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First Research on Bat Bacteria in Burkina Faso (West Africa)

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Abstract

The world is in turmoil with the emergence of various diseases in which bats play a key part. Indeed, bats are known to host bacteria that can create major public health problems. The investigation into bat bacteria was carried out from December 2020 to September 2021 at seven sites in Burkina Faso. Bat specimen collection occurred from 6 pm to 5 am with mist nets. On each bat captured, an oral and rectum swab was taken to search for bacterial species using standard bacterial culture methods. A total of 204 bats representing 11 species were captured. 183 bat specimens were infected by at least one bacterium with a prevalence of 89.7%. 54 species of bacteria divided into 30 genera were identified from the 183 specimens. Bacterial species richness was the highest in the bat *Mops condylurus* (A. Smith, 1833) followed by *Epomophorus gambianus* (Ogilby, 1835). Genus *Escherichia* was the most frequent of the bat species. Genus *Pseudomonas* alone is represented by six species. The most infected site was the rectum, from which we isolated 44 species of bacteria out of the 54 species. The most infected locality was Ouagadougou. Bacteria are highly pathogenic to humans and may be responsible for public health problems, such as *Shigella* sp. was identified and bacteria known to cause harm to bats such as *Yersinia* and *Pasteurella* were also isolated. From this study, decisions on the management of public health problems can be considered drown to avoid the emergence and re-emergence of certain zoonotic diseases.

Keywords

Chiroptera, Bacteria, Prevalence, Diversity, Burkina Faso

1. Introduction

Bats are an ancient and diverse group of mammals, comprising almost a quarter of all mammalian diversity and inhabit in all continents, other than Antarctica [1] [2]. Bats play a critical role in the ecosystem and are ecologically and economically advantageous to humans [3] [4]. Indeed, numerous studies have demonstrated the role of Chiroptera in regulating insect populations, pollination and seed dispersal of many ecologically important plants [5]. Bats are a food source and traditional medicine in many countries, as discussed by Ejotre *et al.* [6]. Despite the important ecological role played by bats worldwide, they are more often than not neglected and constitute the potential reservoir of parasites, vectors of several diseases [7] [8] [9] [10].

However, with the appearance of emerging diseases, several studies have been carried out on bat pathogens worldwide. The drivers of disease emergence include anthropogenic changes to the environment (e.g. agricultural, intensification), climate change and the encroachment of human populations into wildlife habitats [11]. Research on bat-borne viruses attracted significant attention in recent years mainly [12]. Also, on bat bacteria [13], studies have also focused on the search for bacteria in bat ectoparasites [14]. In fact, several studies have shown that these ectoparasites are responsible for transmitting bacteria to bats [8] [15]. Unfortunately, the prevalence of pathogenic bacteria in bats and their impact on bats have been largely overlooked, especially in Africa. Some of the identified bacteria are potentially pathogenic to humans, such as *Leptospira* sp. [16]. Several enteric pathogenic bacteria (e.g. Salmonella sp., Escherichia coli) are transmitted by arthropods [8]. To date, the pathogenicity of bacteria has rarely been revealed in bats, suggesting a coevolution between them and bacteria [17]. However, a fungus (*Pseudogymnoascus destructans*) affects bat health and causes high mortality [18]. This fungus causes severe damage to bats, especially juveniles [19] [20]. Research into understanding bacterial and fungal infections in bats is growing and has led to the identification of potentially pathogenic bacterial species in bats [21] [22].

In Africa, very few studies have been conducted on bat bacteria. In Gabon, Nguema *et al.* [23] focused on antibiotic resistance of enterobacteria in fruit bats. The work of Nowax *et al.* [24] highlighted the presence of *E. coli* in bats in Congo. Oluduro *et al.* [25] worked on antibiotic resistance of *E. coli* in bats in Nigeria. However, in Burkina Faso, studies on bats and their pathogens are very fragmentary [9] [26] [27]. This study aimed to provide knowledge of the bacteria of bats in Burkina Faso.

2. Materials and Methods

2.1. Study Area

This study was conducted in seven sites in Burkina Faso. Burkina Faso is a landlocked country located in the center of West Africa between latitudes 9˚20' and

15˚3' North, and longitudes 2˚20' East and 5˚3' West. It covers an area of 274,400 km^2 and is limited to the east by Niger, to the north and northwest by Mali, to the south by Ghana and Togo, to the southwest by Côte d'Ivoire and to the southeast by Benin. These sampling points were chosen based on the presence of waterways, forest galleries, caves and abandoned houses, which are the bats' preferred locations. Burkina Faso has an alternating wet and dry season. The wet season starts gradually between May and June, but ends abruptly between the end of September and mid-October. Rainfall is highly variable in space and time. Over the last forty years or so, rainfall has shown a downward trend, with a reduction of more than 40 mm. In each sampling site, bats were captured at different sampling points (Figure 1).

2.2. Bat Capture and Handling

Bats typically emerge at dusk to feed. Bats were captured from December 2020 to September 2021. Mist nets were used to capture bats. Mist nets were monitored regularly to remove any bats that were caught to avoid injury from entanglement or predation. Care was taken to free the bats, and particular attention was paid to wing clearances because bats enter the nets with their wings spread and then

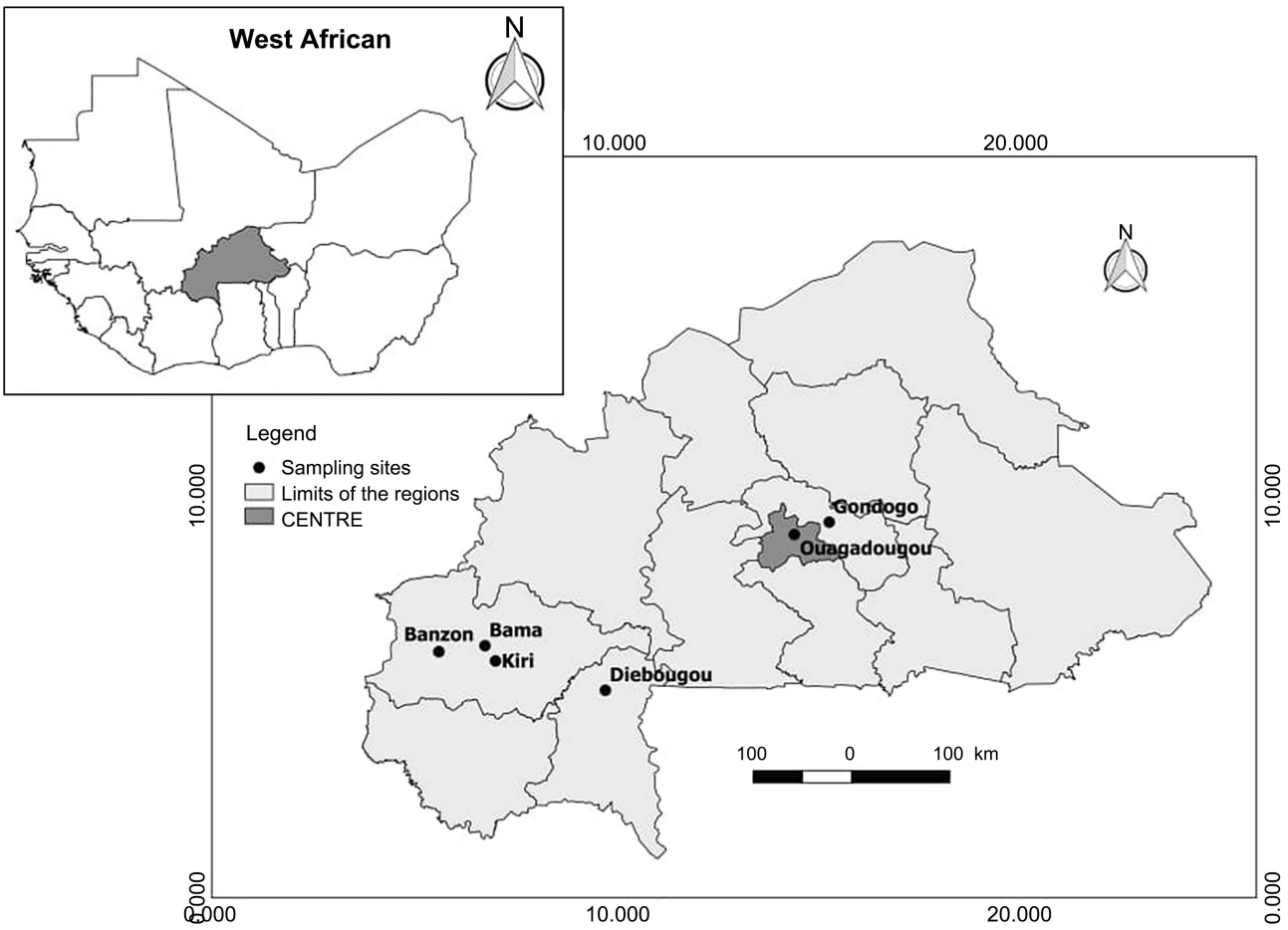


Figure 1. Site of capture of bats with the abundance of bats captured on each site.

fold them back up. The nets were opened at nightfall from 6 pm to 5 am depending on the activity of the bats. All bats were identified using the identification keys of [28] [29].

2.3. Identification of Bats

Each bat specimen was placed in a porous cotton bag and kept until the time of sampling. The risks of contamination were minimized as much as possible by using protective suits during the capture and handling of the bats. To identify bats, we determined weight, sex, age class, reproductive status, and forearm length [30].

2.4. Microbiology Analyses

Bacteria were collected by swabbing. After swabbing, bacteriological analysis was carried out in three stages: enrichment of swabs, inoculation of culture agar and identification of bacteria.

2.4.1. Swabbing

Sterile swabs were used for oral and anal bacterial sampling. Swabs were removed from their packaging, avoiding contamination of the swab tips. Buccal swabs were then taken by rolling gently inside the bat's mouth and behind the tongue. Rectal swabs were collected by inserting the entire tip of the swab into the rectum. Any excess fecal material was then gently shaken from the swab before being placed in the cryovial.

2.4.2. Swab Enrichment

Each swab was first enriched with 9 mL of buffered peptone water, a non-inhibitory nutrient medium, and then incubated at 37˚C for 16 to 20 hours.

2.4.3. Inoculation

The enriched sample was used to inoculate four agar plates: MH, EMB, Uriselect, CLED and Uriselect agar. All these agar plates, after inoculation into petri dishes, were incubated at 37˚C for 20 to 24 hours. MH (Muller Hinton) agar was used for the isolation of all bacterial strains. EMB (Methylene Eosin Blue) agar and Hecktoen and SS agars were used for the isolation of Enterobacteriaceae. EMB agar is a specific culture medium for *Escherichia coli*, and SS agar is specific for *Salmonella* spp. and *Shigella*. Uriselect and CLED (Cysteine Lactose Electrolyte Deficient) agars have been used for the isolation of many bacteria (e.g. *Escherichia coli*, *Enterococcus* spp. and *Klebsiella* spp.). Uriselect agar was also used to directly identify certain Cocci species such as staphylococci and micrococques.

2.4.4. Identification of Bacteria

After incubation, Petri dishes are examined for the presence of characteristic colonies. Each colony is subjected to two methods of identification: gram staining and biochemical tests.

- **Gram staining**

Gram staining was performed according to the method of [31]. Slides were stained successively with crystal violet and iodine for one minute in each solution. The slides were then decolorized with alcohol and counterstained with safranin for 30 seconds. Gram-positive bacteria stain blue-violet and Gram-negative bacteria stain red-pink.

- **Biochemical tests**

Gram-negative bacilli were identified using the API 20E (Analytical Profile Index) gallery. Colonies were first placed in sterile water to obtain a bacterial suspension, which was then placed in each microtube of the gallery. After incubation, reactions were reflected by spontaneous changes in coloration revealed by the addition or non-addition of reagents. Gram-positive Cocci were identified using the catalase test, which yields either positive or negative catalases. To do this, part of the colony was placed on a slide containing a drop of hydrogen peroxide for identification of the genus *Streptococcus* and *Staphylococcus*.

To identify *Staphylococcus* down to species level, the Chapman method was used.

To identify *Streptococcus* down to species level, the agglutination test method was used by Burriel and Brendle [32]. Colonies were placed in agglutination kits (Strept-check Kit) containing antigens of six different species (Strep A, B, C, D, F, G latex reagent). Positivity was revealed by an agglutination fringe indicating the presence of the species.

3. Statistical Analysis

Statistical analysis of the data was carried out, with R. 4.1.0 statistical software. A Shapiro-Wilk test was used to check for the normality of the data. That proved the data not to be normally distributed; therefore, non-parametric tests were used in further analysis. Statistical tests (Kruskal-Wallis rank sum test, Pearson's Chi-squared test) and calculations of proportions were performed using the "tbl_summary" and "add_p" functions of the "gtsummary" package. Host-bacteria analysis was used to explore interactions by focusing on the host species level [33]. A host-parasite matrix (presence/absence data) was created using the "vegan" and "bipartition" packages [34] in R 4.2.1 software. A bipartite network graph was generated with the "plotweb" function showing infections in each host species. The average number of interactions per species, the average number of shared organisms and the variance ratio (V. ratio) were calculated using the "grouplevel" function in the "bipartition" package to determine the existing relationships between bacteria and their hosts and between the bacteria themselves.

4. Results

4.1. Inventory and Diversity

The search for bacteria involved 204 bat specimens divided into 11 species (*Epo-*

mophorus gambianus, *Hyposideros caffer*, *Hyposideros jonesi*, *Epomophorus pusillus*, *Mops condylurus*, *Mops midas*, *Mops pumilus*, *Nycteris hispida*, *Pipistrellus nanulus*, *Rhinolophus alcyone* and *Scotophilus leucogaster*). All 11 bat species were infected with at least one bacterium (Table 1). 54 species of bacteria in 30 genera were isolated. The bat species richest in bacteria were *M. condylurus*, followed by *E. gambianus* and *S. leucogatser*. *Pseudomonas* genus alone was represented by six species (*Pseudomonas aeroginosa*, *Pseudomonas amygdali*, *Pseudomonas anthropi*, *Pseudomonas fluorescens*, *Pseudomonas putida* and *Pseudomonas* sp.) (Table 1).

Table 1. Distribution of bacteria species according to bat species.

Bacteria	*Eg*	*Ep*	*Mc*	*Mm*	*Mp*	*Hc*	*Hj*	*Sl*	*Pn*	*Ra*	*Nh*	*Er*	*Eb*
*Acinetobacter calcoaceticus**	−	−	+	−	−	−	−	−	−	−	−	+	−
*Acinetobacter baumaani**	+	−	+	−	−	−	−	−	−	−	−	+	−
Acinetobacter sp.*	+	−	+	−	−	+	−	+	+	+	−	+	−
*Aeromonas hydrophyla**	+	+	−	+	−	−	−	+	+	−	−	−	+
Aeromonas hydrophyla gr.2*	−	+	−	+	−	−	−	−	−	−	−	+	−
Bordetella sp.	−	−	−	−	−	−	−	−	−	−	−	+	−
Cedecae davise	−	+	−	−	−	−	−	−	−	−	−	+	−
Chryseomonas luteola	−	+	−	−	−	−	−	−	−	−	−	+	−
*Citrobacter braakii**	−	+	−	−	−	−	−	−	−	−	−	+	−
*Citrobacter freundii**	−	+	−	−	−	−	−	−	−	−	−	+	−
Citrobacter sp.*	+	+	+	−	+	−	−	+	+	+	−	+	+
*Escherichia coli**	+	+	+	+	−	+	−	+	+	+	−	+	+
*Enterobacter aerogenes**	−	+	−	−	−	−	−	−	−	−	−	+	−
*Enterobacter cloacea**	+	−	+	−	−	−	−	−	+	−	−	+	−
*Enterobacter gergoviae**	−	+	−	−	−	−	−	−	−	−	−	−	+
*Enterobacter sakazakii**	+	+	−	−	−	−	−	+	−	−	−	+	−
Enterobacter sp.*	+	−	+	−	−	−	−	+	−	−	−	+	−
Enterococcus sp.	+	+	+	−	−	−	−	+	+	−	−	−	+
Hafnia alvei	−	−	+	−	−	−	−	−	−	−	−	+	−
*Klebsiella oxytoca**	+	−	−	+	−	−	−	+	+	−	−	+	−
*Klebsiella planticola**	−	−	+	−	−	−	−	−	−	−	−	+	−
Klebsiella sp.*	+	+	+	+	−	−	+	+	+	−	−	+	+
*Listeria monocytogenes**	−	+	−	−	−	−	−	−	−	−	−	+	−
Microcrococcus sp.	+	−	+	+	−	+	−	+	+	−	+	−	+
Moraxella sp.	−	−	+	−	−	−	−	−	−	−	−	+	−
*Morganella morganii**	+	−	−	−	−	−	−	−	−	−	−	+	−
*Ochrobactrum anthropi**	−	−	+	−	−	−	−	−	−	−	−	+	−
Pantoea sp.	−	−	−	−	−	−	−	+	−	−	−	+	−
Pasterella sp.	−	−	+	−	−	−	−	+	+	−	−	−	+
Phobacteria dansela	+	−	+	−	−	−	−	+	−	−	−	+	−

Continued

*Prodencia rettgeri**	−	−	−	−	−	−	−	−	+	−	−	+	−
*Proteus mirabilis**	+	−	+	−	−	−	−	−	−	−	−	+	−
Proteus sp.*	+	−	−	−	−	−	−	−	−	−	−	+	−
*Proteus vulgaris**	−	+	+	+	−	−	−	−	−	−	−	+	−
*Pseudomonas aeroginosa**	+	+	+	−	−	−	−	+	−	−	−	+	+
*Pseudomonas amygdali**	+	−	+	−	−	−	−	−	−	−	−	−	+
*Pseudomonas anthropi**	−	−	+	−	−	−	−	+	−	−	−	+	−
*Pseudomonas fluorescens**	+	−	+	−	−	−	−	−	−	−	−	+	+
*Pseudomonas putida**	−	−	+	−	−	−	−	−	−	−	−	+	−
Pseudomonas sp.*	+	+	+	+	+	−	−	+	+	+	−	+	+
*Salmonella paratyphi**	+	+	+	−	+	−	−	+	+	−	−	+	−
Salmonella sp.*	+	−	+	−	−	+	+	+	+	+	−	+	−
*Salmonella typhi**	+	−	+	−	−	−	−	−	−	−	−	+	−
Serratia sp.*	+	+	−	−	−	−	−	−	+	−	−	+	−
*Serratia liquefaciens**	−	+	−	−	−	−	−	−	−	−	−	+	−
Shewanella putrefaciens	−	−	+	−	−	−	−	−	−	−	−	+	−
Shigella sp.**	+	−	−	−	−	−	−	−	−	−	−	+	−
*Staphylococcus aureus**	+	−	+	−	−	+	+	+	−	−	−	−	+
Staphylococcus epidermis	−	−	−	−	−	−	−	−	−	−	−	−	+
Staphylococcus sp.	+	−	−	−	−	−	−	+	−	−	−	−	+
*Stenotrophomonas maltophila**	+	+	+	+	−	−	−	+	−	−	−	+	−
Streptococcus sp.*	+	−	+	−	−	+	−	+	+	+	−	−	+
*Yersinia enterocolitica**	−	−	+	−	−	−	−	−	−	−	−	+	−
Yersinia sp.*	−	−	+	−	−	−	−	−	−	−	−	+	−
Specific richness	**28**	**21**	**33**	**9**	**3**	**6**	**3**	**22**	**16**	**6**	**1**	**44**	**16**

+: Presence of bacteria; −: Absence of Bacteria; *: Pathogenic bacteria; **: Highly pathogenic bacteria, Eg: *Epomophorus gambianus*; Ep: *Epomophorus pusillus*; Mc: *Mops condylurus*; Mm: *Mops midas*; Mp: *Mops pumilus*; Hc: *Hyposideros caffer*; Hj: *Hyposideros jonesi*; Sl: *Scotophilus leucogaster*; Pn: *Pipistrellus nanulus*; Ra: *Rhinolophus alcyone*; Nh: *Nycteris hispida*; Er: Rectal swabbing; Eb: Oral swabbing.

4.2. Effect of Sex, Age Class, Reproductive Status and Site of Capture of Host Bats on Prevalence

Of the 204 bats swabbed, 183 were infected with at least one bacterium, with a prevalence of 89.7%. Prevalence was 100% in five bat species (*H. jonesi*, *E. pusillus*, *M. midas*, *M. pumilus*, *N. hispida*, *R. alcyone*).

Male bats had a prevalence of 91.91% versus 85.18% for females. Thus, the sex of the bats was not related to the presence of bacteria according to the chi-square test of independence (p-value = 0.3). Of the 105 female bats captured, the abundance of infected bats was 92 (87.61%) and of the 99 male bats, the abundance of infected bats was 91 (91.91%).

The presence of bacteria in bats appears to be related to bat age class according to Fisher's exact test (p-value = 0.026) (Table 2). Of 183 infected bats, 157

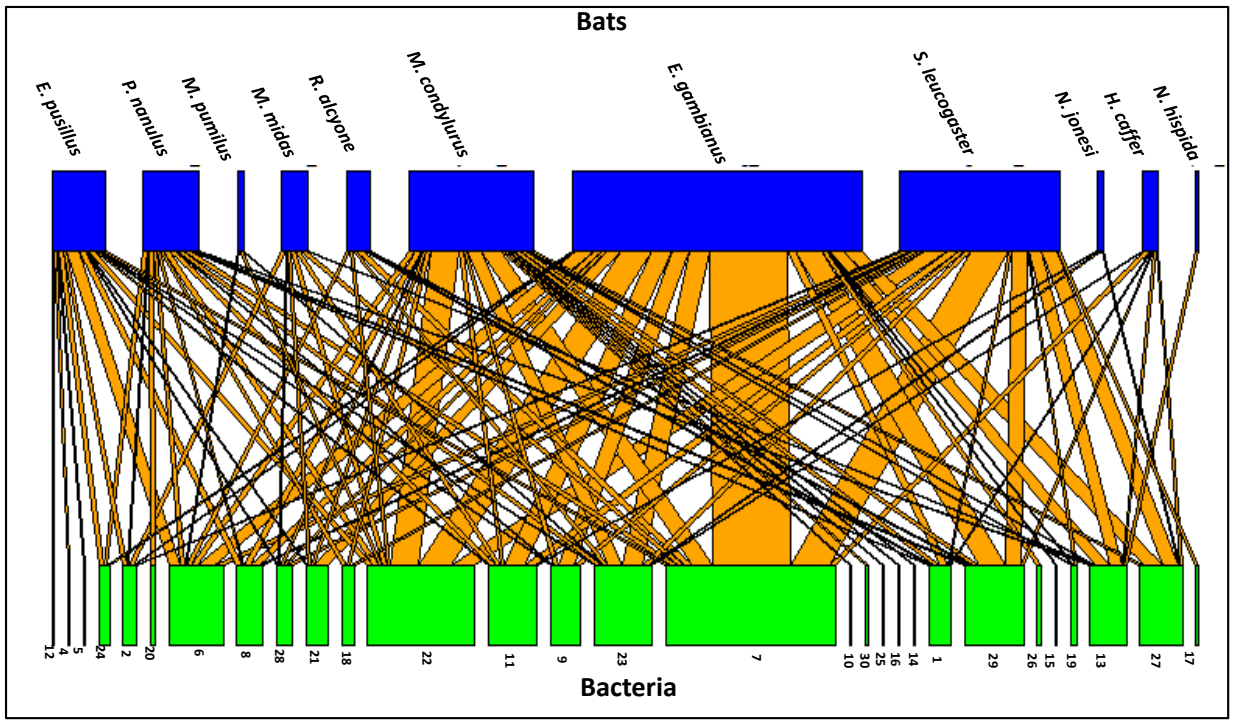
Table 2. Effect of sex, age class, reproductive status, capture area and bat species on the presence of bacteria.

Characteristics	Infested	Prevalence	Total
Sex			
F	92 (50%)	85.18%	105 (51.47%)
M	91 (50%)	91.91%	99 (48.53%)
Age class			
Adult	157 (86%)	91.81%	171 (83.82%)
Juvenile	14 (7.7%)	87.5%	16 (7.84%)
Sub-adult	12 (6.6%)	70.58%	17 (8.34%)
Species			
Epomophorus gambianus	43 (23%)	78.18%	55 (27%)
Epomophorus pusillus	15 (8.2%)	100%	15 (7.4%)
Hyposideros caffer	6 (3.3%)	85.71%	7 (3.4%)
Hyposideros jonesi	2 (1.1%)	100%	2 (1.0%)
Mops condylurus	38 (21%)	95%	40 (20%)
Mops midas	7 (3.8%)	100%	7 (3.4%)
Mops pumilus	2 (1.1%)	100%	2 (1.0%)
Nycteris hispida	1 (0.5%)	100%	1 (0.5%)
Pipistrellus nanulus	20 (11%)	90.90%	22 (11%)
Rhinolophus alcyone	9 (4.9%)	100%	9 (4.4%)
Scotophilus leucogaster	40 (22%)	90.90%	44 (22%)
Hyposideros jonesi	2 (1.1%)	100%	2 (1.0%)
Mops condylurus	38 (21%)	95%	40 (20%)
Sites			
Bazon	13 (7.1%)	92.86%	14 (7%)
Bama	25 (14%)	86.20%	29 (14.21%)
Kiri	18 (9.8%)	100%	18 (8.82%)
Gondogo	19 (10%)	100%	19 (9.31%)
Diebougou	14 (7.7%)	100%	14 (7%)
Ouagadougou	94 (51.36%)	85.45%	110 (53.6%)
Ziniare	19 (10%)	100%	19 (9.3%)

were adults, followed by 14 juveniles and 12 sub-adults. Bats were tested for bacteria in seven capture sites. All sites contained at least one bat infected with bacteria. The percentage of infection was highest at Ouagadougou. However, the prevalence was 100% in four sites: Ziniare, Diebougou, Gondogo and Kiri (Table 2).

4.3. Structure of Bacterial Genera within Bat Species

Figure 2 illustrates the network of interactions between bacterial genera and bat



Legend

: Abundance of bat species;
: Abundance of a genus of bacteria in a species of bats
: Overall abundance of bacterial genera

1 : *Acinetobacter* ; 2 : *Aeromonas* ; 3 : *Bordetella* ; 4 : *Cedecae* ; 5 : *Chryseomonas* ; 6 : *Citrobacter* ; 7 : *Escherichia*; 8 : *Enterobacter* ; 9 : *Enterococcus* ; 10 : *Hafnia* ; 11 : *Klebsiella* ; 12 : *Listeria* ; 13 : *Microcrococcus* ; 14 : *Moraxella* ; 15 : *Morganella* ; 16 : *Ochrobactrum* ; 17 : *Pantoea* ; 18 : *Pasteurella* ; 19 : *Phobacteria* ; 20 : *Prodencia* ; 21 : *Proteus* ; 22 : *Pseudomonas* ; 23 : *Salmonella* ; 24 : *Serratia* ; 25 : *Shewanella* ; 26 : *Shigella* : 27 : *Staphylococcus* ; 28 : *Stenotrophomonas* ; 29 : *streptococcus* ; 30 : *Yersinia*

Figure 2. Bacterial genus diversity by bat species.

species. This network was constructed using only bacterial genera, due to the large number of bacterial species (54). The average number of interactions per genus was 5.62 for helminths and 14 for bats, while the average number of shared organisms for bacteria was 1.73 and 4.54 for bats. The different bacterial genera appear to live in aggregation across the V. ration equal to 3.68.

Twenty genera of bacteria were found in the *Mops condylurus* species. *Salmonella* genus was the most widely distributed among bat species, followed by the *Escherichia* and *Pseudomonas* genus. *Nycteris hispida* was the only species infected by a single bacterial genus (*Microcrococcus*).

4.4. Bacteriofauna Structure by Swab Site

Bats were swabbed both buccally and anally. Of the 54 species of bacteria found in the bats, 44 species were isolated from the rectum (81.48%) and 16 species from the mouth (18.52%) (Table 2). The six bacterial species (*Pseudomonas* sp., *Pseudomonas fluorescens*, *Pseudomonas aeroginosa*, *Klebsiella* sp., *Escherichia coli* and *Citrobacter* sp.) were isolated from both swab sites (buccal and anal) (Figure 3).

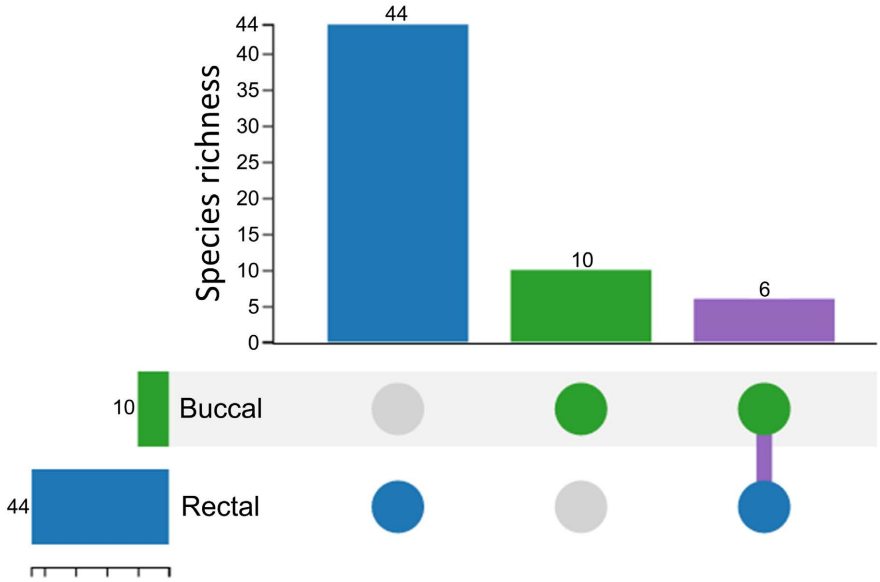


Figure 3. Distribution of bacteria according to swab site.

4.5. Structure of Bacteriofauna According to Pathogenicity

Of the 204 bats examined, 69.60% (142/204) were infested with pathogenic bacteria. Among all the bacterial species isolated in this study, 41 are pathogenic to humans and pose public health problems. 38 species of pathogenic bacteria were present in the rectum (e.g. *Morganella morganii*, *Proteus vulgaris*, *Shigella* sp...) and 12 were present in the mouth (e.g. *Aeromonas hydrophyla*, *Enterobacter gergoviae*, *Klebsiella* sp.). The most dangerous of the 41 is the *Shigella* genus, recognized as a major contributor to public health problems. Bacteria capable of causing health damage in bats were *Yersinia* and *Pasteurella* genera. Among the bacterial species isolated, 13 are recognized as commensals such as (*Escherichia coli*, *Pantoea* sp., *Cedecae davise*...) (**Table 1**).

5. Discussion

In this study, we isolated a large number of bacteria. 54 species of bacteria were identified in bats in this study, with a prevalence of 89.7%. This richness could be explained by the close proximity of bats to humans and the variability of their ecological niches, which favours the transfer of pathogens. Some of these bacteria are pathogenic to both men and bats. Despite the presence of these bacteria, none of the bat specimens showed any signs of disease. This high diversity is reflected in the cohabitation and coevolution that exists between bacteria and bats. Indeed, this trend has been reported by Voigt *et al.* [35] and Mühldorfer *et al.* [36].

All 11 bat species investigated were infested with at least one bacterium. *Mops condylurus* was the bat species with the highest diversity and abundance of bacterial species, followed by *Epomophorus gambianus*. This is reflected in their ability to colonize several living environments and live promiscuously with humans on trees and abandoned houses [37]. *E. coli* was the most prevalent in the

bats studied. This is explained by its dual character, *i.e.* it can be pathogenic and commensal in its host. In Gabon, Nguema *et al.* [23] also isolated more *E. coli* in Pteropodidae samples, with a percentage of 37.93%.

Salmonella genus, divided into three species, was isolated in this study. However, salmonellosis is a major cause of gastroenteritis in both humans and animals and is a global bacterial disease of public health and economic importance to the livestock industry [38]. *Staphylococcus*, *Streptococcus* and *Micrococcus* are gram-positive cocci described in nosocomial infections and also implicated in cerebrospinal meningitis [39]. *Pasteurella* genus has been recognized in several studies as the causative agent of severe pneumonia and subcutaneous abscesses in bats [40]. 13 species of commensal bacteria isolated in this study (*Pantoea* sp., *Cedecae davise*...) have been reported to be widely present in the environment, as well as in the small intestines of animals [41].

The aggregation behavior of bats within their roosts is of particular importance, as this dense grouping increases the potential for bacterial transmission between individual bats via contact [42]. Other bat behavioral factors such as frequent indoor movements at roosts and long-distance migrations can increase transmission between bat species and different colonies and consequently the exchange of bacteria within different bat populations [43].

Bats are generally infected via contaminated food and water, or by bat-to-bat contact with infected animals.

Of all the male and female bats captured in this study, sex was not a factor influencing the presence of bacteria. In fact, male and female bats live in communities and share the same ecological niches, so there's just as much chance of a female or a male being infected by at least one bacterium. On the other hand, age could be a factor influencing the presence of bacteria in bats. Adult bats were more infected than sub-adults and juveniles. Bats can often live up to 34 years, depending on the species, so this gives adults a greater chance of encountering the bacteria.

At all the capture sites, 100% of the bats were infected with at least one bacterium. These sites included abandoned houses, schools and riverbanks, all of which are favored by certain bat species known to be highly rich in bacteria. Bats were swabbed both buccally and anally. Of the 54 species of bacteria isolated, 81.48% were found in the anal region, compared with 18.52% in the buccal region. This indicates that the anal region is the preferred site for bacteria. In fact, the digestive tract of bats provides bacteria with a wealth of nutrients that encourage their proliferation. Six species of bacteria have been isolated from the mouth and anal tract of bats, three of which (*Pseudomonas* sp., *P. fluorescens*, *P. aeroginosa*) are from the *Pseudomonas* genus. According to Scaccabarozzi *et al.* [44], *Pseudomonas* genus is responsible for both foodborne and nosocomial infections.

6. Conclusion

In this survey, we isolated a large number of bacteria. This richness indicates the

coevolution that can exist between bacteria and bats. Some of these bacteria are highly pathogenic to both men and bats. For example, *Yersinia* genus can have a negative impact on the bat's immune system and other organs, opening the door to other pathogens. Histological examinations can, therefore, be used to assess the effect of these bacteria on bats. In addition, an assessment of the antibiotic resistance of these bacteria will enable us to understand their involvement in public health problems.

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Authors' Contributions

NGT conceived and designed the study. NGT, GJG, MK, BMAC, AO and MB carried out fieldwork and bat sampling. NGT, GJG, AMD and JS performed bacteriological analysis. All authors conducted data gathering and wrote the article.

Ethical Approval and Consent for Publication

Authorization to collect bats was given to our laboratory at the University Joseph Ki-Zerbo by the Ministry of the Environment, Green Economy and Climate Change (MEECVCC) (permit no. 21-091 MEECVCC/SG/DGEF/DFRC).

It was approved by the ethics committee on animal experimentation of Joseph Ki-Zerbo University with the number: CEEA-UJKZ/2021-04.

Conflicts of Interest

The authors declare there are no conflicts of interest.

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