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# Metabarcoding of Bacterial Pathogens in a Rodent Pest: Which Organ?

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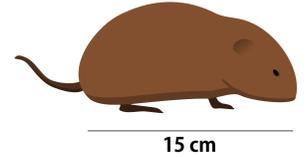
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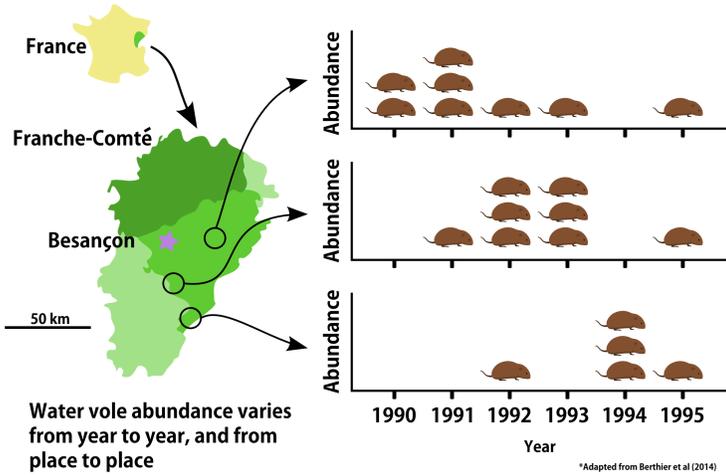
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The water vole, *Arvicola terrestris*



## Water voles (*Arvicola terrestris*) are pests in Franche-Comté



When they are abundant, they can cost a single farmer thousands of euros in damage per year



Water voles can carry tapeworms that are dangerous to humans

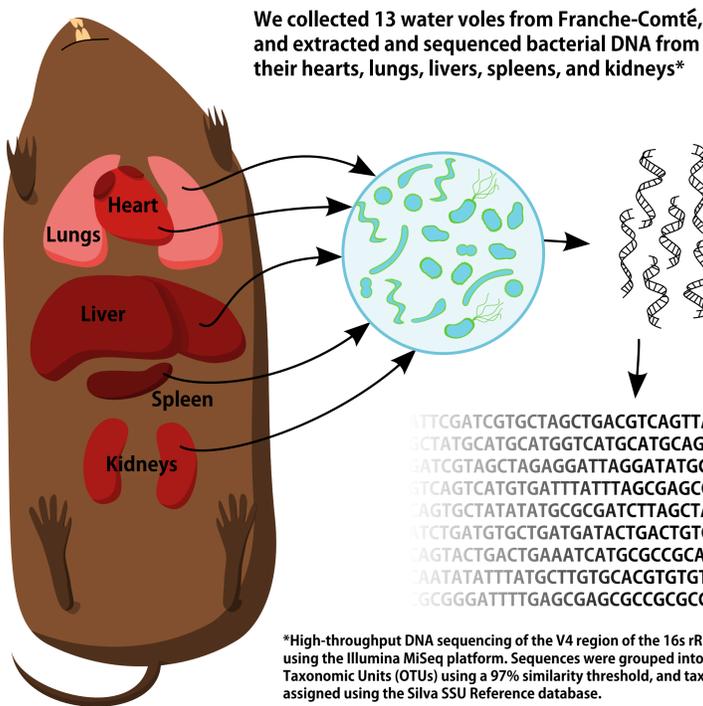


We know little about the bacteria hosted by this rodent; bacteria may drive changes in vole abundance, and may also pose a risk to human health



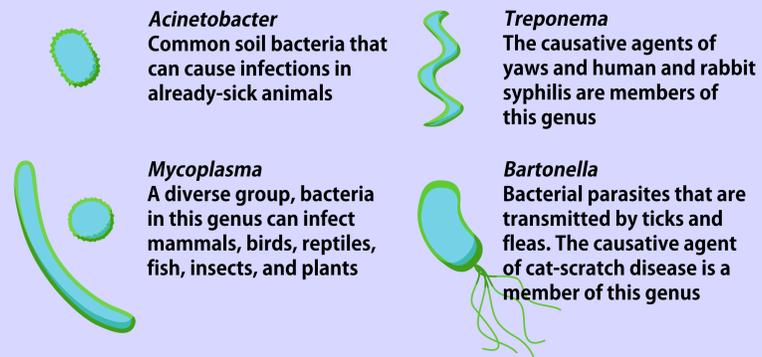
## With which organ should we look for bacteria?

We can use DNA sequencing technology to search for bacteria, but we need to know which organs to look in.



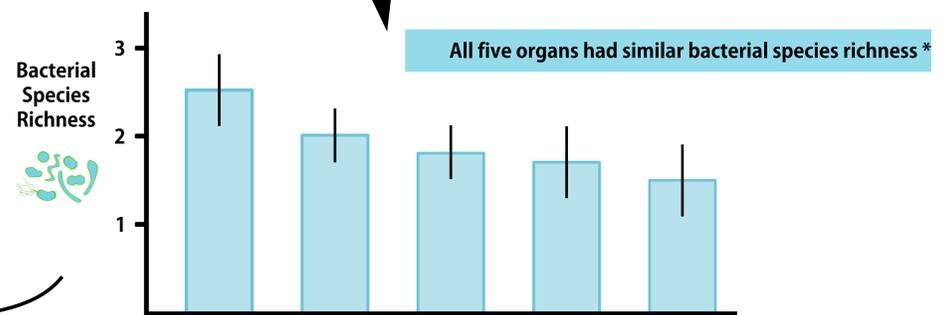
## We found 25 potentially pathogenic bacteria in our voles

These are bacteria that we know can cause disease in animals, and may be causing disease in our voles. The 5 most prevalent bacteria we found:

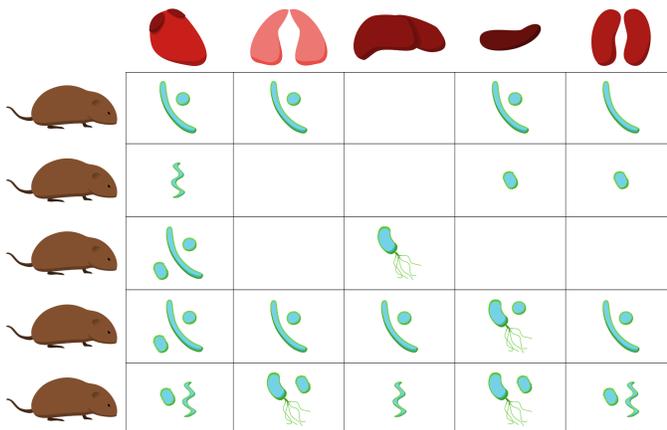


### Other bacteria we found:

- Avibacterium*
- Pasteurellaceae*
- Helicobacter*
- Aerococcus*
- Chryseobacterium*
- Corynebacterium*
- Leptospira*
- Peptococcus*
- Spingomonas*
- Streptococcus*
- Ureaplasma*



## We found different bacteria in different organs



But...



These patterns of different bacteria in different organs appear random\*

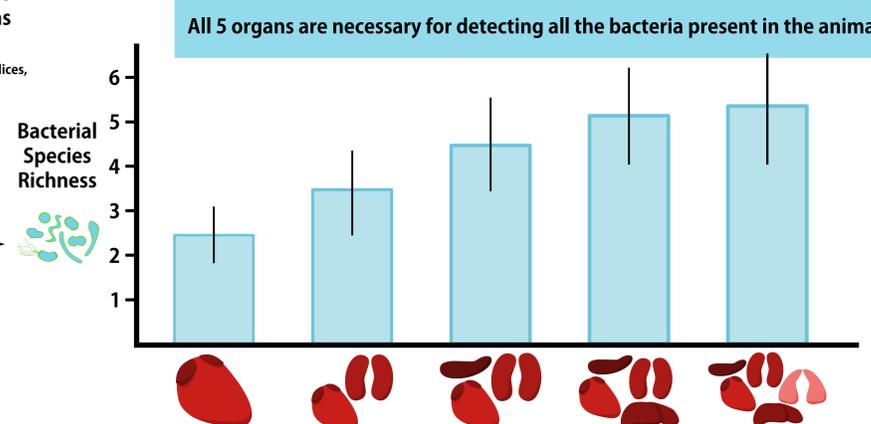
\*PERMANOVA with Jaccard dissimilarity indices, pseudo-F<sub>4,51</sub> = 1.34, p=0.120

And...

If we pool all organs within an animal, we find an average of 5.4 bacterial species per animal\*

\*5.4 ± 0.7 (mean ± standard error), which is 2.9 ± 0.9 species (bootstrapped mean and 95% confidence interval) greater than the mean bacterial richness of the heart, the organ with the highest bacterial richness.

All 5 organs are necessary for detecting all the bacteria present in the animal\*



## Conclusion: We should use all five organs when we are looking for bacteria in water voles

Different organs host different bacteria, and bacteria are not concentrated in a single organ

In addition, all 5 organs are necessary to detect host-population-level differences in bacterial assemblages. The animals sampled here are from two different populations; we found that organ bacterial richness does not vary with location (generalized linear mixed-effects model for average OTU richness within organs, with animal and location as random effects, fit using maximum likelihood, a Poisson distribution, and log-link function), but differences in pooled, liver, and lung bacterial assemblages map to host populations (ordination and PERMANOVA analysis of Jaccard dissimilarities). Livers and lungs are prone to having no detectable bacteria, making them poor candidates for studying host-population level bacterial assemblages, thus pooling organs within animals is the "best" choice.