



# ISWAVLD 2023

International Symposium of the World  
Association of Veterinary Laboratory  
Diagnosticians

29 JUNE-1 JULY  
2023  
Congress Centre  
Lyon

*Towards  
the veterinary  
diagnostics  
of the  
future*

Main topic : Surveillance and control of emerging diseases

## **Spatio-temporal variations of zoonotic hazard associated with small mammal communities along a gradient of forest anthropization.**

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### Introduction

These last decades, the world has experienced a growing number of emerging zoonotic diseases. Their emergence is attributed to the erosion of biodiversity that results from human activities. Dilution effect, the decrease of disease risk with increasing host diversity (1), has been the subject of numerous studies. It could serve as a nature-based solution to mitigate the circulation of zoonotic agents and zoonoses emergence. Gibb et al (2) analyzed the impact of anthropogenic disturbance on host communities and showed an increase in competent host species in anthropogenic ecosystems. Hence, it is crucial to examine not only the specific richness but also the composition of host communities to better understand the relationships between biodiversity and zoonotic risk (3).

Here, we addressed this question by examining rodent-borne diseases along a gradient of forest urbanization. Rodents are main reservoirs of zoonotic agents due to their taxonomic diversity, ability to colonize diverse habitats and their close proximity to humans (4). Besides, forests and large urban green spaces are environments where rodents are abundant and human/domestic-wildlife interactions are likely. As such, it is essential to carefully assess the circulation of zoonotic agents within small mammal communities in these ecosystems and to analyze how urbanization affects the relationships between biodiversity and zoonotic risks.

### Methods

During 2,5 years, we surveyed small mammal communities and their zoonotic pathogens along a gradient of urbanization in Eastern France, including biological reserves, managed forests and urban parks. We used trapping success index as a proxy for the relative abundance of each species. We combined molecular and serological approaches to describe pathogen prevalence. 16S metabarcoding was applied on spleen samples to detect pathogenic bacteria with no a priori. Specific quantitative PCR of the *LipI32* gene was performed to detect pathogenic leptospires. Lastly, serological analyses based on immunofluorescence assays (IFA) were performed to detect antibodies against Orthopoxvirus. We analyzed spatiotemporal variations of the prevalence of each pathogen. We used generalized linear models to investigate the relationship between the prevalence of each pathogen and the structure of small mammal communities.

### Results

We trapped 1593 small mammals representing 15 species of rodents and soricomorphs. Urbanization strongly shaped the composition of these communities, with urban avoiders, adapters and dweller species. Moreover, we observed marked variations of the abundance of these species between seasons and years.

The use of 16S metabarcoding enabled to reveal the circulation of six bacteria genera (*Anaplasma*, *Orientia*, *Borrelia*, *Neorhlichia*, *Bartonella*, *Francisella*), with potentially high levels of prevalence in forests. Leptospire were detected in all sites surveyed, with prevalence ranging from 0% to 28%. We detected high seroprevalence of Orthopoxvirus, in particular in the biological reserves surveyed (resp. 42% and 60%). Hyper-reservoir species (species found to carry several pathogens) were mainly urban adapter species.

### Conclusions

Geography and urbanization emerged as important factors driving the composition of small mammal communities and the prevalence of zoonotic agents. The relationships between the circulation of zoonotic rodent-borne pathogens and the diversity of small mammal communities appeared to be idiosyncratic, depending on the pathogens that were studied.