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Rodents as Reservoirs of Zoonotic Diseases in Guinea: Implications for Surveillance and Public Health

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Abstract

In the Republic of Guinea, rodents are an important reservoir and vector for numerous zoonoses. However, the mechanisms of transmission and the influence of environmental and anthropogenic factors remain poorly understood. The present study aimed to analyse the dynamics of circulation of rodent-borne zoonotic agents in order to propose effective strategies for the surveillance, prevention and control of emerging and re-emerging diseases. Between 10 July 2023 and 15 August 2024, an inventory of small mammal fauna was carried out in several prefectures of the country (N'Zérékoré, Lola, Yomou, Beyla, Macenta, Gueckédou, Faranah, Kindia, Kankan, Siguiri, Labé, Dalaba and Dubréka). A total of 1855 individuals belonging to 18 species, including *Rattus rattus*, *Mus musculus* and *Mastomys natalensis*, were captured using Sherman and Formizon traps. The specimens collected underwent biometric and pathological analyses, supplemented by blood and tissue samples subjected to molecular investigations (PCR, centrifugation and sequencing). The results revealed the presence of Lassa virus RNA in *Mastomys natalensis*, as well as *Coxiella burnetii* infections in *Xerus erythropus*, representing a potential risk to human health. In addition, *Borrelia spp.*, *Leptospira spp.*, *Anaplasma spp.* and *Ehrlichia spp.* were detected, indicating active circulation of these pathogens within the rodent populations studied. These results highlight the need to strengthen sur-

veillance of small mammals in Guinea and to adopt appropriate biosecurity measures, particularly in areas of high interaction between wildlife and human communities.

Keywords

Zoonoses, Rodents, Surveillance, Emerging Diseases, Guinea

1. Introduction

Rodents are reservoirs for approximately 40% of known zoonoses and have been responsible for major epidemics and pandemics throughout history. Zoonoses associated with rodents can be viral (such as smallpox), bacterial (such as plague), helminthic (such as schistosomiasis) or protozoan (such as toxoplasmosis). Some of these diseases can spread between humans and cause more than 400 million cases worldwide each year. In addition, rodents are likely to carry as yet undiscovered parasites that could cause new emerging diseases [1].

Their strong affinity for urban environments, their phylogenetic proximity to humans, their anthropophilic nature and the subsequent spread of certain invasive alien species—such as the house mouse and black rat—through global trade make rodents crucial players in the multi-scale spread of zoonoses. Recent studies in several West African countries (such as Benin, Niger and Senegal) have shown that rodents carry zoonotic pathogens (e.g., *Lassa virus*, leptospires, plague bacilli, typhus infectious agent), which are responsible for particularly harmful epidemic episodes and are unfortunately often neglected in terms of anticipation, consideration and/or management [1].

Lassa fever is a viral haemorrhagic fever with a rodent host, *Mastomys natalensis*, and is endemic in certain regions of West Africa. There have been repeated epidemics of Lassa fever in Sierra Leone, Nigeria, Liberia and even Guinea [2].

The disease is mainly transmitted to humans through direct or indirect contact with rodent bodily fluids such as urine, faeces, saliva and blood. Secondary human-to-human transmission occurs through contact with bodily fluids or household objects, or during healthcare [3]. Human-to-human transmission can also occur through the secretion of aerosols in the form of sneezing, expectoration, faeces, urine, blood and fluid [4]. There is no vaccine, and prevention is recommended through improved hygiene practices, including food storage, rodent control measures, and infection prevention practices [2].

The latest report on human infectious diseases showed that there are nearly 1407 pathogens affecting humans worldwide. Of these, 800, or 58%, are caused by zoonotic pathogens transmitted to humans by animals. Another study identified 335 human infectious diseases that have emerged over the past six decades. This figure represents 25% of all human infectious diseases. Of these 335 recently emerged human diseases, 202 (60%) are caused by zoonotic pathogens and 144 (43%) are

caused by pathogens whose main source is wildlife. The rate of disease emergence has increased over the last six decades [5].

Rodents are both pets and laboratory animals. In these areas, they are valued for their qualities. However, as wild rodents, they are important in public health, which is why they sometimes, and rightly so, have a bad reputation. Indeed, they are particularly hated because they carry serious diseases such as the plague [6].

Moreover, a recent study conducted in Senegal revealed a remarkable diversity of pathogens in rodents, including *Bartonella spp.*, *Borrelia crocidurae*, members of the *Anaplasmataceae*, as well as several protozoa (*Piroplasmida*, *Hepatozoon* spp., *Kinetoplastidae spp.*). Notably, molecular analyses enabled the identification of two potentially novel agents: *Candidatus* "*Theileria senegalensis*" and *Candidatus* "*Ehrlichia senegalensis*". These findings confirm that West African rodents are not only reservoirs of known pathogens but also a likely source of emerging and yet undescribed diseases, thereby reinforcing the need for enhanced surveillance [7].

Infectious diseases (zoonoses), the subject of our study, are the result of damage caused to their host by microparasites. These organisms include viruses, bacteria, fungi and protists, to which prions [6] can be added.

Whenever we attempt to control human and animal diseases in order to limit their socio-economic and ecological impacts, we act by modifying certain aspects of their ecology. Consequently, the ecology of diseases is a crucial scientific field for those involved in their management and control. This concept is often illustrated by a triangle of interactions. **Figure 1** illustrates the interactions between hosts, pathogens, and the environnemental factors, such as climate and habitat, in the dynamics of infections (see **Figure 1**).

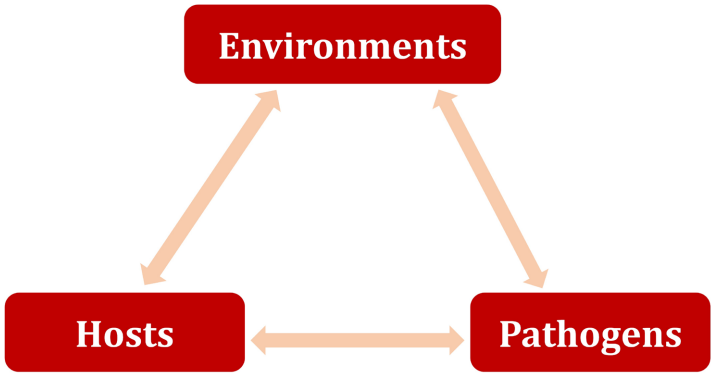

Figure 1. Ecological model of disease transmission.

The study conducted here therefore aims to prove the zoonotic importance of rodents in contact with humans in order to demonstrate the need to find new ways of controlling rodents that carry zoonoses.

General Objective

To analyse the zoonotic dynamics of rodents in Guinea in order to assess their impact on public health and develop effective prevention strategies.

Specific objectives:

- Determine the species of rodents present in different regions.
- Conduct analyses to detect viruses, bacteria or parasites that are potentially transmissible to humans.
- Analyse the mechanisms of pathogen transmission between rodents and humans.
- Develop recommendations to limit contact between humans and rodents.

2. Materials and Methods

2.1. Study Environment

Given the diversity of ecosystems in our country, we chose prefectures by natural region where diversity would be reasonable.

2.2. Materials

Biomaterial: The biomaterial consists of rodents captured in the various study areas. Capture campaigns were carried out between 10 July 2023 and 15 August 2024.

The collection of biomaterials was conducted using a stratified random sampling method, considering the ecological characteristics of the sites (forests, agricultural areas, urban zones). This approach ensured the representativeness of the different environmental strata in which rodents occur.

2.3. Study Setting

The International Centre for Tropical Infections Research in Guinea (CIRIT-Guinea) was our study setting. It is located in the prefecture of N'Zérékoré, within the grounds of the N'Zérékoré Regional Hospital, and has a staff of ten, including trainees. The infrastructure comprises four offices and four analysis laboratories.

2.4. Working Methods

Small mammals were captured using Sherman and Formizon traps baited with dried fish. The traps were set directly in dwellings, warehouses, barns, vegetable gardens and agricultural fields. At these locations, we marked the spots where the traps would be set. The size of a site is 72 by 135 metres. The traps on this site were placed at exactly the same distance from each other. All traps at each site were of the same type and were numbered.

Captures at each site were carried out four times a year: dry season (early and late), October-April and rainy season (early and late) June and September.

Each trapping session lasted approximately 8 days. The traps were checked twice a day, in the morning and evening, at 12-hour intervals.

The captured rodents were placed in breathable cotton bags, which had been moistened beforehand to prevent dehydration. All rodents used in this study were handled in accordance with international guidelines on animal welfare, including those of the Guide for the Care and Use of Laboratory Animals and the AVMA

Guidelines for the Euthanasia of Animals (2020) [8].

Some of the captured animals were released immediately after testing, while those transported to the laboratory were all euthanised.

The animals were euthanised by inhalation of isoflurane followed by a confirmatory physical method. More specifically, each animal was placed individually in an induction chamber containing a pad impregnated with isoflurane (>5%) until deep anaesthesia was achieved (absence of pincer reflex). Death was then induced by rapid cervical dislocation, in accordance with current ethical standards.

A post-mortem examination was performed, preceded by weighing, measuring the animal, determining its sex, place of capture, animal ID, trap number and species identification, followed by the collection of internal organ tissue (brain, lungs, liver, kidneys, spleen, blood and urine). The carcasses were disposed of via the establishment's secure biosafety circuit [9]-[11].

2.5. Molecular Study

Blood samples were centrifuged for 10 minutes at 800 rpm to precipitate red blood cells and obtain serum. The serum obtained was then centrifuged for 10 minutes at 14,000 rpm to precipitate white blood cells. Total RNA was extracted from the precipitated white blood cells and, separately, from 100 to 500 µl of blood plasma.

Tissue samples were homogenised in 500 µl of saline solution. Next, nucleic acids were extracted from 100 µl of 10% homogenate using the Amplisense Ribo Prep kit.

For certain animal species, species identification was confirmed by sequencing the cytochrome oxidase (cox1) gene region. For this purpose, amplification was performed with the primers described in [12].

The sequences obtained were compared using the blast algorithm with the sequences deposited in GenBank.

In addition, animal tissue samples were examined by PCR for the presence of RNA from *Lassa virus*, *Ebola virus*, *Marburg virus*, *Jingmen tick virus*, *Crimean-Congo haemorrhagic fever virus*, *Flavivirus*, *Orthobunyavirus* and *Hantavirus*. The presence of DNA from *Borrelia spp.*, *Rickettsia spp.*, *Anaplasma spp.*, *Ehrlichia spp.* and *Coxiella burnetti* was also investigated.

2.6. Statistical Analyses

The data were statistically processed using SPSS (20.0) and Statistica (version 8.0) software.

$$\text{Prevalence} = \frac{\text{Number of patients}}{\text{Total population}}$$

3. Results

During this study, five families of rodents and insectivores were identified: *Muridae*, *Soricidae*, *Nesomyidae*, *Sciuridae and Gliridae*, divided into 14 genera (*Mus*, *Rattus*, *Lemniscomys*, *Mastomys*, *Praomys*, *Dasymys*, *Lophuromys*, *Crocidura*,

Cricetomys, *Xerus*, *Heliosciurus*, *Funisciurus*, *Epixerus* and *Graphiurus*), comprising a total of 18 species. Among these, the Muridae family proved to be the most diverse, with 11 out of 18 species, reflecting its significant ability to adapt to the different environments studied. The *Sciuridae* family came in second place with four species identified, mainly arboreal. In contrast, the *Soricida*e, *Nesomyidae* and *Gliridae* families were poorly represented, with only one species each. (Table 1)

Table 1. Inventory of rodents captured.

Order	Families	Species
Rodentia	Muridae	*Mus musculus* (Linnaeus, 1758) ou spp.
		Mus spp. (Linné, 1758)
		Mus setulosus (Peters, 1876)
		Rattus rattus (Linnaeus, 1758)
		Lemniscomys zebra (Heuglin, 1864)
		Mastomys natalensis (Smith, 1834)
		Praomys daltoni Thomas, 1892)
		Praomys rostratus (Miller, 1900)
		Dasymys rufulus (Meunier, 1900)
		Lemniscomys striatus (Linnaeus, 1758)
		Lophuromys sikapusi (Temminck, 1853)
	Soricidae	*Crocidura spp.* (Walger, 1832)
	Nesomyidae	*Cricetomys gambianus* (Waterhouse, 1840)
	Sciuridae	*Xerus erytropus* (Desmarest, 1817)
		Heliosciurus gambianus (Ogilby, 1835)
		Funisciurus pyrropus (Cuvier, 1833)
		Epixerus ebii (Temminck, 1853)
	Gliridae	*Graphiurus kelleni* (Reuvens, 1890)

This faunal diversity highlights the predominance of Muridae, recognised as the main reservoirs of zoonotic pathogens, but also emphasises the presence of less common species, which could nevertheless play a significant local epidemiological role.

Analysis of the data reveals significant variation in the distribution of rodents across prefectures and species. Kindia Prefecture recorded the highest number, with 239 specimens, followed by Faranah (210) and Dubréka (196). In terms of taxonomy, *Rattus rattus* dominated the catches with 556 individuals, confirming its commensal nature and its significant ability to adapt to urban and peri-urban environments. It was followed by *Mus musculus* (230 individuals) and *Cricetomys gambianus* (157 individuals), two species that are also well represented in environments frequented by humans. (Table 2)

Table 2. Summary of rodent species captured by prefecture.

Pathogens \ Prefectures	N'Zérékoré	Kindia	Lola	Yomou	Beyla	Macenta	Guéckédou	Kankan	Siguiri	Labé	Dalaba	Dubréka	Faranah	Total
Mus musculus	24	47	5	3	13	10	20	12	13	14	7	39	23	**230**
Mus spp.	13	18	6	5	11	7	12	9	9	7	6	17	14	**134**
Rattus rattus	48	57	49	17	39	45	42	40	43	35	52	46	43	**556**
Mastomys natalensis	12	13	5	4	9	12	8	8	8	6	4	12	15	**116**
Crocidura spp.	7	18	5	2	6	7	8	3	3	13	5	13	11	**101**
Lophuromys sikapusi	10	13	7	6	12	8	0	9	9	5	7	13	16	**115**
Dasymys rufulus	15	15	4	8	20	14	0	5	4	7	5	15	11	**123**
Lemniscomys striatus	5	16	3	4	13	5	0	10	0	3	4	11	12	**86**
Mus setulosis	0	5	3	1	5	4	0	0	3	2	6	3	7	**39**
Cricetomys gambianus	6	18	11	12	14	16	4	10	10	17	12	15	12	**157**
Xérus erytropus	2	11	1	5	9	7	2	5	0	13	3	12	15	**85**
Lemniscomys zébra	5	3	3	3	8	6	0	2	1	7	0	0	11	**49**
Praomys daltoni	3	3	0	0	0	1	0	1	0	2	0	0	0	**10**
Praomys rostratus	2	2	0	0	0	0	0	0	0	1	0	0	2	**7**
Funisciurus pyrropus	0	0	0	0	1	0	0	0	0	0	0	0	4	**5**
Heliosciurus gambianus	0	0	0	0	3	1	0	0	0	3	0	0	5	**12**
Epixerus ebii	1	0	0	2	1	3	0	0	0	4	0	0	7	**18**
Graphiurus kelleni	1	0	0	1	2	1	0	0	0	5	0	0	2	**12**
Total	**154**	**239**	**102**	**73**	**166**	**147**	**96**	**114**	**103**	**144**	**111**	**196**	**210**	**1855**

Conversely, certain species are poorly represented: *Epixerus ebii* (18 individuals), *Graphiurus kelleni* (12), *Heliosciurus gambianus* (12), *Funisciurus pyrropus* (5), *Praomys daltoni* (10) and *Praomys rostratus* (7). This low abundance could reflect a more restricted distribution, a naturally low density or lower capture rates linked to their ecological behaviour.

These results suggest that the dominant species, particularly *Rattus rattus* and *Mus musculus*, could play a central role in the dynamics of zoonotic disease transmission, given their proximity to human habitats. On the other hand, less abundant species, although in the minority, should not be overlooked as they could constitute specific reservoirs for certain pathogens.

Analysis of the results using molecular methods showed the presence of *Borrelia spp*. Bacterial DNA, with infections found in various rodents captured in different prefectures. The infected rodent species are *Mus musculus*, *Mus spp.*, *Rattus rattus*, *Mastomys natalensis*, *Dasymys rufulus*, and *Lemniscomys zebra*. Forty-two positive samples were identified, indicating the potential circulation of *Borrelia spp*. among rodents in the Republic of Guinea.

Further studies, such as sequencing and microagglutination reaction, are needed to assess the pathogenicity of this bacterium to humans. In addition, blood sediment samples were analysed, showing the presence of DNA from the bacteria *Anaplasma spp.*, *Leptospira spp.*, and *Ehrlichia spp.* Four (4) cases indicating the presence of *Ehrlichia spp.* were detected in *Cricetomys gambianus*, and four positive cases were identified for *Leptospira spp.*, distributed as follows: 1 *Lemniscomys striatus* and 3 *Dasymys rufulus*, while for *Anaplasma spp.*, 5 cases were identified in *Lemniscomys striatus* and *Crocidura spp.* (Table 3)

Table 3. Distribution of pathogens by rodent species.

Prefectures / Pathogens	*Borrelia spp.*	*Mamarenavirus lassa*	*Anaplasma spp.*	*Leptospira spp.*	*Ehrlichia spp.*	*Coxiella burnettii*	Total
Mus musculus	12	0	0	0	0	0	**12**
Mus spp.	9	0	0	0	0	0	**9**
Rattus rattus	15	0	0	0	0	0	**15**
Mastomys natalensis	2	2	0	0	0	0	**4**
Crocidura spp.	0	0	3	0	0	0	**3**
Lophuromys sikapusi	0	0	0	0	0	0	**0**
Dasymys rufulus	2	0	0	3	0	0	**5**
Lemniscomys striatus	0	0	2	1	0	0	**3**
Mus setulosis	0	0	0	0	0	0	**0**
Cricetomys gambianus	0	0	0	0	4	0	**4**
Xérus erytropus	0	0	0	0	0	1	**1**
Lemniscomys zébra	2	0	0	0	0	0	**2**
Praomys daltoni	0	0	0	0	0	0	**0**
Praomys rostratus	0	0	0	0	0	0	**0**
Funisciurus pyrropus	0	0	0	0	0	0	**0**
Heliosciurus gambianus	0	0	0	0	0	0	**0**
Epixerus ebii	0	0	0	0	0	0	**0**
Graphiurus kelleni	0	0	0	0	0	0	**0**
Total	**42**	**2**	**5**	**4**	**4**	**1**	**58**

Analysis of brain tissue samples from *Mastomys natalensis* detected the presence of Lassa virus RNA in samples from 2 *Mastomys natalensis*.

The analyses conducted highlight the diversity and active circulation of several zoonotic pathogens among rodents in the Republic of Guinea. (Table 4)

Lassa virus: detected in *Mastomys natalensis* in N'Zérékoré, this result confirms the role of this species as the main reservoir of the virus and highlights the persistence of a major epidemiological risk in the forest region.

Coxiella burnetii: found in *Xerus erythropus* in N'Zérékoré, this is an important finding, as this agent is responsible for Q fever, a zoonosis that can be transmitted to humans.

Table 4. Distribution of agents by prefecture.

Pathogens \ Prefectures	N'Zérékoré	Kindia	Lola	Yomou	Beyla	Macenta	Guéckédou	Kankan	Siguiri	Labé	Dalaba	Dubréka	Faranah	Total
Borrelia spp.	9	8	2	1	0	2	1	5	3	4	2	5	0	**42**
Mamarenavirus lassa	2	0	0	0	0	0	0	0	0	0	0	0	0	**2**
Anaplasma spp.	2	1	0	0	0	0	1	1	0	0	0	0	0	**5**
Leptospira spp.	1	1	0	0	0	0	0	0	0	0	0	2	0	**4**
Ehrlichia spp.	2	1	0	0	0	0	0	1	0	0	0	0	0	**4**
Coxiella burnettii	1		0	0	0	0	0	0	0	0	0	0	0	**1**
Total	**17**	**11**	**2**	**1**	**0**	**2**	**2**	**7**	**3**	**4**	**2**	**7**	**0**	**58**

Anaplasma spp. and *Ehrlichia spp.*: their detection in several species (*Cricetomys gambianus*, *Lemniscomys striatus*, *Crocidura spp.*) spread across different prefectures indicates a wider circulation of these bacteria, which are often associated with arthropod vectors (ticks).

Borrelia spp.: confirmed in various prefectures, it reflects widespread distribution and a potential threat to human health, particularly through recurrent fevers.

Leptospira spp.: cases detected in Samoé (N'Zérékoré) indicate a localised but active outbreak, which may be a source of human infection linked to water contaminated by rodent urine.

Guinea Forest appears to be the main zoonotic hotspot, accounting for the majority of positive cases and the diversity of pathogens detected.

The results confirm the central role of *Mastomys natalensis* in the transmission of the Lassa virus.

The detection of various bacterial agents (*Coxiella*, *Borrelia*, *Leptospira*, *Anaplasma*, *Ehrlichia*) highlights the complexity of the risks and the need for an integrated surveillance approach (One Health).

These data justify the implementation of targeted surveillance programmes, particularly in Guinea Forestière, and the adaptation of prevention strategies to take into account the specific ecological characteristics of each region.

In Forest Guinea, the number of captures was highest, with 738 specimens out of a total of 1855, followed by Lower Guinea (435) and Upper Guinea (427), while Middle Guinea recorded the lowest number (255). In terms of the presence of pathogens, Guinea Forest had the highest number of cases, with 24 infected individuals (1.29%), compared to 18 cases (0.97%) in Basse Guinée. These results indicate that Forest Guinea is a high zoonotic risk area, requiring enhanced surveillance and targeted actions to limit transmission. In Lower Guinea, although the prevalence appears to be slightly lower, the number of cases observed remains a cause for concern due to the large number of rodents captured. The analysis therefore highlights the need to adapt prevention and control strategies to the specific ecological and epidemiological realities of each region. (Table 5)

Table 5. Distribution of rodents carrying pathogens by natural region.

Natural Region	Number of rodents captured	Pathogen Carriers	Percentage %
Lower Guinea	435	18	0.97
Middle Guinea	255	6	0.32
Upper Guinea	427	10	0.54
Forest Guinea	738	24	1.29
Total	**1855**	**58**	**3.13**

Examination of brain tissue, blood sediments and organs detected 58 pathogens, representing an overall prevalence of 3.13%, including 38 cases (2.05%) in females and 20 cases (1.08%) in males. These results reveal a higher prevalence in females, suggesting that they may play a specific role in the transmission dynamics of infectious agents. This difference between the sexes highlights the need to integrate the gender dimension into the study of zoonoses. Further exploration of the underlying ecological and behavioural factors could help refine surveillance and prevention strategies, taking into account the specific characteristics of each sex. Table 6 presents the number of pathogens identified by sex in each studied prefecture, while Figure 2 provides a visual representation of this distribution. This allows for the comparison of pathogen diversity and prevalence between prefectures and helps identify areas with higher pathogen loads (see Figure 2 and Table 6).

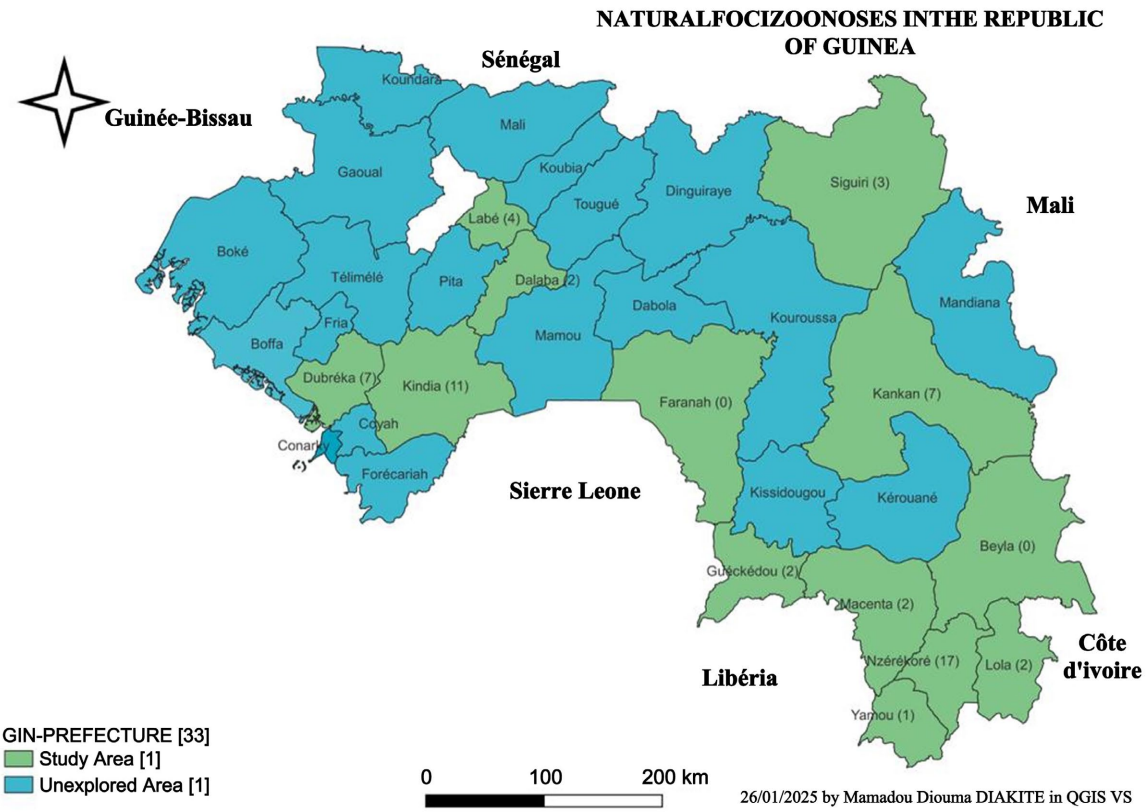

Figure 2. Map showing the prevalence of pathogens by prefecture. (Source: Bonaventure Kolié)

Table 6. Distribution of positive cases by gender.

Gender	Number of rodents captured	Positive cases	Percentage %
Male	982	20	1.08
Femelle	873	38	2.05
Total	1855	58	3.13

4. Discussion

The composition of the populations at the various study sites during the two years of research was as follows: 18 species found compared to 11 species listed by Inapogui P. *et al.* in 2000. The greatest species richness was found in the Kindia region, where we captured 16 different species compared to 12 species listed by Kéita, N. in 2021 in Kindia [13] [14]. This variation can be explained by several ecological and anthropogenic factors.

On the one hand, urbanization and agricultural expansion have altered natural habitats, favoring generalist species such as *Rattus rattus* and *Mus musculus*, which adapt easily to human-modified environments, to the detriment of more specialized species that tend to disappear.

On the other hand, climate change (changes in rainfall patterns, rising temperatures) may influence resource availability and the reproductive success of certain species, leading to the emergence of new species from neighboring areas or the decline of more sensitive species.

In addition, human activities (trade, transport of goods, livestock production) can also contribute to the passive introduction of new species into certain regions, thereby reshaping local community structures.

These shifts in species composition have major epidemiological implications, as the arrival or disappearance of specific species may alter the dynamics of zoonotic pathogen circulation, increasing or reducing the risk of transmission to humans depending on the host species involved.

In 2000, Inapogui P. *et al.* noted that the rodent population in the selected areas was largely polyspecific and representative of the central regions of Guinea. The main family characteristics of West Africa are represented there. They had listed 11 species, including 8 species of *Muridae*, one species of *Soricidae* and one species of *Gerbillidae*, which represented the bulk of the rodent fauna. All these species are likely to play an epidemiological role in the transmission of diseases or as predators of crops and harvests.

With the exception of (*Mus minutoides*, *Praomys tulbergi*, *Dasymys incomtus*, *Hyllomyscus alleni*, *Malacomys longipes spp.*, *Uranomys* spp.), it can be assumed that these species have become very rare or even extinct. We did not encounter any such fauna during our study.

However, we did record 13 other new species in the study areas (*Mus spp.*, *Mus setulosus*, *Lophyromys sikapusi*, *Dasymys rufulus*, *Lemniscomys struatus*, *Cricetomys gambianus*, *Xérus erytropus*, *Lemniscomys zébra*, *Praomys daltoni*, *Pra-*

omys rostratus, *Funisciurus pyrropus*, *Epixerus ebii* and *Heliosciurus gambianus*).

Among the truly emerging diseases, we focused primarily on zoonoses linked to wild animals, as relatively little data is available describing or reporting the emergence of diseases in this area [15].

Our results after PCR testing of blood and organ samples detected two cases of *Lassa Mammarenavirus*. This result confirms the statements made by the Guinean health authorities regarding a fatal case of *Lassa haemorrhagic fever* and more than 30 contacts recorded in the prefecture of Yomou during May 2021, which was also detected in a 17-year-old patient from the sub-prefecture of Kassadou, Guéckédou Prefecture on 20 April 2022. All this shows that rodents are reservoirs of pathogens and are a source of infection for ectoparasites and humans [16].

Blood plasma samples from all rodents were tested for the presence of hantavirus RNA using genus-specific primers. The result was negative—no hantavirus RNA was detected.

Coxiella burnettii

Blood sediment samples from all rodents were analysed for the presence of *Coxiella burnettii* bacterial DNA. The pathogen was detected in tissue samples from *Xerus erythropus* killed by a hunter in the prefecture of N'Zérékoré. This pathogen can cause serious human disease, so caution should be exercised when cutting and preparing infected animals.

Anaplasma spp. and *Ehrlichia spp.*

Blood sediment samples from all rodents were analysed for the presence of DNA from the bacteria *Anaplasma spp.* and *Ehrlichia spp. Ehrlichia spp.* bacteria were detected in samples from *Cricetomys gambianus* captured in Kindia and Kankan. *Anaplasma spp.* DNA was detected in two animals: *Lemniscomys striatus* N'Zérékoré (Samoé) and *Crocidura spp.* in Gueckedou.

Borrelia

Blood sediment samples taken from all rodents were tested for the presence of *Borrelia spp.* DNA. *Borrelia spp.* was detected in animals captured in Labé, Dubréka, N'Zérékoré (Samoé) and Kankan. Three animals (*Dasymus rufulus*, *Lemniscomys Zebra*, *Mus* spp.) from Samoé were infected with *Borrelia spp.* In Labé, Bubréka and Kankan, synanthropic rodents (*Rattus rattus*, *Mastomys natalensis* and *Mus musculus*) were infected. Sequencing is required to genotype *Borrelia* species.

Leptospira

Blood sediment samples taken from all rodents were tested for the presence of bacterial DNA from *Leptospira spp.* Four positive samples were identified, all taken in N'Zérékoré (Samoé). Leptospires were detected in Dasymus rufulus and *Lemniscomys striatus*. This result indicates that *Leptospira spp.* circulates among rodents in Samoé. Further studies (sequencing, microagglutination reaction) are needed to determine its pathogenicity to humans.

Rodents are one example of reservoirs of diseases that can be transmitted to

humans. Other more common diseases, such as arboviruses, and in particular those transmitted by mosquitoes (dengue, chikungunya, etc.), are also closely linked to climatic and environmental conditions. However, these conditions for propagation are a reflection of human activities, which disrupt ecosystems and erode biodiversity.

Analysis of the results of our work shows that the areas at risk are the N'Zérékoré and Kindia regions (where expertise is located and which are densely populated by rodents).

5. Conclusions

At the end of our research in the four natural regions of the Republic of Guinea on the zoonotic dynamics linked to rodents in the Republic of Guinea: implications for the surveillance and prevention of emerging diseases, several specimens were caught and divided into different families and species.

A total of 1855 small mammals captured across 13 prefectures were screened for zoonotic pathogens. Lassa virus RNA was detected in two *Mastomys natalensis* from N'Zérékoré, confirming this species as a key reservoir. No hantavirus was identified. However, several bacterial agents were detected: *Coxiella burnetii* in *Xerus erythropus* (Lola), *Ehrlichia spp.* in *Cricetomys gambianus* (Kindia, Kankan), *Anaplasma spp.* in *Lemniscomys striatus* and *Crocidura spp.*, *Borrelia spp.* in multiple species including *Rattus rattus*, *Mus musculus*, and *Mastomys natalensis* (Labé, Dubréka, N'Zérékoré, Kankan), and *Leptospira spp.* in *Dasymus rufulus* and *Lemniscomys striatus* (N'Zérékoré).

These findings highlight the wide range of pathogens circulating in Guinean rodents and their potential public health risks, particularly in forested areas. They underscore the urgent need for integrated surveillance, further molecular characterization (sequencing, genotyping), and community awareness, especially among hunters and rural populations, to mitigate zoonotic transmission.

PCR and RT-PCR analyses, combined with bacteriological examinations of rodent tissues and organs, have enabled us to assess the health situation and confirm the role of rodents as reservoirs for certain zoonoses.

Based on our observations, the overall health situation appears to be of little concern, although the presence of zoonoses that are potentially dangerous to humans, particularly professionals, cannot be overlooked.

These diseases are transmitted from host to host when favourable conditions are present, reflecting their dependence on ecosystem disturbances.

Thus, it is likely that these diseases and their vectors circulate within a borderless area, increasing the risk of contamination for humans. Since wild animals are a major reservoir of zoonotic pathogens, it is essential to identify and understand the routes of transmission between wildlife and humans.

Study Limitations

Trapping success may have varied depending on habitat and season, potentially affecting the representativeness of captured species. Additionally, the geographic

coverage was limited to certain prefectures, restricting the generalizability of the results. Finally, the lack of complete molecular typing for some pathogens reduces the precision of the assessment of zoonotic risk.

6. Recommendations

Pathogens affecting animals can also cause serious diseases in humans. In the absence of a vaccine, the only way to reduce the risk of human infection is to raise awareness among the general public and all healthcare professionals about the risk factors and to recommend measures to limit exposure to the virus. These measures include:

1) Human Community Health

Rodent control: The detection of *Borrelia spp.* in *Rattus rattus* and *Mus musculus* highlights the need for safe rodent control near human settlements, using traps and carefully applied rodenticides.

Epidemic prevention: Infestation by flea vectors carrying pathogens suggests that homes should be insecticide-treated before rat elimination during outbreaks (e.g., plague) to prevent vector displacement to humans.

Safe handling of wild animals: The presence of *Coxiella burnetii* in *Xerus erythropus* requires the use of gloves and strict hygiene when hunting and preparing these animals for consumption.

2) Animal Health

Surveillance and prevention: The pathogens detected in rodents, wildlife, and certain organic fertilizers underline the need to integrate disease prevention and surveillance into government animal health services.

Strengthening OIE surveillance: The diversity of microorganisms identified emphasizes the necessity for enhanced monitoring and systematic reporting to anticipate emerging zoonoses.

3) Governmental and Institutional Involvement

Service integration: Cross-species transmission observed necessitates coordinated action between public health, animal health, and environmental management services, following the "One World, One Health" approach.

Collaboration and communication: Preventing zoonoses requires continuous information sharing among agencies and institutions.

Interdisciplinary research and surveillance: The identification of new pathogens and vectors calls for promoting interdisciplinary research to better understand and control zoonotic dynamics.

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Conflicts of Interest

The authors declare no conflicts of interest for this article.

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