



Bats and Antibiotic Resistance: A Culprit or a Victim?

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ABSTRACT

In the last decades, the increase of antimicrobial resistance bacteria has become a concern for public health. Bats' ability to fly, form colonies for a long lifespan, and inhabit a variety of diverse ecological niches make them successful species in terms of adaptation and distribution on earth. Moreover, these characteristics let them act as the potential natural reservoir of numerous zoonotic pathogens (bacteria, viruses, fungi). Bat bacteriome knowledge is still very scarce, but a few studies have indicated that bats are hosts of antimicrobial resistance and play an important role in the dispersion of resistance in the environment. Moreover, bats are vulnerable to acquiring these pathogens since they sometimes live in close contact with humans and domestic animals. Therefore, the present study aimed to compile the latest studies that describe the presence of antibiotic-resistant in bats. Based on the papers analyzed for this review, it is possible to conclude that bats are hosts of pathogenic bacteria that carry numerous antibiotic resistance. Extended-spectrum b-lactamases (ESBLs) or Methicillin-resistant *Staphylococcus* which nowadays days are a great public health concern, have already been reported in these animals, with some isolated strains being of Human origin. Although not completely understood regarding the dynamics and transmission routes, bats seem to have an important role in the dissemination and acquisition of antibiotic resistance in the environment. They can be contaminated by bacteria with antibiotic resistance and disperse through the environment. However, they also can be the host of bacteria that carry antibiotic resistance.

Keywords: Antibiotic-Resistant, Bacteria, Bat, Chiropters, Zoonoses

INTRODUCTION

Bats are mammals that belong to the order Chiroptera, which is classified into two suborders, including Megachiroptera and Microchiroptera (Fenton and Simmons, 2015; Wilson and Mittermeier, 2019). They are an incredibly diverse group of mammals with the ability to fly and cover long distances during seasonal migrations. Most of the species are nocturnal and prefer to roost in large colonial populations on caves, trees, or human constructions. Some species hibernate during the winter (Neuweiler, 2000; Kunz and Fenton, 2006) and are characterized by using echolocation to capture their prey (Kunz and Fenton, 2006).

This order corresponds to nearly 20% of all classified mammal species worldwide, with over 1400 species reported. Bats are present on almost every continent, except for extremely cold regions, such as Antarctica or the Arctic continent. Their diet is very diverse, depending on the specie can include insects, fruit, nectar and blood or other animals (Neuweiler, 2000; Kunz and Fenton, 2006; Wilson and Mittermeier, 2019). Chiropterans provide humans and ecosystems with various benefits, being essential to the ecosystem's health and economics. Plant pollination, control of insect populations, utilization as fertilizer, rural tourism, and the food source as bushmeat, (Neuweiler, 2000; Kunz and Fenton, 2006; Wilson and Mittermeier, 2019) are some of the services provided by bats.

Antimicrobial resistance (AMR) is a global concern that affects humans, domestic animals, and wildlife. The report of AMR in wildlife has been increasing in the last years, showing their potential role as reservoirs and in the transmission of these pathogens to humans, domestic animals and the environment (Nguema et al., 2020). This subject has been studied under a multidisciplinary and collaborative "One Health" approach, addressing interactions between humans-domestic and non-domestic animals-environment to understand and prevent the dispersion of AMR (Calisher et al., 2006; Mühldorfer, 2013). There is not enough understanding regarding the dynamics and transmission routes among bats and humans (McDougall et al., 2021a).

The ability to fly, form colonies, long lifespan and capability to inhabit a variety of diverse ecological niches make bats one of the most successful species on earth (Neuweiler, 2000) but also made them a potential natural reservoir of numerous zoonotic pathogens (bacteria, viruses, fungi, Mühldorfer, 2013). They have been considered a reservoir of many viruses that occasionally spread into human populations and cause disease outbreaks, such as SARS-CoV-2 (Garcês et al., 2020). The AMR has already been reported in several species of bats. Unfortunately, still little is known regarding bat microbiota and the dynamics of transmission and acquisition of AMR (Calisher et al., 2006; Adesiyun et al., 2009; Nguema et al., 2020). The present study review compiles the latest studies that describe the presence of AMR in bats.

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WEB-BASED LITERATURE SEARCH

To produce this review, we conducted a literature search through the main web search for peer reviews of scientific articles (e.g. original research, case reports, letters, short communications, review articles) and non-peer-reviewed grey bibliographies (e.g. thesis, reports, white papers). To find these references the author placed a specific set of terms in the main search engines available on the internet. The main engines of research were Google Web, ResearchGate, PubMed, and Google Scholar. The search terms included combinations of bats, Chiropterans, antibiotic resistance, zoonoses, bacteria, enteric bacteria, one health, wildlife health, and environment. The languages used in the research were English, Spanish and Portuguese. As inclusion criteria, only works that describe information regarding antibiotic resistance in different bat species were included. Some studies were not used in this review because the information was mixed with other species of mammals or birds and was not possible to retrieve information regarding specie, type of samples or which resistances were observed.

BATS BACTERIOME AND ENTERIC PATHOGENS

Bat bacteriome knowledge is still very scarce. Studies performed have indicated a relatively high diversity and function of bacterial species (Gerbáčová et al., 2020; Nguema et al., 2020). In several studies, it was observed that Gammaproteobacterial (with Enterobacteriaceae family in predominance) appears to be the prevalent bacterial group in the Chiroptera order, while Fusobacteria is less represented in comparison to other mammal species (Gerbáčová et al., 2020). The bacteriome will vary according to several extrinsic and intrinsic factors, such as season, sex, diet type, reproductive stage, and environmental factors (Gerbáčová et al., 2020).

Beyond the bacterial commensal strains, it has been identified in bat's gastrointestinal flora strains similar to the strains of human and animal pathogens in individuals and colonies of different bat species. Bats are a host of pathogenic bacteria such as *Salmonella*, *Shigella*, *Yersinia* and *Campylobacter* (Mühldorfer, 2013). These pathogens usually do not cause disease in the bats but have the potential of causing diseases such as diarrhoea, septicemia, and meningitis, in humans and animals (Nowak et al., 2017; Silveira, 2021). Bats and their guano could serve as reservoirs of numerous pathogenic agents, some of which are zoonotic (Vandžurová et al., 2013). Figure 1 presents some bat-related zoonoses. Bats are hosts of numerous viruses, bacteria, parasites and fungi, that can be transmitted to other animals or Humans and induce diseases.

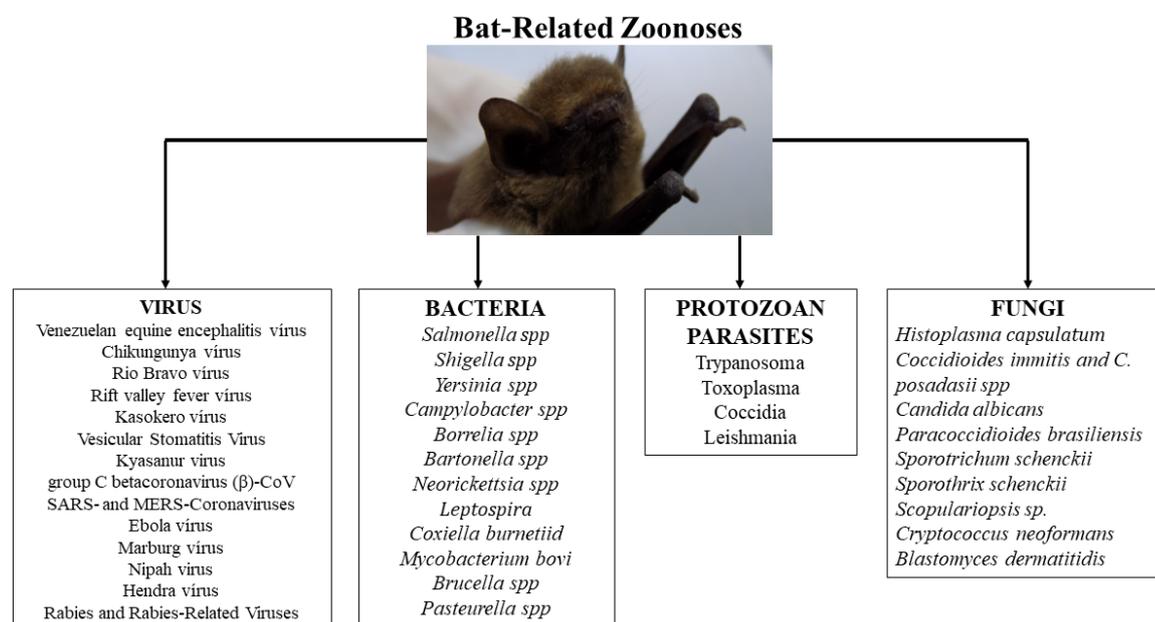


Figure 1. The reports of zoonotic diseases in bat species

BAT DISPERSION AND CONTAMINATION SOURCE OF PATHOGENIC BACTERIA

Due to their specific style of life bats are very prone to spread AMR in the environment and acquire new pathogenic strains. Their flight ability allows them to be in constant movement for food and shelter and to migrate from one region to another (large territorial range of some species). This activity increases the chance of being exposed to antimicrobials, raising the risk of developing, changing, or acquiring a new microbiota (Sens-Junior et al., 2018). Their longevity (some individuals can live up to 30 years) and the realization of periods of hibernation and torpor by some species, allow microorganisms to persist for long periods in the spots where animals are inhabiting and facilitate their transmission between individuals (Sens-Junior et al., 2018).

Figure 2 has represented a scheme considering the possible routes of spread and acquisition of AMR and pathogenic agents by bats. Chiropterans do not build shelters, they often use the natural landscape (e.g., caves or trees) as

places of shelter, to reproduce and hibernate (Voigt et al., 2015). Many species use artificial hideouts in human environments, such as attics and cellars, as permanent, or temporary shelters (McDougall et al., 2021a). Large colonies can be formed inside of these artificial structures, because there are many benefits to the colony, not only obtaining shelter but also having easier access to food sources (Voigt et al., 2015). The use of shelters located very near to the human population, that is specific synanthropization, raises the change of direct and indirect contact of human and domestic animals with the microbiota of bats. Pets (particularly cats) can hunt the bats. Direct contact with bats when these are captured to be reallocated, or the contact of an aerosol of bat's faeces (guano), are some of the routes by which humans and domestic or non-domestic animals can acquire these pathogenic bacteria from bats (Nowakiewicz et al., 2020; McDougall et al., 2021a).

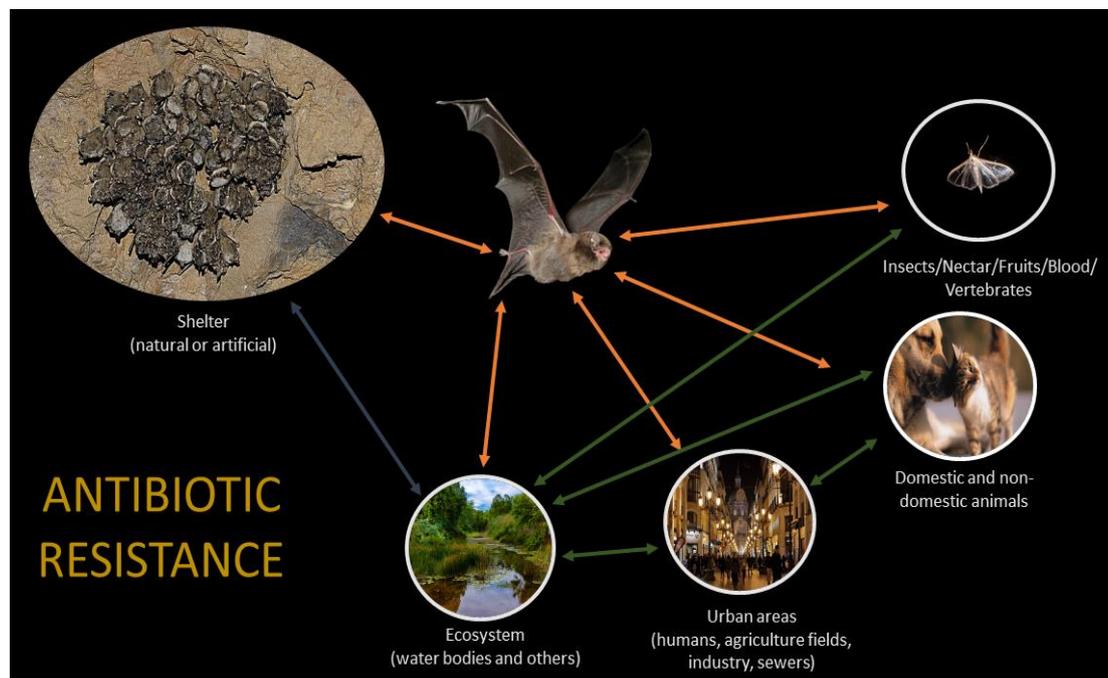


Figure 2. The possible routes of spread and acquisition of antibiotic resistance and pathogenic agents by bats

Another source of contamination due to direct contact with humans is tourists that visit large colonies that are an attraction in some regions. Tourists are responsible for introducing resistant strains of bacteria in and out of the cave, spreading AMR into the ecosystems (Mulec et al., 2020). To prevent the dissemination of these strains should be performed a regular cleaning of the tourist footpaths and a disinfectant barrier at the tourist cave entrance and exit (Mulec et al., 2020). Environmental compartments (e.g., water bodies) can also serve as reservoirs for multiresistant bacteria and resistance genes (Gharout-Sait et al., 2019). The origin of these agents is diverse. Rivers and seas are exposed to discharges with microbial contaminants from industrial, agricultural, and domestic sources, such as faecal sludge from dairy farms, discharges from aquaculture, hospitals, sewers, wastewater treatment plants and surface waters, and others (Sherley et al., 2000; Gharout-Sait et al., 2019). In some countries, antimicrobials agents are still used in domestic animals for their protection and improver, such as prophylaxis of diseases. These animals can act as a source of environmental contamination (Sens-Junior et al., 2018). In many caverns, there is a network of underground water channels that have contact with the exterior environment. These underground water bodies can be contaminated with AMR due to the infiltration of bat faecal matter during the rainy seasons or introduce contaminated water into the caves (Mulec et al., 2020).

The surface of bodies of water is typically rich in insects and other invertebrates, which are an important food source to many species of bats. Bats can acquire and transmit strains of resistant bacteria when in contact with these contaminated water bodies but also from consuming their food source. Insects are also hosts of multidrug-resistant bacteria and have the potential to spread through the environment. Studies have shown that fly guts are carried antimicrobial-resistant bacteria that share the same genotypes as strains isolated on humans and other animals and can occur horizontal transfer of plasmids bearing antibiotic resistance genes inside their gut. (Gharout-Sait et al., 2019). Other sources of food such as fruits, flowers and blood from other animals also can be a source of acquisition of AMR by bats. Plants can be contaminated with water and faecal matter that are contaminated with AMR bacteria. Hematogenous species can also feed on animals and humans that are also carriers of multidrug-resistant bacteria (Nowakiewicz et al., 2020; McDougall et al., 2021b).

ANTIBIOTIC RESISTANCE IN CHIROPTERANS

Overall, the present study presents a total of 32 works, between the years 1985 to 2021. Of the 32 papers (presented in table 1) the majority, 31.3 % (10/32) were performed in individuals from the Pteropodidae family, 25 % (8/32) in the Vespertilionidae Family and the remaining studies in individuals of several families from the Chiroptera Order. In 34.4% (n = 11/32) papers the study was performed in colonies that harboured mixes of individuals from different families. In one study, the specie was not determined.

Table 1. Antibiotic resistance in Chiropterans regarding specie, family, country, year, type sample, bacteria isolated, antibiotic resistance and resistance genes

Specie	Family	Location of colonies	Country	Year	Type of sample	Isolated Bacteria	Antibiotic resistance	Resistance genes	Reference
<i>Cynopterus tittecheilus</i> , <i>C. brachyotis javanicus</i> , <i>C. sphinx angulatus</i> , <i>Myotis muricola</i>	Pteropodidae Vespertilionidae	Cave near and in coastal village	Indonesia	1985	Faecal	<i>Escherichia coli</i> , <i>Klebsiella</i> spp., <i>Enterobacter</i> spp.	<i>E. coli</i> to almost every antibiotic tested, with 10 strains resistant to trimethoprim and cephalothin. <i>Klebsiella</i> spp. was sensitive to almost every antibiotic except 9 strains resistant to ampicillin, cephalothin, trimethoprim and tetracycline. <i>Enterobacter</i> spp. all isolates presented resistance, between 1-6 different agents.		(Graves et al., 1988)
<i>Myotis</i> , <i>M. blythii</i>	Vespertilionidae	Church tower	Slovakia	2010	Faecal (guano)	<i>Staphylococcus nepalensis</i>	Nalidixic acid, aztreonam, tetracycline, chloramphenicol and erythromycin.		(Vandžurová et al., 2013)
<i>Carollia perspicillata</i> , <i>Sturnira lillium</i> , <i>Artibeus lituratus</i> , <i>Artibeus planirostris</i>	Phyllostomidae	Fragment forest near city	Brasil	2018	Oral and perianal region	<i>Escherichia coli</i> ; <i>Enterobacter aerogenes</i> , <i>Enterobacter agglomerans</i> , <i>Serratia liquefaciens</i>	All individuals had resistant strains, with a few of them presenting multi-resistance to antimicrobials.		(Sens-Junior et al., 2018)
<i>Rhinolophus pumilus</i>	Rhinolophidae	Cave	Japan	2014	Faecal	<i>Escherichia coli</i> , <i>Klebsiella pneumoniae</i> , <i>Citrobacter freundii</i>	One <i>E. coli</i> isolate was resistant to chlortetracycline and streptomycin and 4 <i>K. pneumoniae</i> and 5 <i>C. freundii</i> were resistant to sulfadimethoxine.	Five of the ten resistant isolates exhibited the transmissible R plasmid.	(Obi et al., 2014)
<i>Myotis daubentonii</i> , <i>Eptesicus serotinus</i> , <i>Myotis nattereri</i> , <i>Plecotus auritus</i> , <i>Nathusius Pipistrellus pipistrellus</i> ,	Vespertilionidae	Urban area	Poland	2021	Faecal	<i>Enterococcus faecalis</i>	69% of the isolates were multi-drug resistant. Resistance to tetracycline, rifampicin and erythromycin. High-level aminoglycoside resistance (HLAR) was detected in 41.6% of strains.	In all strains the presence of at least one gene encoding resistance: tetM, ermBoraph (30)-IIIaI, geIE, aac (60)-Ie-aph (200)-Ia and ant (6)-Ia).	(Nowakiewicz et al., 2021)
		Urban area	Poland	2020	Faecal	<i>Escherichia coli</i>	71% of the isolated strains were multi-drug resistant. The highest resistance was observed in the case of ampicillin, kanamycin, sulfamethoxazole/trimethoprim, and streptomycin.	Two isolates produced extended-spectrum beta-lactamases (ESBL) (bla CTX-M-3, bla CTX-M-15, bla TEM-1).	(Nowakiewicz et al., 2020)
<i>Eidolon helvum</i> , <i>Nycteris hispida</i>	Pteropodidae Nycteridae	Trees near a market and caves	Nigeria	2021	Samples liver, spleen, and intestines	<i>Escherichia coli</i>	22.9 % of the isolates were multidrug-resistant-	Two isolates were cefotaxime-resistant, ESBL-producers and harboured the blaCTX-M-15. tet(A), int1 and blaTEM genes were also found. Three isolates contained the eae gene.	(Obodoechi et al., 2021)
<i>Tadarida brasiliensis</i> , <i>Histiotus velatus</i> , <i>Molossus molossus</i> , <i>Eptesicus brasiliensis</i>	Molossidae Vespertilionidae	Urban area	Brasil	2018	Faecal	<i>Staphylococcus aureus</i> , <i>Yersinia enterocolitica</i>	70.59% of the <i>S. aureus</i> were resistant to methicillin		(Silveira, 2021)
<i>Eidolon helvum</i> , <i>Epomops franqueti</i> , <i>Hypsignathus monstrosus</i> , <i>Myonycteris torquata</i> , <i>Rousettus aegyptiacus</i>	Pteropodidae	National parks and reserves	Republic Congo	2009-2010	Intestine, liver, lung, kidney	<i>Escherichia coli</i>	Extended-Spectrum ESBL phenotype was detected in 60% of the samples.	Were detected sequence types (e.g., ST69, ST127, and ST131) and pathotypes (e.g., ExPEC, EPEC and atypical EPEC).	(Nowak et al., 2017)
<i>Barbastella barbastellus</i> , <i>Eptesicus serotinus</i> , <i>Miniopterus schreibersii</i> , <i>Myotis capaccinii</i> ,	Vespertilionidae Miniopteridae Rhinolophidae	Caves	Slovenia	2020	Swab samples from tourist	<i>Escherichia coli</i>	Several isolates from rivers and swabs exhibited a multidrug-resistant phenotype		(Mulec et al., 2020)

						footpaths				
<i>M. daubentonii, M. oxygnathus, M. myotis, M. nattereri, Nyctalus noctula, Pipistrellus pipistrellus, P. pygmaeus, Rhinolophus ferrumequinum, R. hipposideros</i>										
<i>Desmodus rotundus</i>	Phyllostomidae	Farms	Peru	2015	Faecal	<i>Escherichia coli</i>	ESBL in 4.94 % of the isolates	Expression of blaCTXM-15 genes carried by plasmids	(Benavides et al., 2018; Mendoza, 2017)	
<i>Pteropus poliocephalus</i>	Pteropodidae	Urban and rural areas	Australia	2017-2018	Faecal	<i>Klebsiella pneumoniae, Klebsiella africana and Klebsiella variicola subsp. variicola</i>		Trimethoprim and fluoroquinolone resistance genes in 3 <i>K. pneumoniae</i> isolates.	(McDougall et al., 2021b)	
		Urban and rural areas	Australia	2020	Faecal	<i>Escherichia coli</i>	3.8% <i>E. coli</i> were amoxicillin-resistant with 38.5% isolates exhibiting multi-resistance. One isolate presented resistance to carbapenem and fluoroquinolone resistance. Two isolates presented resistant to third-generation cephalosporins. 69.2% of isolates presented resistance to tetracycline and trimethoprim-sulfamethoxazole.	38.5% of isolates had class 1 integrons. 69.2% of isolates harboured extraintestinal virulence factors.,	(McDougall et al., 2019; McDougall et al., 2021a)	
<i>Epomops franqueti, Megaloglossus woermanni</i>	Pteropodidae	Forest area and trees near village	Gabon	2020	Faecal	<i>Enterobacteriaceae</i>	ESBLs in 20.69% <i>E. coli</i> isolates, 13.79% <i>K. pneumoniae</i> isolates, and 3.45% <i>E. cloacae</i> isolate.	41.67% ESBL had CTX-M-15- gene and, 16.67% CTX-M-15+SHV-11. has presented <i>E. coli</i> , In the <i>K. pneumoniae</i> isolates 8.33% ha CTX-M-15- and 25% CTX-M-15+SHV-11 CTX-M-15 was detected in 8.33% <i>E. cloacae</i> .	(Nguema et al., 2020)	
<i>Molossus rufus</i>	Molossidae	Forest area	Brasil	2019	Samples of stomach and intestine	<i>Lactobacillus spp. Enterobacteriaceae</i>	21% isolates where multiresistant		(Mateus-Vargas et al., 2017)	
<i>Chironax melanocephalus</i>	Pteropodidae	National park	Indonesia	2020	Oral and rectal swab	<i>Proteus mirabilis, Serratia marcescens subsp. marcescens</i>	<i>P. mirabilis</i> and <i>S. marcescens</i> are resistant to oxacillin and susceptible to amikacin Antibiotic-resistant profiles also show <i>P. mirabilis</i> susceptible against cefoxitin (and amoxicillin-clavulanic acid, while <i>S. marcescens</i> resistant against these two antibiotics.		(Masrukhin et al., 2021)	
<i>Tadarida brasiliensis</i>	Molossidae	Housing ceilings	Brasil	2015-2016	Faeces	<i>Enterococcus faecalis, E. casseliflavus, E. gallinarum, and E. mundtii</i>	Resistance to rifampicin, erythromycin, norfloxacin, ciprofloxacin and tetracycline.	Resistance genes detected: tetM, rnC, gyrA, vanA, vanB, vanC1 and vanC2-3 r. Virulence genes observed: gelE, ace, agg, cylA and esp.	(Costa et al., 2019; Frazzon and Alegre, 2018)	
<i>Eidolon helvum</i>	Pteropodidae	Urban areas	Nigeria	2017	Faeces	<i>Citrobacter spp., Enterobacter spp., Salmonella spp., Klebsiella spp., and Escherichia coli</i>	Resistance to multiple antibiotics	35.9% of isolates were ESBL Resistance genes MultiDHA and TEM and virulence Biofilm, PAPC, ISS and eaeAgenees were detected.	(Aladejana, 2019)	
		Housing ceilings	Nigeria	2008-2010	Faeces	<i>Staphylococcus aureus</i>	The majority are susceptible to the antibiotic tested.	92.9% coagulase type VI, and accessory gene typing classified 69 isolates into the following: type I (12; 17.1%), type II (3; 4.3%), and type III (1; 1.4%) and type IV (53; 75.7%).	(Akobi et al., 2012)	

<i>Artebius sp., Carollia perspicillata, Desmodus rotundus, Diaemus youngi, Glossophaga sp, Molossus major, Molossus ater, Mormoops sp., Noctilio leporinus, Phyllostomus hastatus, Phyllostomus discolor, Pteronotus parnelli</i>	Phyllostomidae Molossidae Noctilionidae Mormoopidae	Urban and rural areas	Trinidad	2006-2006	Gastrointestinal tract	<i>Salmonella</i> spp., <i>Escherichia coli</i> , <i>E. coli</i> O15, <i>Campylobacter</i> spp.	82% of the <i>E. coli</i> isolates exhibited resistance to antibiotic: erythromycin (61%), (27%), gentamycin - (0%) and sulphamethoxazole/trimethoprim (2%).	(Adesiyun et al., 2009)	
<i>Myotis myotis, Rhinolophus hipposideros</i>	Vespertilionidae Rhinolophidae	Housing ceilings	Slovakia	2020	Faecal	<i>Enterococcus faecalis</i> , <i>E. mundtii</i> , <i>Lactobacillus</i> spp., <i>Pseudomonas</i> spp., <i>Bavillus</i> spp., <i>Carnobacterium maltaromaticum</i> , <i>Staphylococcus nepalensis</i> , <i>Arthrobacter</i> sp., <i>Kocuria</i> sp.	Isolates from the Micrococcaceae family were resistant to ampicillin (7%), chloramphenicol (50%) and vancomycin (50%). <i>Kocuria</i> sp. resistance to chloramphenicol (18%) and vancomycin (18%). Vancomycin resistance was observed in <i>Staphylococcus nepalensis</i> (94%).	(Gerbáčová et al., 2020)	
<i>Asellia tridens, Rhinolophus blasii, Rhinolophus clivosus, Rhinolophus euryale</i>	Hipposideridae Rhinolophidae	Cave	Algeria	2016	Guano	<i>Staphylococcus aureus</i>	36.3% were resistant to penicillin G, cefoxitin and fusidic acid. Four isolates were resistant to methicillin (MRSA).	MRSA isolates harboured a SCCmecIV Q6GD50 (fusC). Virulence genes including sea, eeg enterotoxin locus, sec, sel, tst.	(Mairi et al., 2021)
<i>Tardarita teniotis</i>	Molossidae	Bridges	Portugal		Faecal	<i>Escherichia coli</i>	9.6% of samples were ESBL	Detected genes were blaCTX-M-1, blaCTX-M-3, blaSHV, blaTEM, blaOXA, blaCTX-M-9, tet(A), tet(B) and fimA.	(Garcês et al., 2017)
		Bridges	Portugal		Faecal	<i>Escherichia coli</i>	Resistance to ampicillin (57.14%) and streptomycin (52.38%)	Virulence gene fimA and antimicrobial resistance blaOXA, blaSHV, blaTEM, tet(A), tet(B), adA and strA-strB	(Garcês et al., 2019)
Various species	Undetermined	Urban and rural areas	Bangladesh	2016-2017	Faecal	<i>Salmonella</i> spp., <i>Staphylococcus</i> spp., <i>Escherichia coli</i>	<i>Salmonella</i> spp. presented resistant to Tetracycline (93%), Sulphamethoxazole-Trimethoprim (80%), Amoxicillin-Clavulanic acid (42%), Azithromycin (76%) and Chloramphenicol (62%). <i>Staphylococcus</i> sp. resistance to Ampicillin (55%), Methicillin, Oxacillin, Streptomycin and Tigecycline by 12%. <i>E. coli</i> resistance against Cefepime (16%) and Ampicillin (13%).		(Uddin et al., 2020)
		Trees near urban areas	Nigeria	2012	Faecal	<i>Escherichia coli</i>	Resistance to augumentin (92%), to ciprofloxacin, ofloxacin and pefloxacin (1%).		(Oluduro, 2012)
		Urban and rural areas	Nigeria	2012-2014	Fecal	<i>Escherichia coli</i>	50% of the isolates were resistant or immediately resistant to cefuroxime, ceftazidime and cefotaxime.		(Ngozi et al., 2018)
		Cave	Algeria	2016	Fecal	<i>Klebsiella pneumoniae</i>	2/100 carbapenem-resistant isolates	Carbapenemase-producing isolates harboured the blaOXA-48 gene (CS34) and blaKPC-3 gene (CS63). Other genes observed were blaTEM-1 and aac (6ε)-Ib genes.	(Gharout-Sait et al., 2019)
Undetermined	Undetermined	Veterinary hospital	Germany	2008	Swab wound	<i>Staphylococcus aureus</i>	Resistant to Methicillin (MRSA).	mecA gene	(Walther et al., 2008)

The type of sample predominately was fecal material (anal swabs, droplets, and gastrointestinal samples) in almost every paper, except for two works that had samples from other organs (Walther et al., 2008; Obodoechi et al., 2021). The countries with the greatest number of studies were in decedent order as follows: Nigeria, Brazil (n=5), Slovakia, Australia (n = 3), Indonesia, Peru, Portugal, Poland, Algeria (n = 2), Japan, Republic of Congo, Slovakia, Trinidad, Germany, Bangladesh, Gabon (n = 1). Since most of the studies were performed in fecal samples, the bacteria isolated were mostly the microbiota of faecal flora, and *Escherichia coli*(*E. coli*) was the most common microorganism in the studies (n=20). The production of extended-spectrum b-lactamases (ESBLs) and carbapenem resistance by Enterobacteriaceae, Methicillin-resistant *Staphylococcus pseudointermedius* (MRSP), and Methicillin-resistant *Staphylococcus aureus* (MRSA) vancomycin-resistant *Enterococci* (VRE), have been some of the main public health concerns in the last years, particularly in human health in the topic of AMR (Garcês et al., 2019; Wangai et al., 2019). Some of these agents have been reported in bats. ESBL was reported in 8 papers and carbapenem resistance in Enterobacteriaceae on 3 as mentioned in Table 1 (Gharout-Sait et al., 2019; McDougall et al., 2019; McDougall et al., 2021a).

A study performed by Obodoechi et al. (2021), detected the blaCTX-M15 gene in ESBL isolated from bats from Nigeria. This gene already had been detected in other bats from Gabon (Nguema et al., 2020), Poland (Nowakiewicz et al., 2020), and Peru (Benavides et al., 2018; Mendoza, 2017). This gene is known for being one of the most predominant ESBL gene types reported in humans, domestic animals and wildlife in many regions of the world. Extended-spectrum b-lactamases type cefotaximase-Munich (CTX-M) is the most widely distributed ESBL in human strains around the world. In the same study, was detected the strain *E. coli* ST2178 was been previously reported in among pets, humans and rodents (Obodoechi et al., 2021). In another study performed in Gabon by Nguema et al., 2020, were detected the presence of blaCTX-M-15 and blaSHV-11 genes in ESBL from insectivorous species. The phylogenetic analyses of the sequences obtained from bats that carry these clustered genes correlate them with one human bacterial strain (Nguema et al., 2020). The presence of these genes in bats populations suggests that the prevalence of antibiotic resistance in bats depends on the antibiotics consumed and the density of human populations in contact with bats.

CONCLUSION

Based on the papers analyzed in the present study, it is possible to conclude that bats do a host of AMR and pathogenic bacteria. Due to their lifestyle bats have an important part in the spread of AMR in the ecosystems. But also, make them more susceptible to acquiring these resistant bacteria from numerous sources such as food, insects, contaminated fruit, animal sources, and environmental factors such as water bodies. Bats are also extremely adaptable animals that sometimes live in close contact with humans and domestic animals. Some colonies of bats are located in urban areas, for example, in old churches or libraries. This proximity to Humans can increase the possibility of the exchange of these bacteria. This cycle of exchange of resistant bacteria between wild animals, including bats, humans, domestic animals and the environment represents a major public health problem. This is because it is extremely difficult to control the flow of these bacteria within wild populations since the mechanism of acquisition and transmission of these bacteria is not yet fully understood.

Bats have undoubtedly an important biological indicator of environmental health, particularly in the case of zoonosis. Nevertheless, there are still gaps in knowledge about the dynamics and mechanisms routes of zoonotic agents and AMR. Often, wild animals such as bats are not included in epidemiological surveillance disease control. In many situations bats have been unfairly accused of being the cause of disease outbreaks, but there is a great possibility that these animals acquired the pathogens elsewhere, for example, in water bodies contaminated with medical wastes, and only act as carriers of those pathogens. As it was possible to observe in this review, numerous EBLs strains of human origin have been reported in different species of bats, from different areas of the globe. Bat are not the cern of the problems, but contribute to its aggravation.

In the future, further studies are needed under the One Health system to determine the role of bats in the dissemination and acquisition of AMR in the ecosystem.

DECLARATIONS

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Competing interests

The author declared no conflict of interest.

Ethical considerations

Plagiarism, consent to publish, misconduct, data fabrication and/or falsification, double publication and/or submission, and redundancy) have been checked by the author.

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