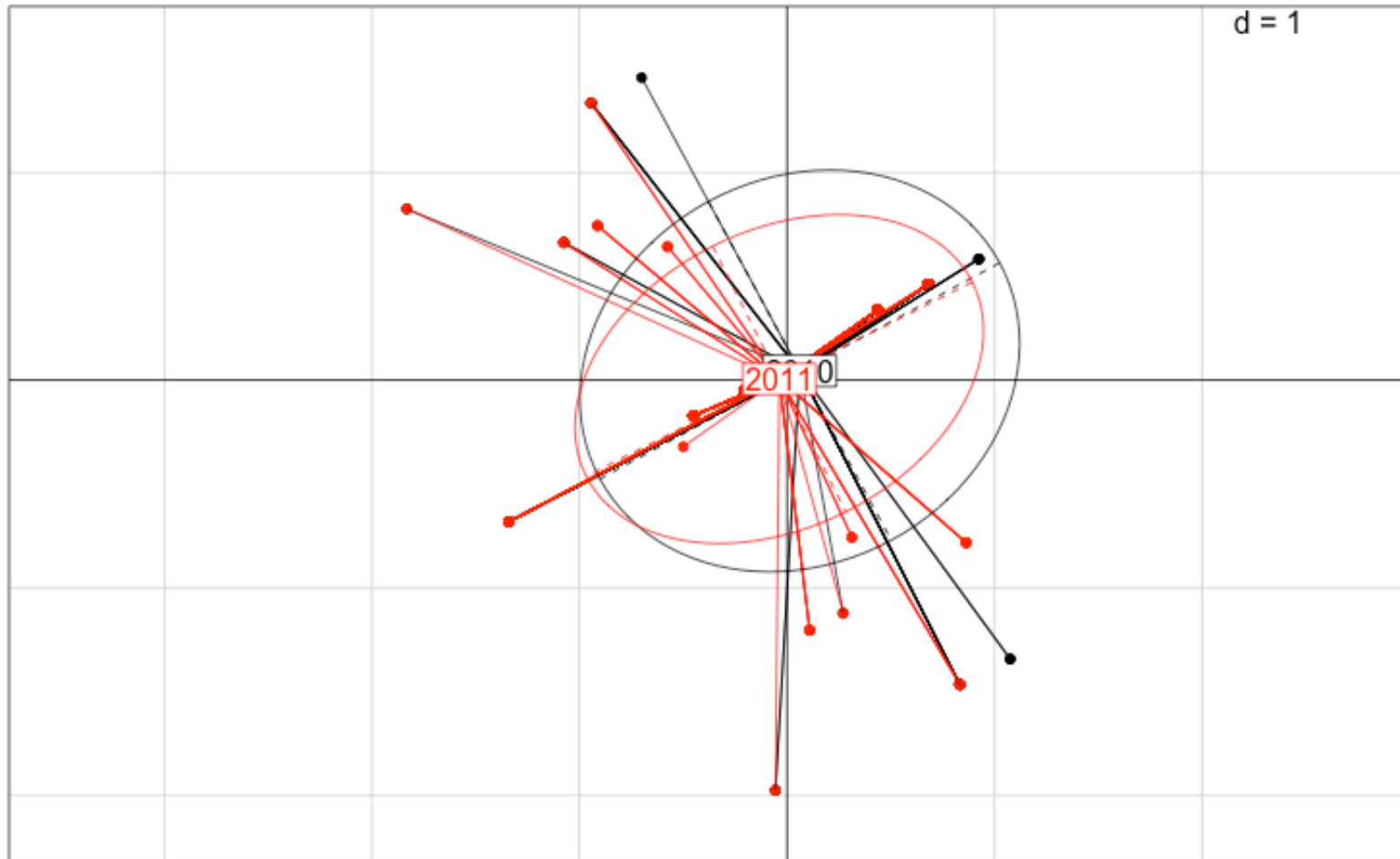


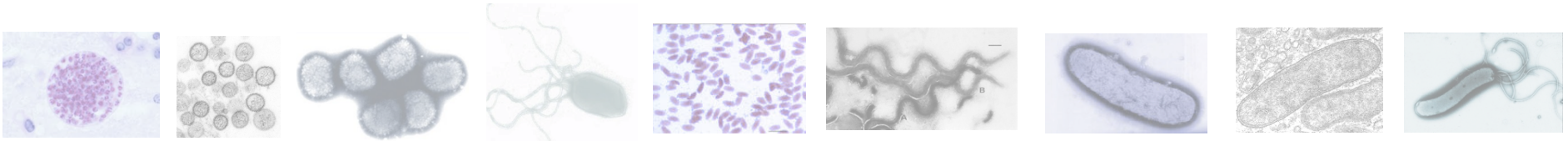
## Multiple Correspondence Analysis (MCA)



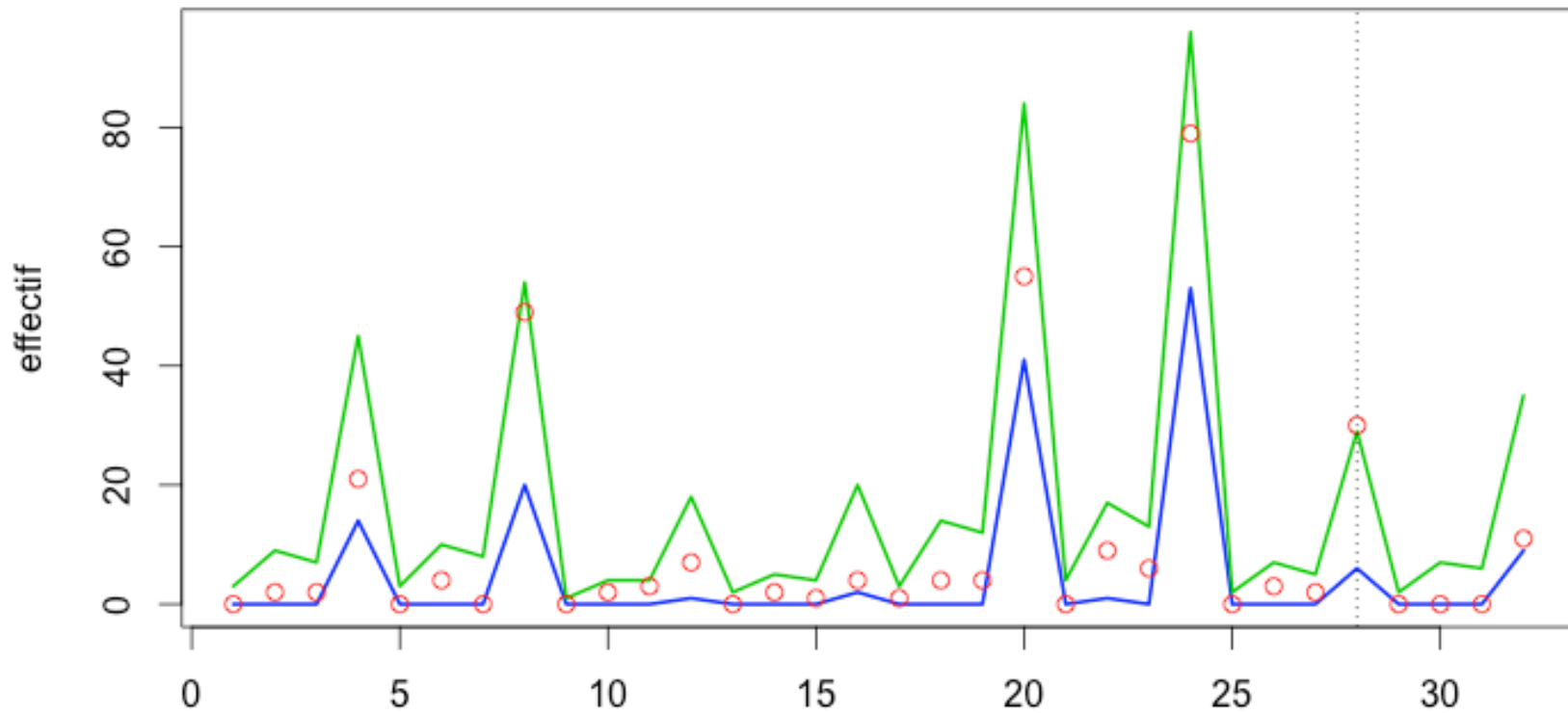


## Multiple Correspondence Analysis (MCA)



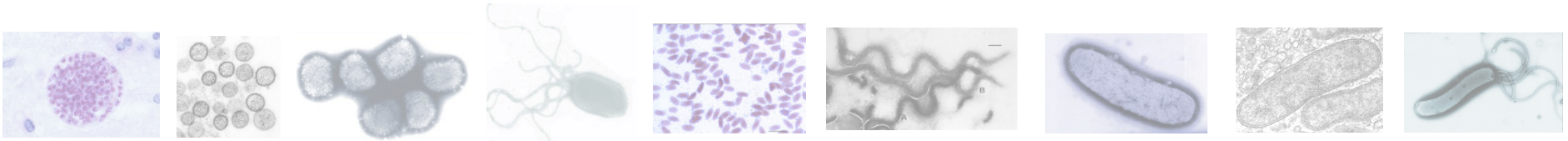


## Screening Analysis

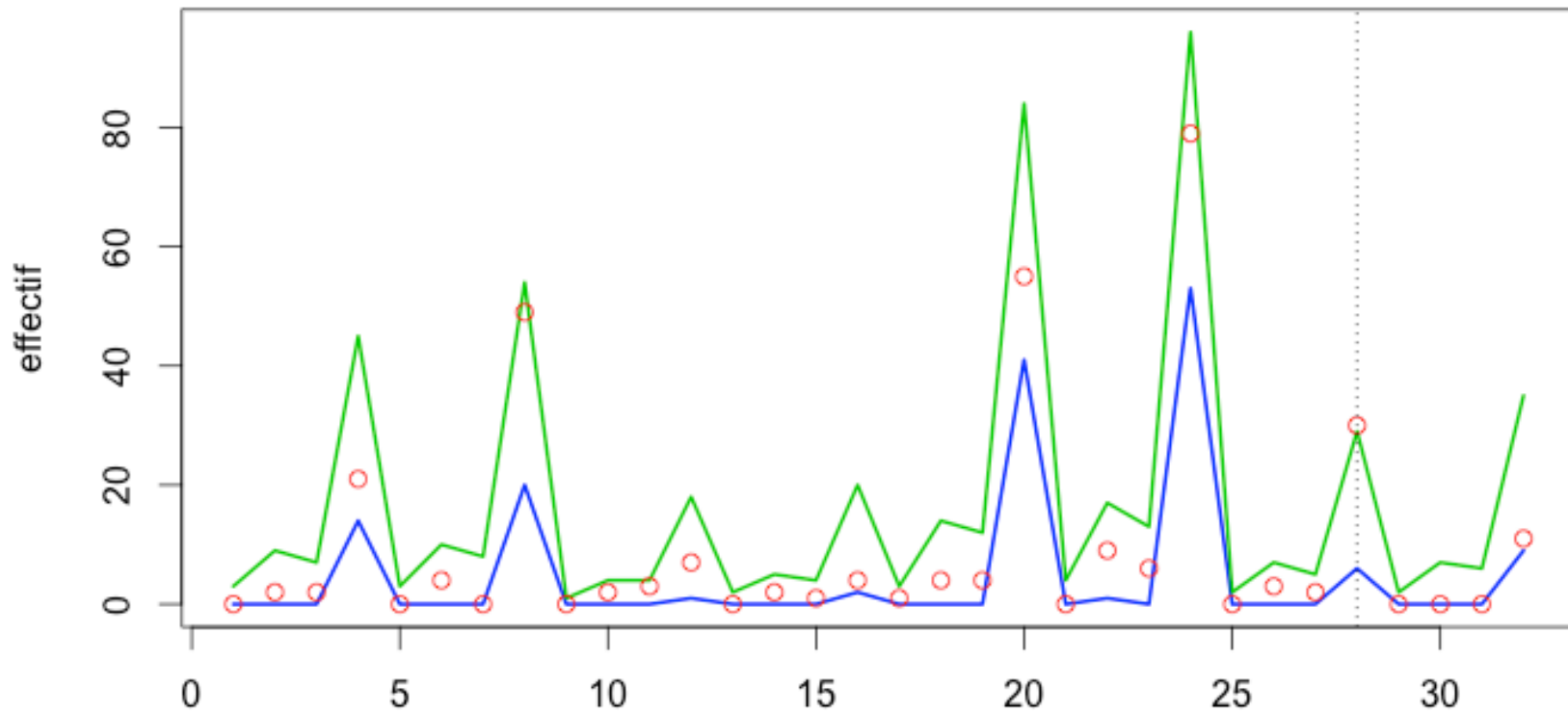


Association Obs - +  
 00100 30 6 29 p= 0.0020





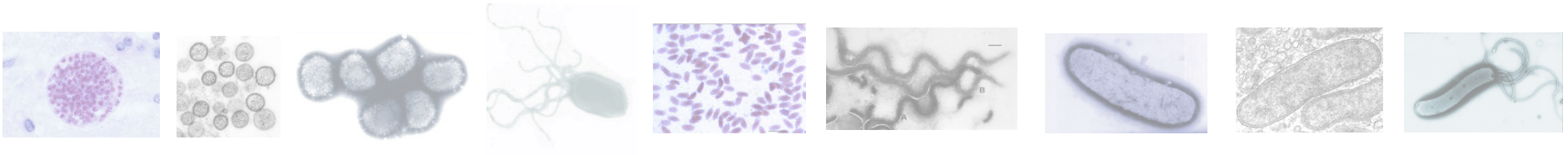
## Screening Analysis



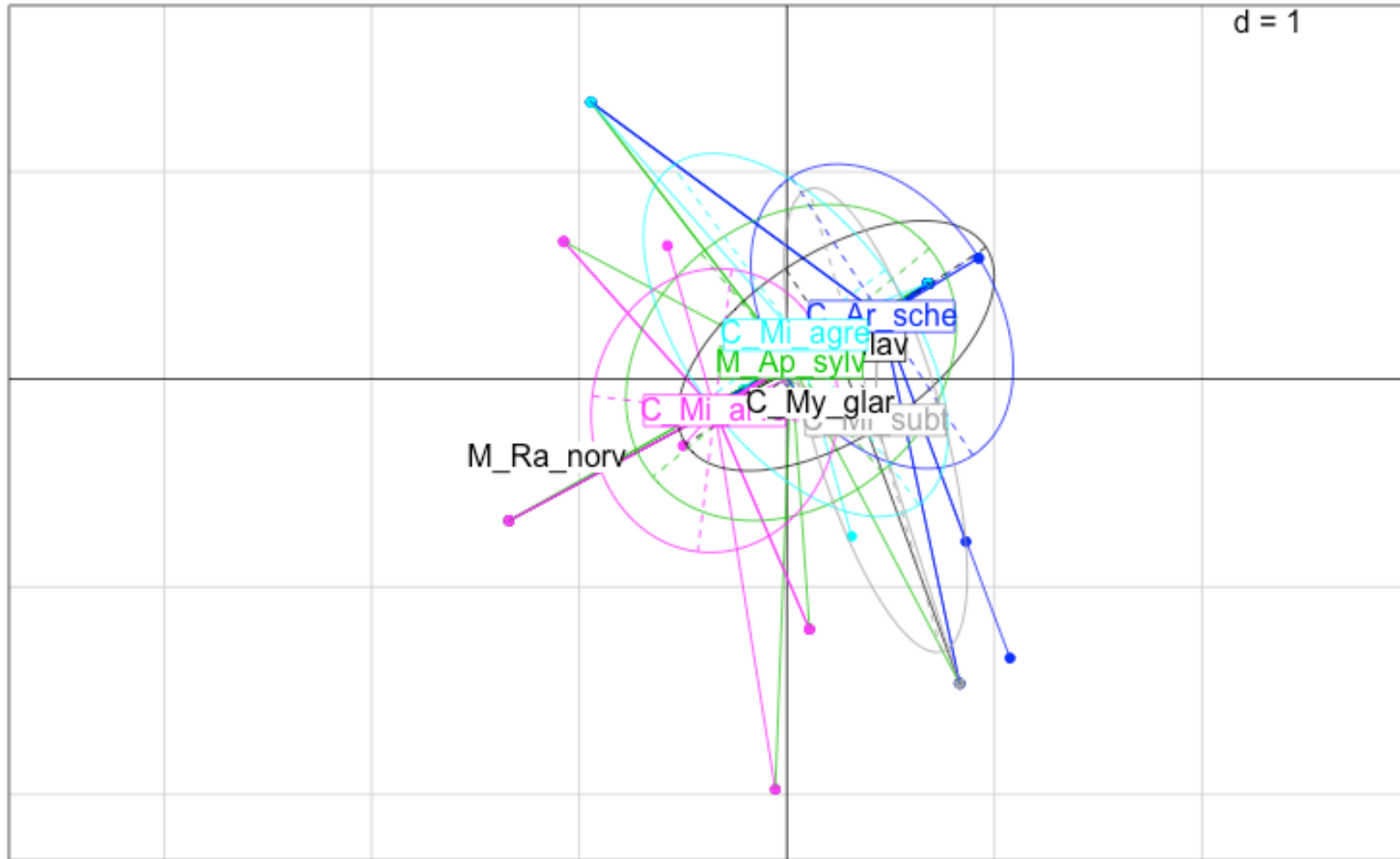
Association Obs - +  
 00100 30 6 29 p= 0.0020

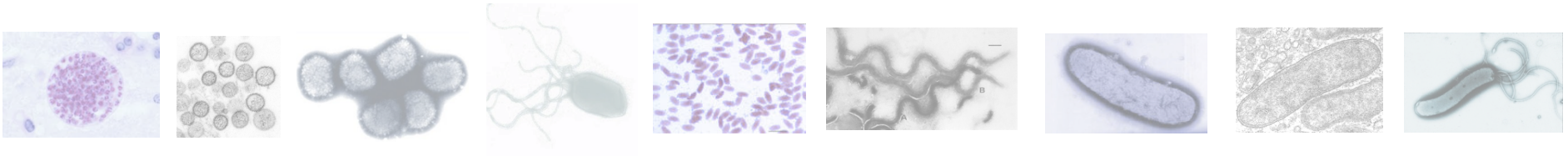
*Mycoplasma* occurs  
 more often by itself  
 than by chance





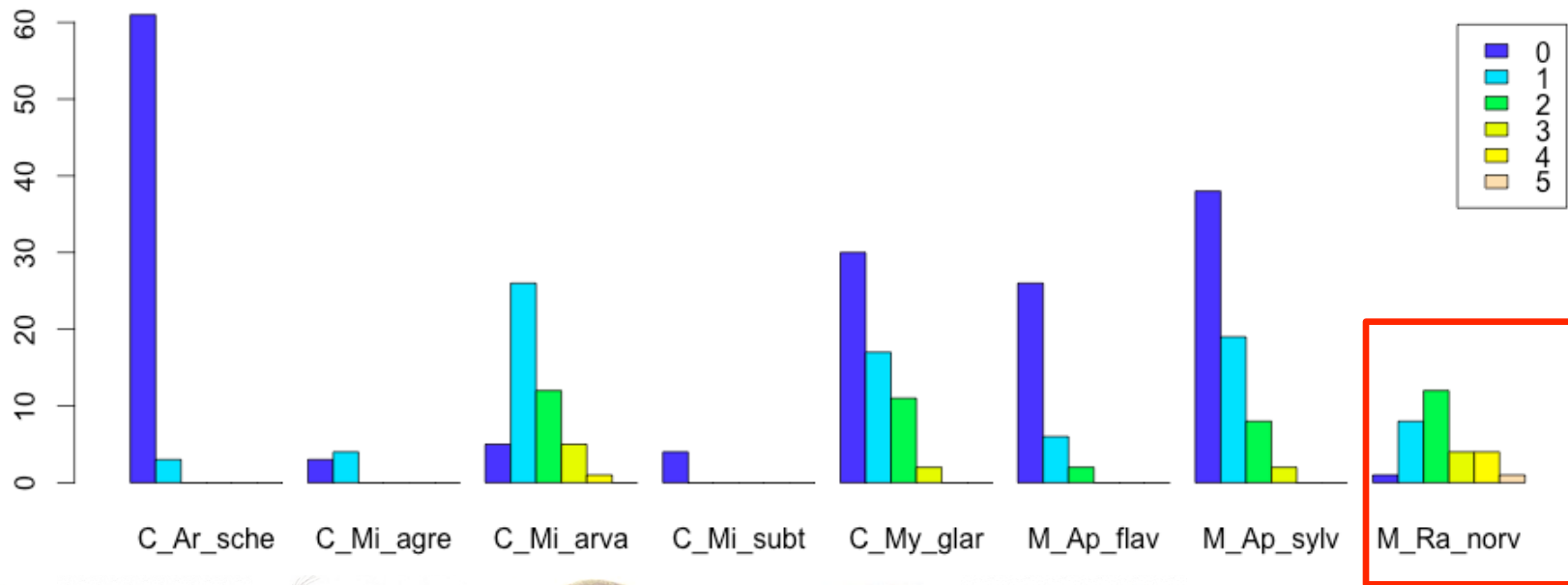
## Screening Analysis



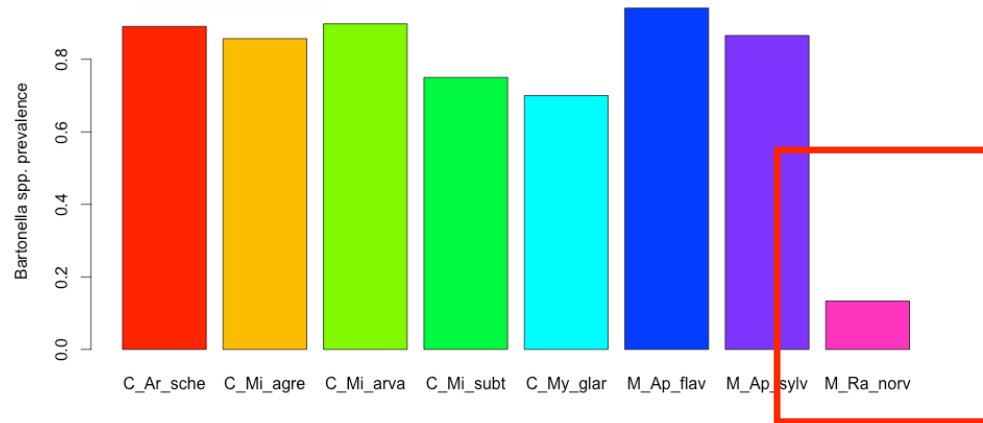
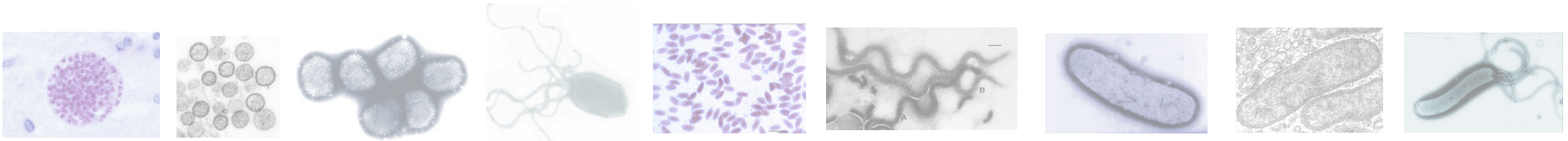


## Screening Analysis

Number of Mycobacterium Species per Individual

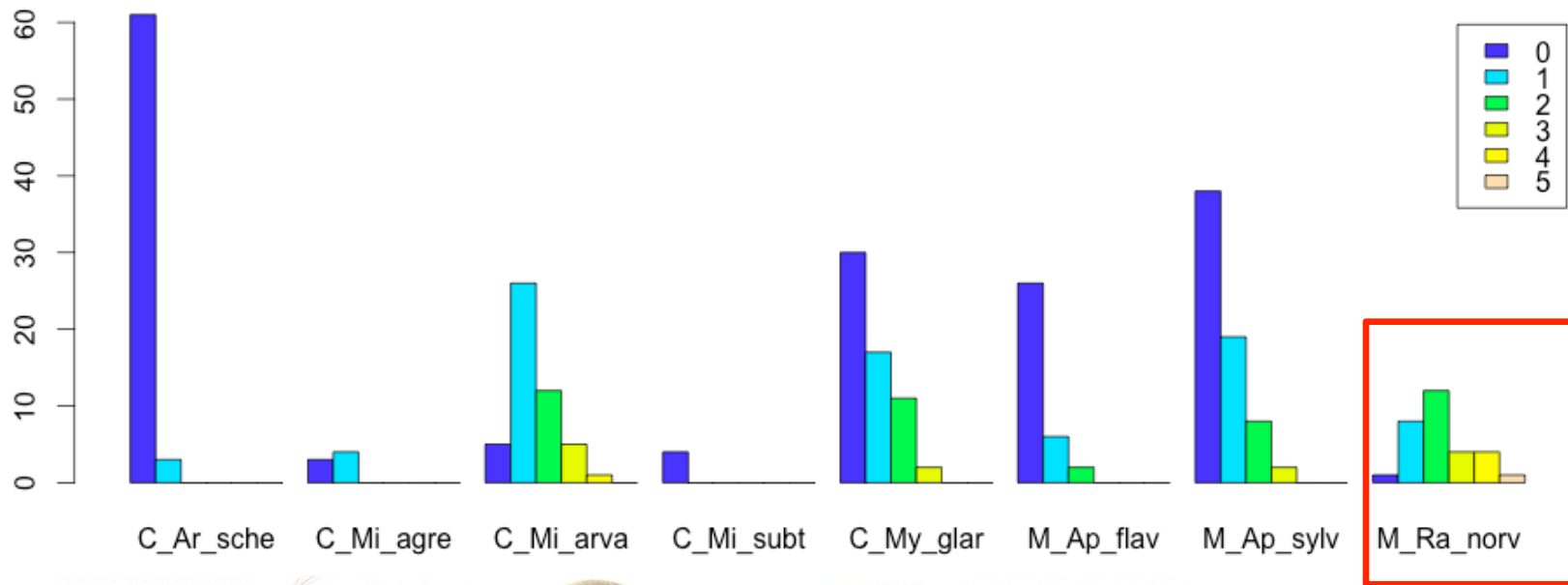






*Bartonella* spp.

### Number of Mycobacterium Species per Individual



*Arvicola scherman*

*Miodes agrestis*

*M. arvalis*

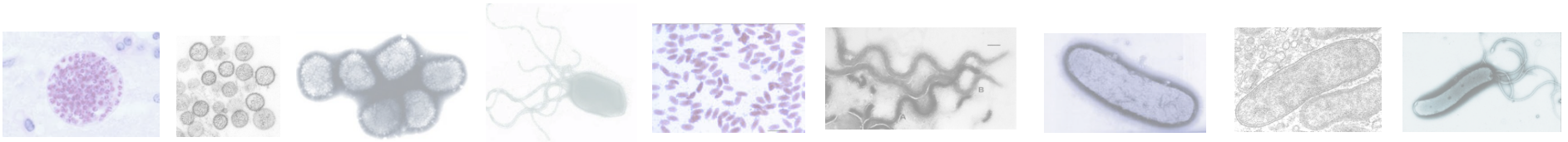
*M. subterraneus*

*Myodes glareolus*

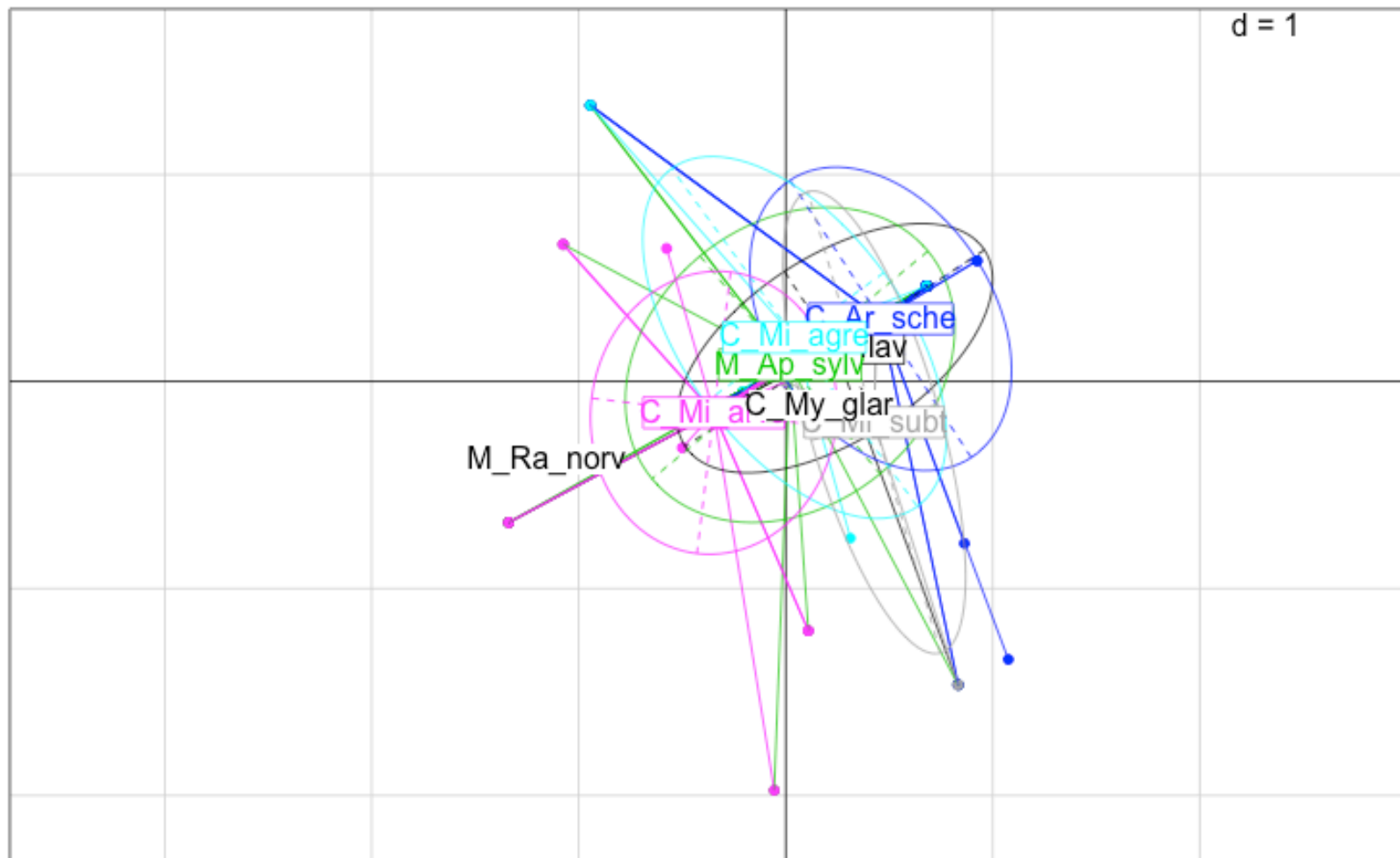
*Apo. flavicolus*

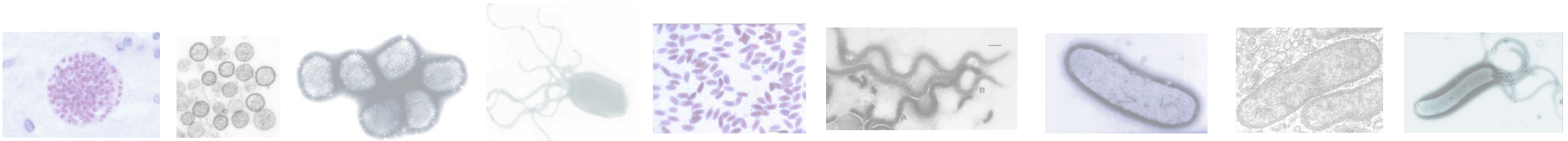
*Apo. Sylvaticus*

*Rattus norvegicus*

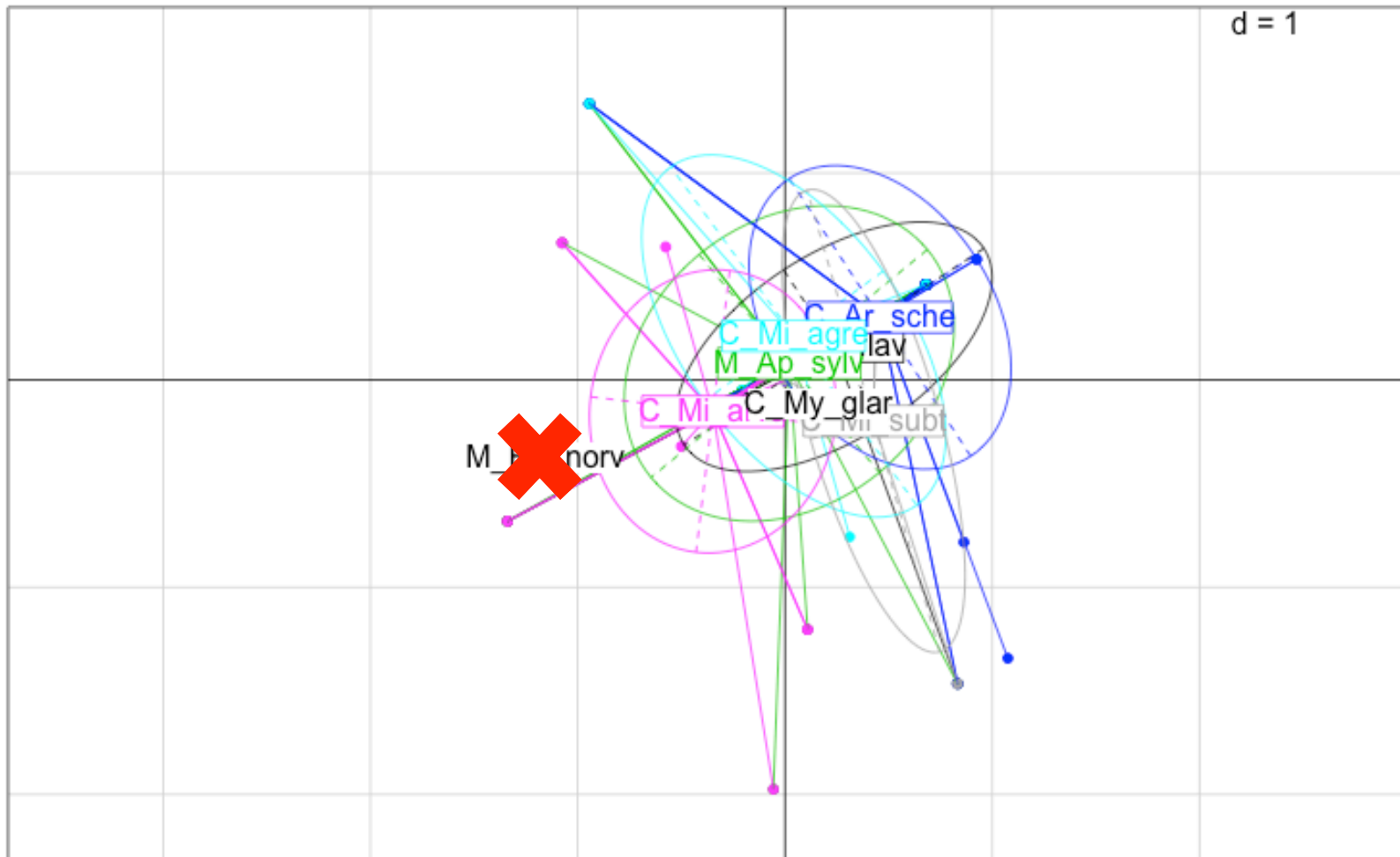


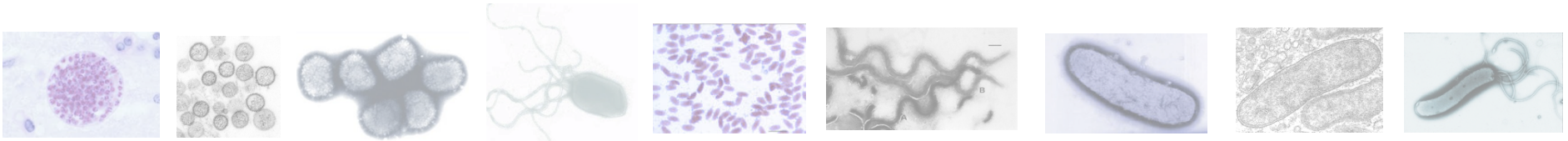
## Screening Analysis



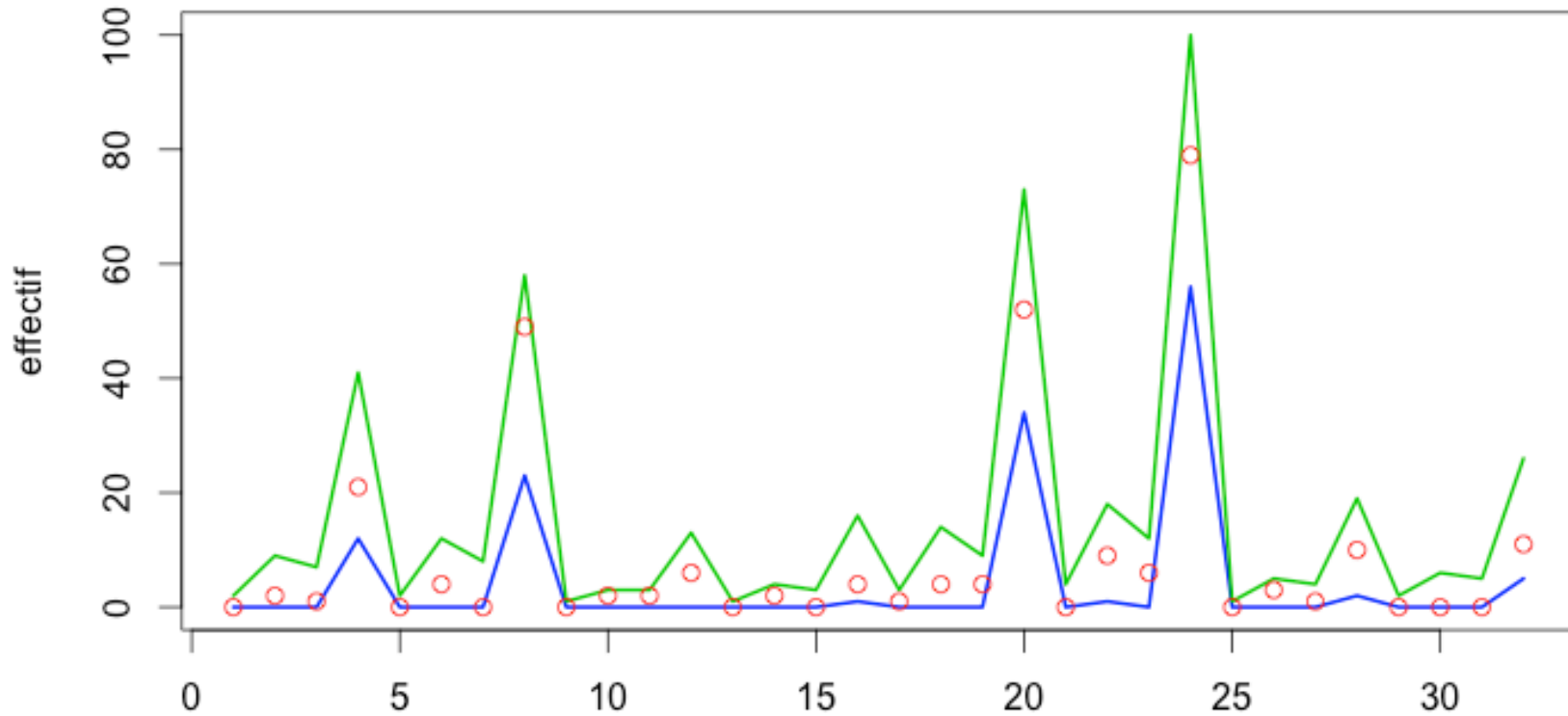


## Screening Analysis





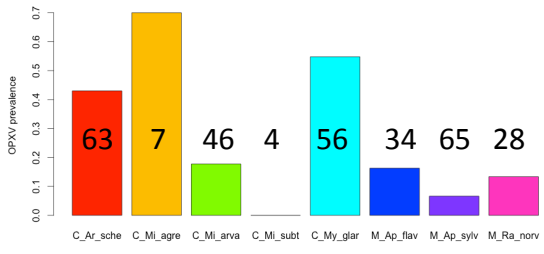
## Screening Analysis



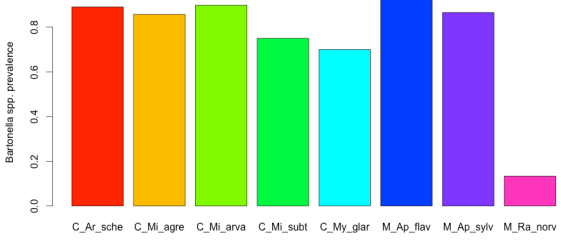
Mycoplasma occurs  
more often by itself  
than by chance



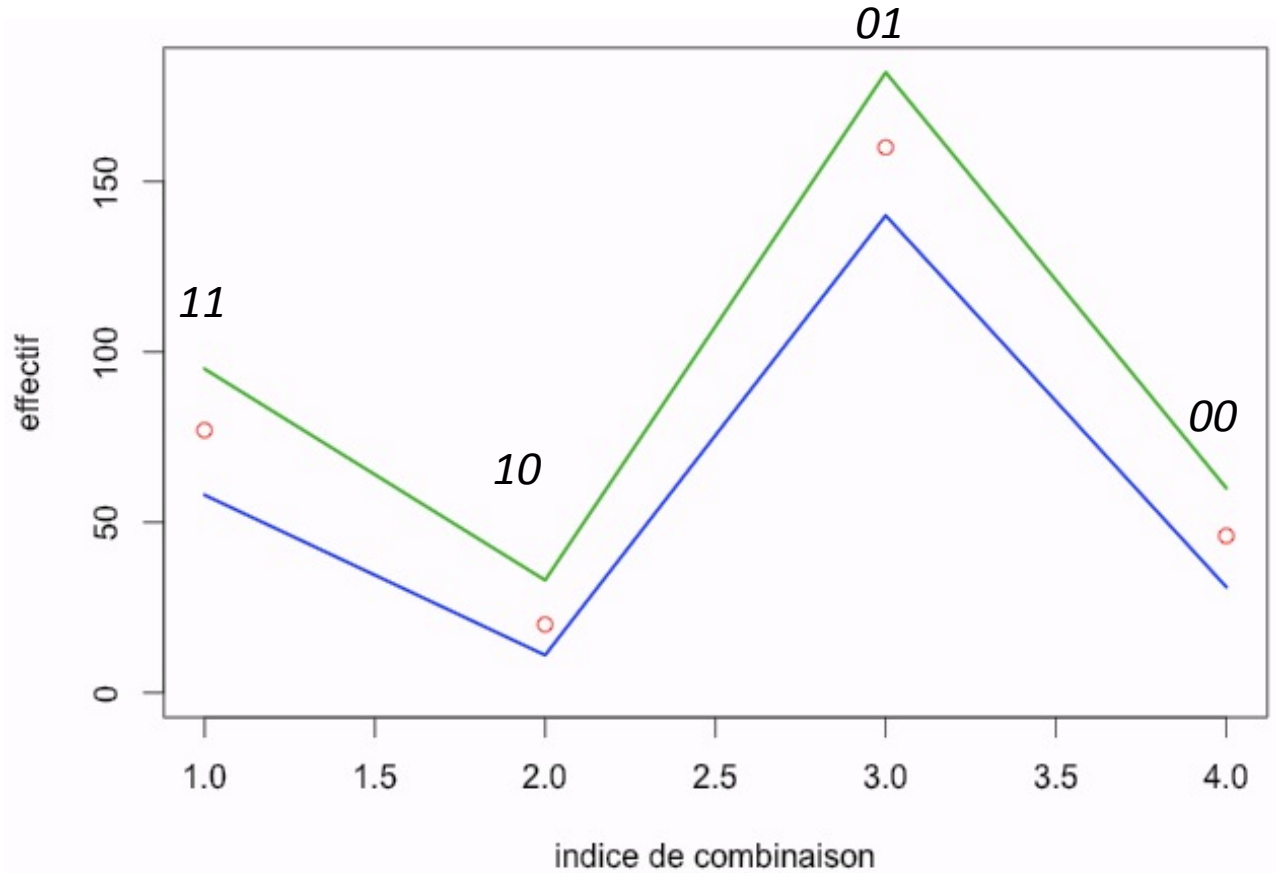
### OPXV antibodies



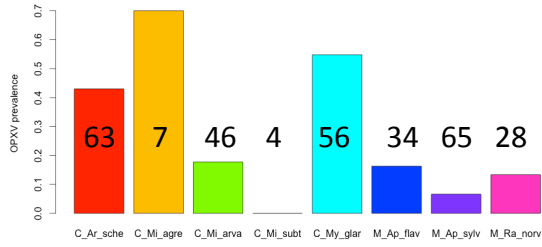
### Overall *Bartonella* spp. prevalence



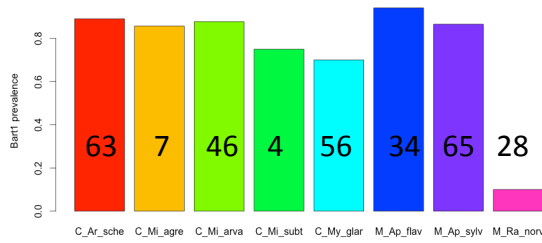
## Screening Analysis



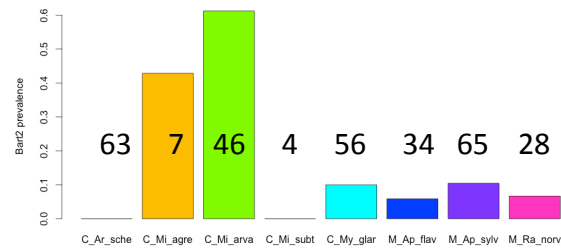
### OPXV antibodies



### Bartonella spp. 1



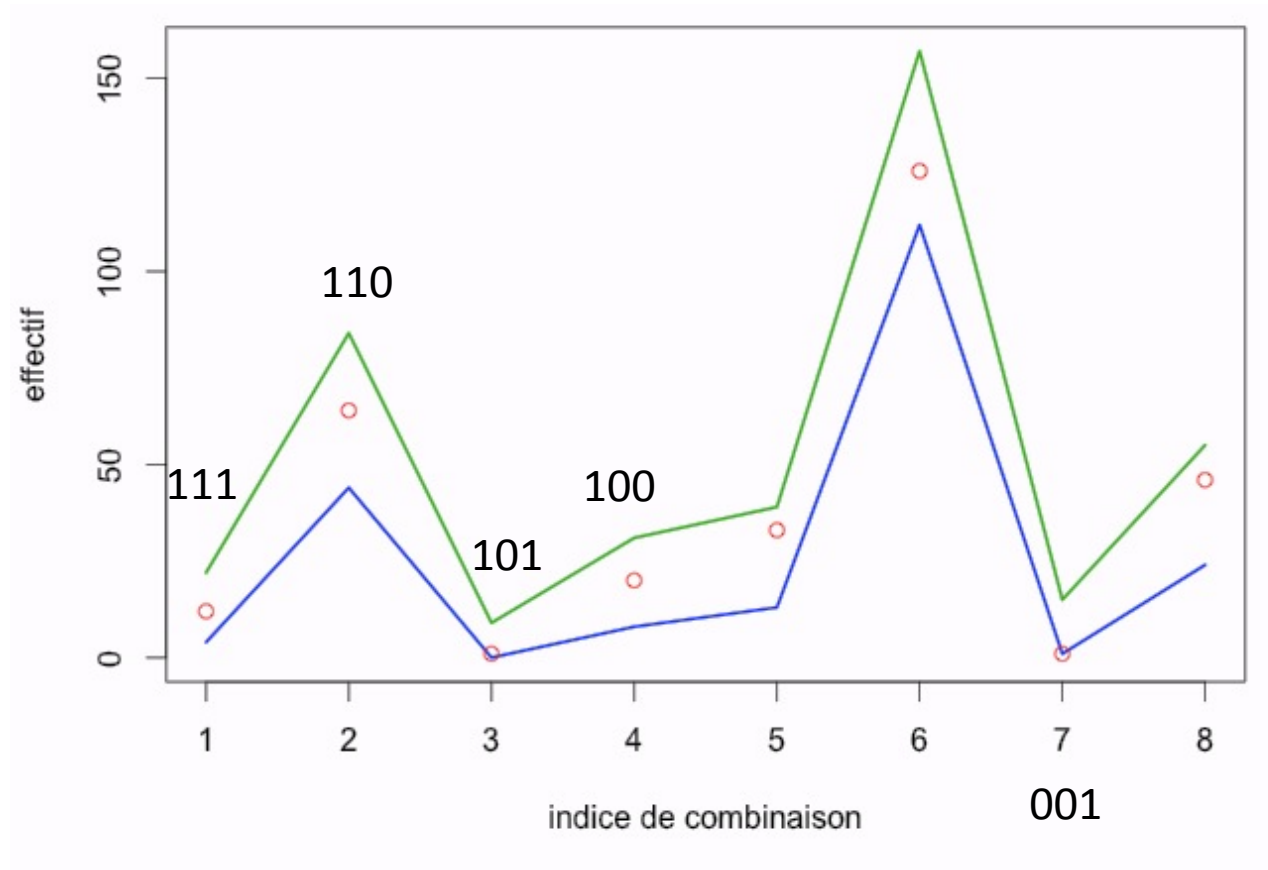
### Bartonella spp.2



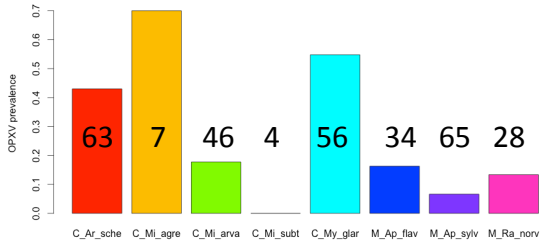
## Screening Analysis

Association Obs - +

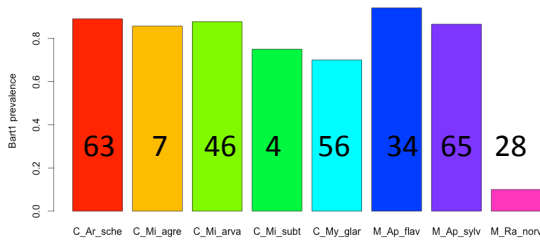
001 1 1 15 p = 0.0116



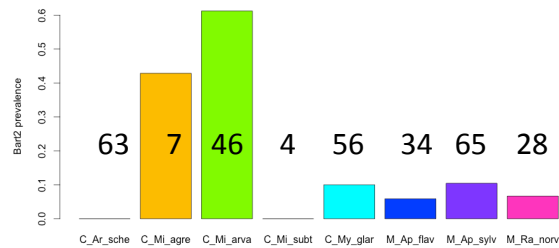
### OPXV antibodies



### Bartonella spp. 1



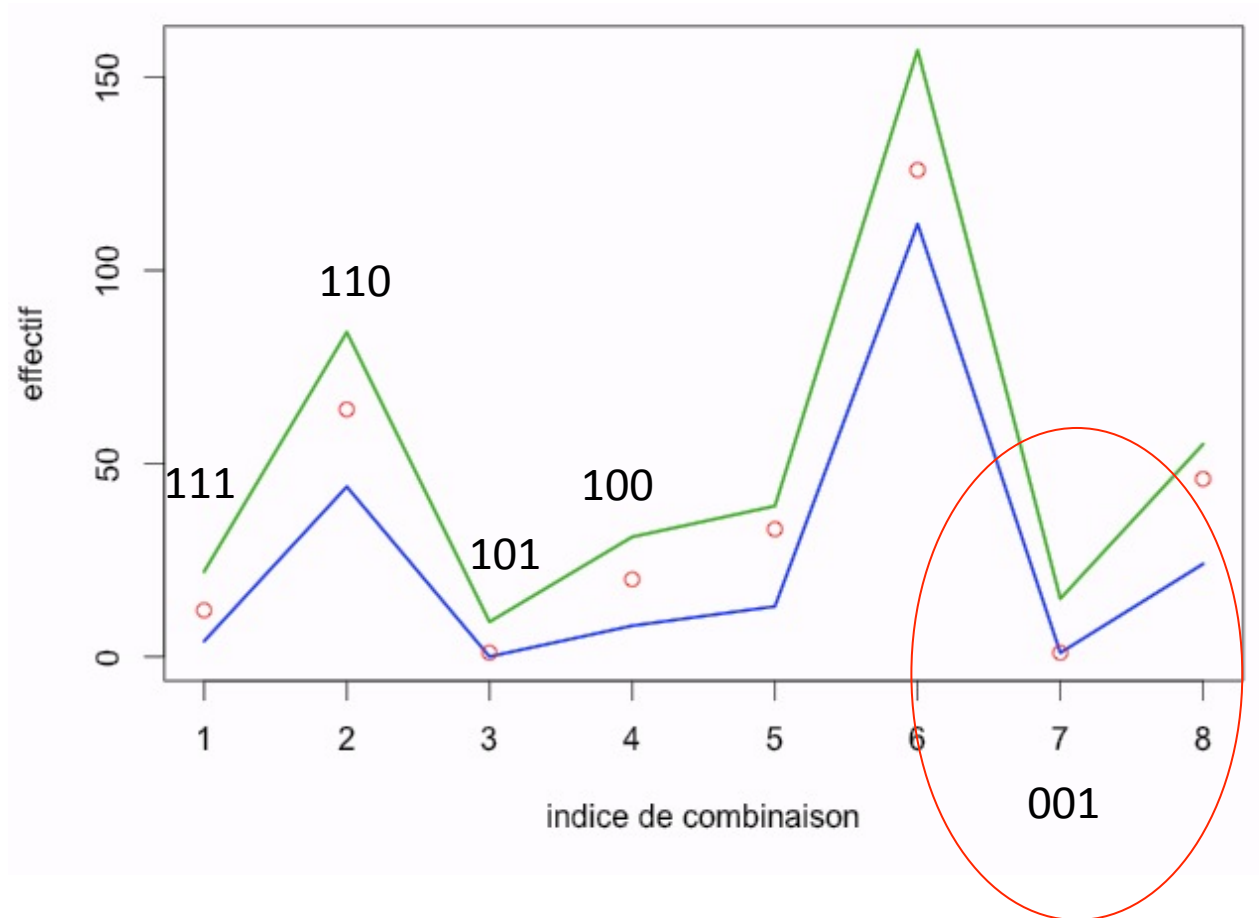
### Bartonella spp.2



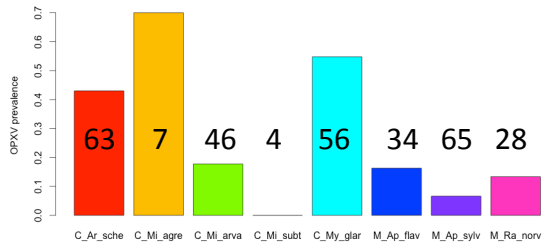
## Screening Analysis

Association Obs - +

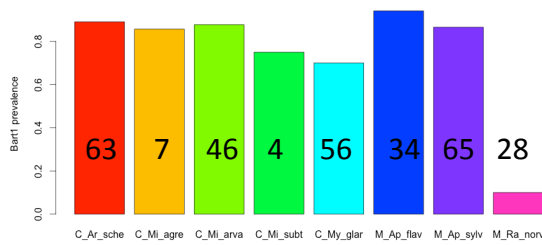
001 1 1 15 p = 0.0116



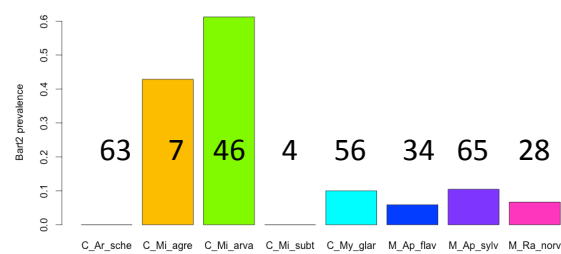
## OPXV antibodies



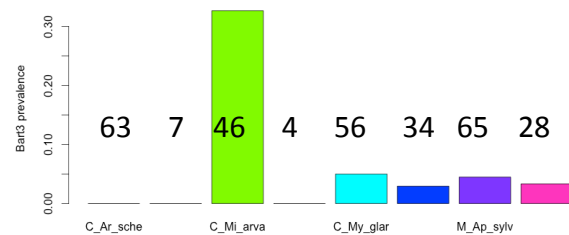
## Bartonella spp. 1



## Bartonella spp.2



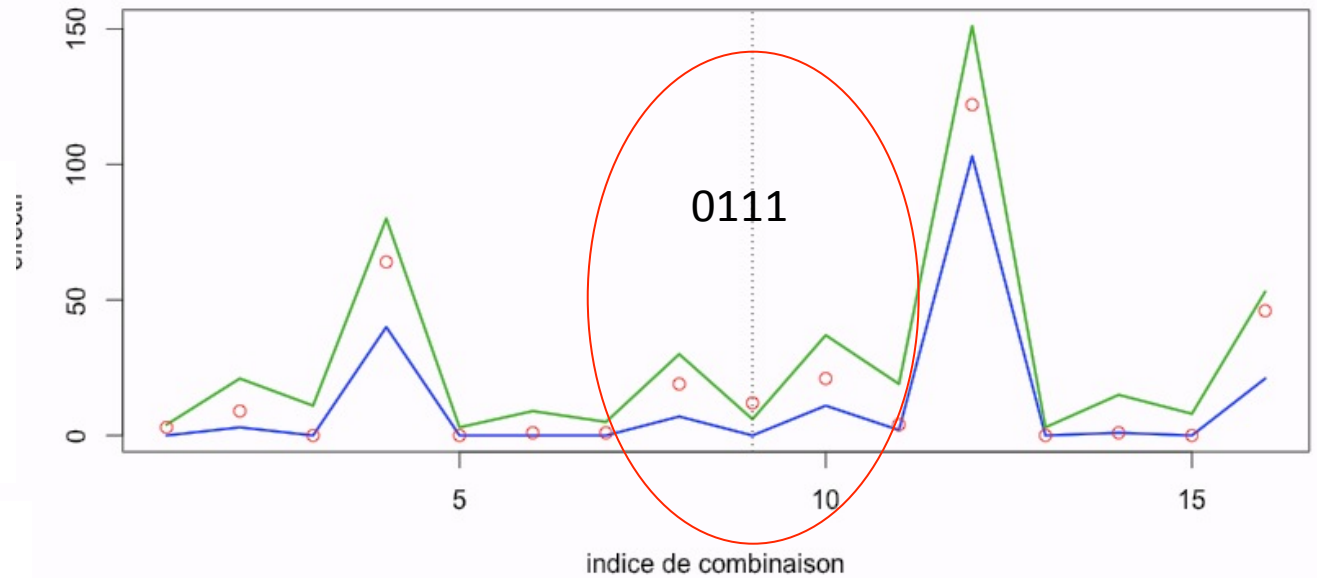
## Bartonella spp.3



## Screening Analysis

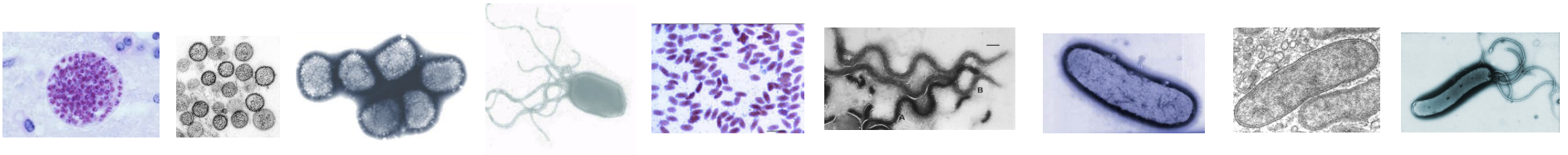
Association Obs - +

0111 12 0 6 p = 0



*Negative association OPXV & Bartonella species richness?*

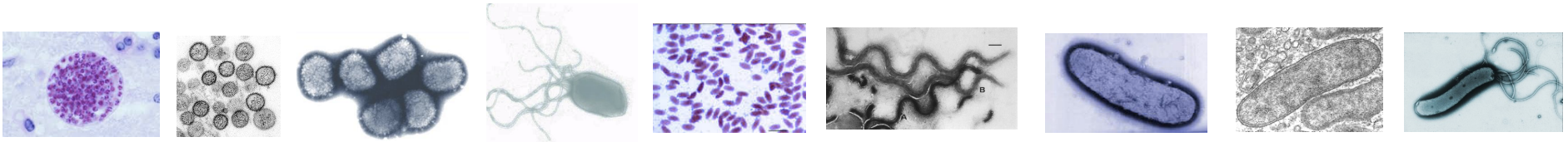




## Summary

- ✓ Do co-infections occur?
- ✓ What determines co-infection rates?
- ✗ Are there associations (+ & -) between parasites (or a history thereof)?

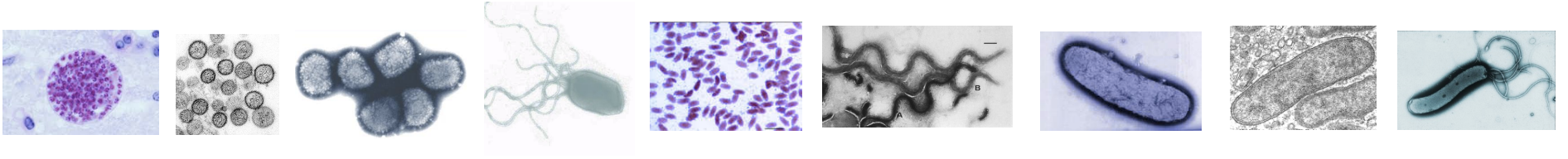




# Perspectives

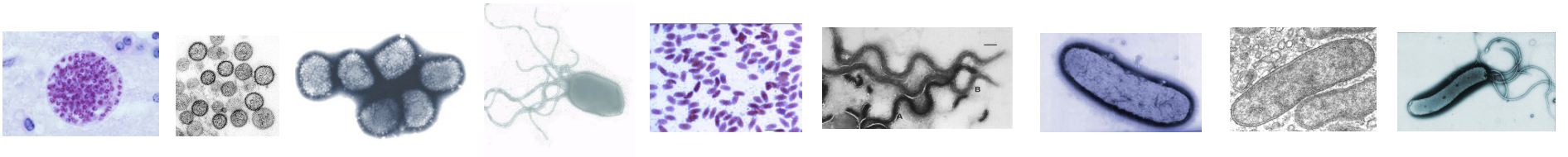
- How does OPXV affect the species-richness of the *pathobiome*?
- What about opportunistic infections of the splenic *microbiome*?
- How does *phylogenetic distance* impact the detection and/or reality of parasite-parasite interactions?





**Thank you!**

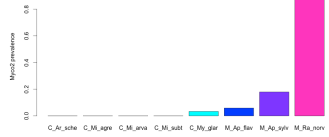




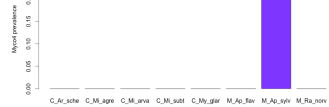
**Bon retrait!**



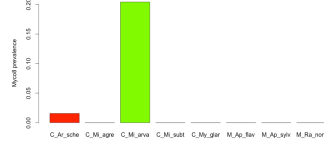
2 (99% rat *M.haemomuris*)



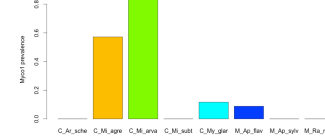
4 (99% *M.coccoides* (mouse)/ *M.haemofelis*)



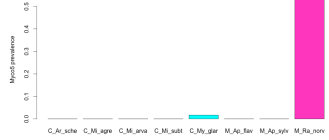
8 (95% bat)



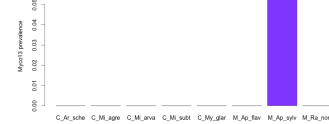
1 (99% Ixodes ticks)



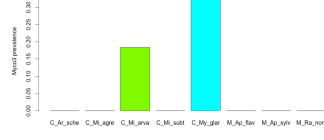
5 (100% rat)



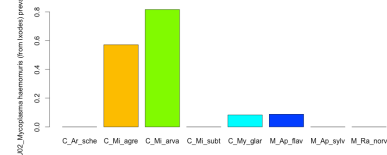
13



3 (99% leopard)



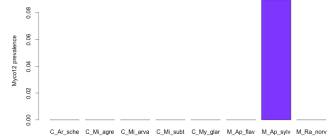
U02 (99% Ixodes ticks)



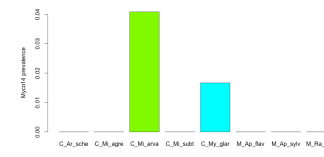
6 (99% mouse, micromys minutus)



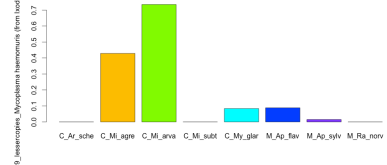
12



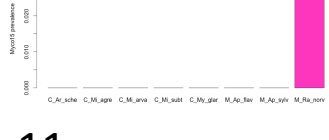
14



U09 (98% Ixodes ticks)



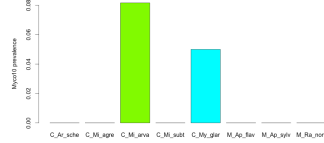
15 (100% murine *M. pulmonis*)



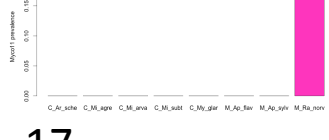
9



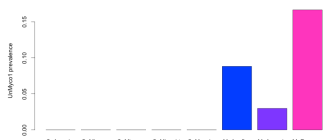
10 (96% leopard / 94% bat)



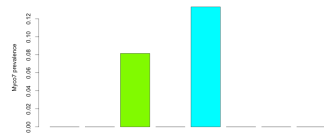
11 (100% mouse *M. ravidulmonis*)



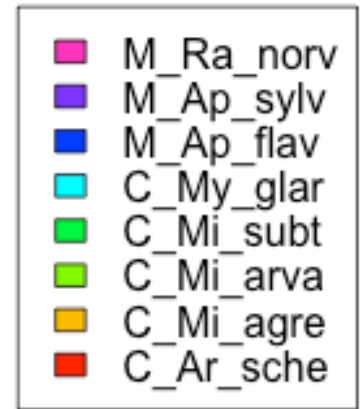
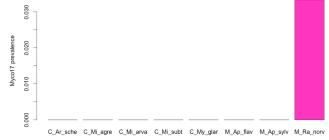
U12 (93% leopard and murine)



7 (96% leopard / 94% rat)



17 (99% rat *M.haemomuris*)



19+ independent *Mycoplasma* OTUs

