

ESBL-producing *bla*TEM-carrying *Escherichia coli* in cave bats of Lombok, West Nusa Tenggara, Indonesia

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Abstract. Agustin ALD, Effendi MH, Tyasningsih W, Khairullah AR, Plumeriastuti H, Riwu KHP, Dameanti FNAEP, Yanestria SM, Tang JYH, Rehman S. 2025. ESBL-producing *bla*TEM-carrying *Escherichia coli* in cave bats of Lombok, West Nusa Tenggara, Indonesia. *Biodiversitas* 26: 3701-3710. Bats are mammals known to carry *Escherichia coli* in their guano and inhabit diverse environments such as caves, forests, and human settlements. Even without prior antibiotic exposure, bats can harbor antimicrobial-resistant *E. coli* that may contaminate the environment and threaten public health. This study investigated bat species in Saung Pengembur Cave, Lombok, West Nusa Tenggara, Indonesia, carrying antibiotic-resistant *E. coli*. Bats were captured using mist nets from 4:00-10:00 PM, and their species identified through morphological measurements. Rectal swabs were collected aseptically, and bacterial isolation was performed using Eosin Methylene Blue Agar, followed by biochemical identification (IMViC test). Antibiotic susceptibility was assessed using the disk diffusion method, and isolates resistant to more than three antibiotic classes were screened for the *bla*TEM gene via PCR, followed by sequencing for phylogenetic analysis. Of 85 bats captured, 77 were *Rhinolophus* sp. and 8 *Hipposideros diadema*. *Escherichia coli* was isolated from 63 (74.1%) individuals, all exhibiting resistance to at least one antibiotic. Multidrug Resistance (MDR) was observed in 19% (12/63) of isolates, with 9 (75%) carrying the Extended Spectrum Beta-Lactamase (ESBL) gene *bla*TEM. The highest resistance rates were to azithromycin (46%), followed by tetracycline (23.8%), amoxicillin (20.6%), sulfamethoxazole/trimethoprim (19%), and ciprofloxacin (16.7%), with no resistance to cefotaxime. Phylogenetic analysis showed close relationships between bat isolates and *E. coli* from human and poultry sources in Southeast Asia and Australia. These findings highlight the role of bats as reservoirs for ESBL-producing *E. coli*, underscoring the need for One Health-based surveillance and public awareness regarding bat guano use, to mitigate environmental contamination and reduce the risk of antimicrobial resistance transmission to humans, animals, and the environment.

Keywords: *Hipposideros diadema*, one health, public health, *Rhinolophus*, wildlife

Antimicrobial Resistance (AMR) is a global health crisis, leading to bacterial infections that are increasingly difficult or impossible to treat (Ansharieta et al. 2021). Gram-negative bacteria like *Escherichia coli* are key vectors of AMR, with resistance to multiple antibiotics exacerbating treatment challenges, economic burdens, and mortality rates in humans and animals (Pradika et al. 2019; Riwu et al. 2022a; Mathur et al. 2023). The rise of AMR

underscores the urgent need for rational antibiotic use, novel antimicrobial development, and robust surveillance systems (Saeed et al. 2023). Resistant bacteria have been detected in humans, livestock, and wildlife, including bats, which serve as environmental sentinels and reservoirs for AMR (Yunita et al. 2020; Widodo et al. 2022; Benavides et al. 2024). Despite minimal direct antibiotic exposure, bats' long-distance mobility, proximity to human settlements,

and longevity make them potential carriers and spreaders of resistant bacteria (Gaeta et al. 2023).

In Indonesia, bat guano used as fertilizer poses a significant public health risk, as it may contaminate soil, water, and food with antibiotic-resistant bacteria (Wibisono et al. 2021; Reis et al. 2024). Studies show that guano alters soil microbial communities and antibiotic resistance profiles, threatening food security (Ajuzieogu et al. 2024; Di Bella et al. 2025). Bats' ecological adaptability and dietary habits further amplify their role in AMR dissemination. Insectivorous bats, for instance, consume insects that often harbor resistant bacteria, while habitat disruption forces them into closer contact with human-dominated landscapes (Rojas-Sereno et al. 2023; Abdullah et al. 2021). Metagenomic analyses reveal that bat gut microbiota carries diverse Antimicrobial Resistance Genes (ARGs), including those resistant to critical drugs like polymyxins (Huang et al. 2025).

In Southeast Asia, AMR in wildlife remains understudied, though evidence suggests alarming trends. For example, 100% of *E. coli* isolates from wild birds in Malaysia exhibited Multidrug Resistance (MDR) (Mohamed et al. 2022), while wild deer and elephants in Thailand showed resistance to multiple antibiotics (Duangurai et al. 2022). Anthropogenic activities, such as antibiotic misuse and environmental contamination, are primary drivers of AMR in wildlife (de la Peña and Kronholm 2024). In Indonesia, resistant *E. coli* has been identified in humans, livestock, and wildlife, including bats, rats, and deer (Sunarno et al. 2023; Riwu et al. 2024). The *bla*TEM gene, a predominant ESBL marker, is

widespread in Indonesian wildlife, highlighting the potential for cross-species resistance transfer (Agustin et al. 2024).

The One Health approach is critical to addressing AMR, yet wildlife remains a neglected component (Garcés et al. 2019; Li et al. 2024). This study focuses on ESBL-producing *bla*TEM-carrying *E. coli* in cave bats of Lombok, Indonesia, to bridge this gap. By examining resistance patterns and genetic linkages, the research aims to elucidate the role of bats in AMR spread and inform strategies to mitigate environmental and public health risks. Findings will contribute to global AMR surveillance and underscore the need for integrated interventions across human, animal, and environmental health sectors.

MATERIALS AND METHODS

Ethical approval

In the current research, bat rectal swabs were carried out that had obtained approval with number No. 1.KEH.046.03.2023 from the ethics commission Airlangga University Animal Care and Use Committee (ACUC).

Bat samples

This was an observational study, conducted from September to December 2023. Live bats captured from a single cave, Saung Pengembur Cave in Central Lombok, West Nusa Tenggara, Indonesia (Figure 1), provided the samples.

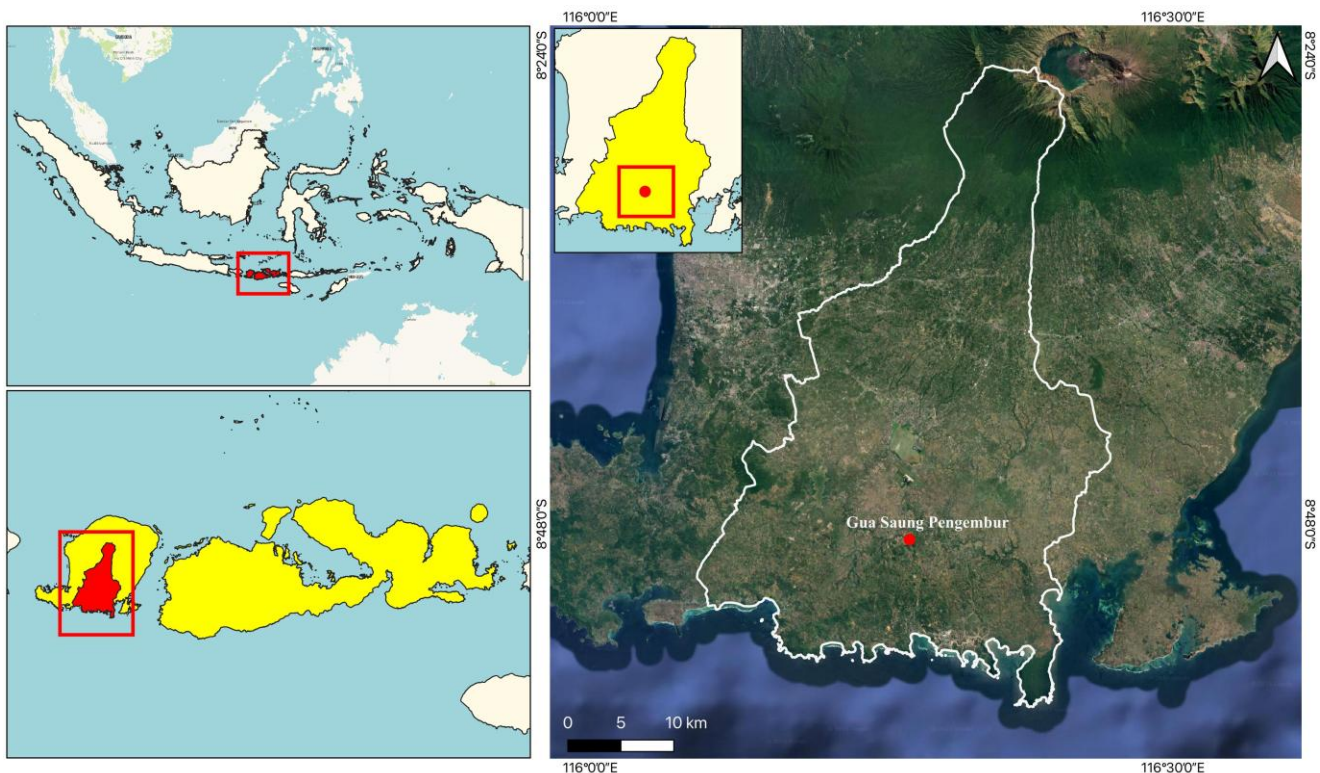


Figure 1. Saung Pengembur Cave area in Central Lombok, West Nusa Tenggara, Indonesia

Samples were collected during a single collection trip using a mist net at the mouth of Saung Pengembur Cave from 4 PM to 10 PM. The captured bats were used as samples in this study. Bats captured in the net were placed in cloth geological specimen bags, and individually removed from the geological specimen bags using protective hard rubber gloves and then anesthetized using isoflurane-oxygen 1.5% and 0.5 L/min O₂ following Wimsatt et al (2005). Physical examination was performed when the bats were anesthetized including measuring body length, wingspan, sex, and photographing the bats and then guano samples were collected from the bats' rectums by cleaning the hair around the anus with 70% isopropyl alcohol to prevent bacteria contamination, followed by inserting a sterile cotton swab into the rectum and swirled for a short while to make sure the germs stuck to it (Obodoechi et al. 2021). We used a carrier medium (Oxoid, UK) to transport samples from the cave to the laboratory in a cool state. In the bacteriology laboratory of the Faculty of Veterinary Medicine, Universitas Airlangga, Surabaya, Indonesia, *E. coli* isolates were identified and their sensitivity tested. All bats were released after they recovered. This research has obtained permission from Balai Besar Konservasi Sumber Daya Alam dan Ekosistem Nusa Tenggara Barat, Indonesia No: SK.76/K.14/TU/KSA.2/8/2023.

Bat identification

The ethics committee has approved that bat identification be carried out one by one with handling bats in a geological specimen bag using protective hard rubber gloves and then anesthetizing using isoflurane-oxygen 1.5% and 0.5 L/min O₂, following Wimsatt et al (2005). Bats (order Chiroptera) are the second-largest order of mammals, comprising over 1,230 species worldwide, which account for nearly 21% of all mammal species. They are divided into two suborders: Yinpterochiroptera (megabats) and Yangochiroptera (microbats) (Montiani-Ferreira et al. (2022). Bat identification was carried out by measuring body length, wingspan using a caliper, and sex according to the identification key by Kitchener et al. (1992) and et al. (1995). After identification and anal swabs were carried out, all bats were released again after they had recovered. Identification is based on body size, fur color, tail shape, and facial structure. Species *Rhinolophus* sp. is distinguished by the presence of a noseleaf and a horseshoe-shaped facial structure and *Hipposideros diadema* is similarly characterized by a horseshoe-shaped nose and face.

Isolation and identification of *Escherichia coli*

By inoculating the sample on media and then incubating it for 18 to 24 hours at 37°C, *E. coli* bacteria were extracted using Eosin Methylene Blue Agar (EMBA) (HI MEDIA M317). Biochemical tests and Gram staining. To identify *E. coli*, IMVIC (indole, methyl red, Voges-Proskauer, citrate) was utilized (Dameanti et al. 2023). Bacterial isolation and sensitivity test at the laboratory of bacteriology, Faculty of Veterinary Medicine, Universitas Airlangga.

Antibiotic sensitivity test

The sensitivity test (disk diffusion method) (HiMedia M173) adapts Mueller-Hinton Agar (MHA) to the Clinical Laboratory Standards Institute (CLSI) (2020). The antibiotic disk (Oxoid, England) used in this study was classified into seven classes: ciprofloxacin 5 µg (CIP) (Oxoid, UK), cefotaxime 30 µg (CTX) (Oxoid, UK), gentamicin 10 µg (CN) (Oxoid, UK), amoxicillin 25 µg (AML) (Oxoid, UK), sulfamethoxazole/trimethoprim 25 µg (SXT) (Oxoid, UK), tetracycline 30 µg (TE) (Oxoid, UK), and azithromycin 15 µg (AZM) (Oxoid, UK). Using a sterile tube, one or two colonies were extracted from EMBA medium, put in physiological NaCl, and had their opacity adjusted to McFarland standard 0.5 (1.5x10⁸ CFU/mL). A sterilized swab was used to apply a loopful of bacterial suspension to the whole MHA. For 16-18 hours, the plate was incubated in an aerobic environment at 35°C. The results were interpreted using CLSI 2020 to alter the diameter of the inhibitory zone (CLSI 2020).

Detection of *blaTEM* genes and phylogenetic analysis of *Escherichia coli* isolates from bats

The ESBL *blaTEM* gene was detected in the *Escherichia coli* bacterial culture in EMBA by employing PCR with primers *blaTEM* (R) and *blaTEM* (F). *E. coli* bacteria were inoculation in MHA medium and cultured for 24 hours at 37°C before extraction. One isolate was used to examine multiple bacterial colonies in a safe-lock Eppendorf tube with 300 µL of TE (10 mM Tris, pH 8, 10 mM Ethylenediaminetetraacetic acid (EDTA)). The solution was vortexed, and the boiling lysis process was then carried out by placing it in the Eppendorf ThermoStat™ for 10 minutes at 98°C. Following that, it was centrifuged for ten minutes at 10,000 rpm. Then, 20 µL reaction mixture (12.5 µL Go tag green master mix, primers *blaTEM*-F gene 5'-ATGAGTATTCAACATTTCCG-3' and TEM-R 5'-CTGACAGTTACCAATGCTTA-3' (Naelasari et al. 2018) with an amplification size of 867bp each -1 µL each, 0.5 µL Dnase water, and 5 µL DNA template) was taken and placed in an Eppendorf tube, then amplified.

The PCR thermal cycle consists of three phases: denaturation, annealing, and extension. There were 35 cycles of annealing at 58°C for 1 minute, followed by extension at 72°C for 1 minute, and a final extension at 72°C for 10 minutes, for amplification. The pre-denaturation temperature was 96°C for 5 minutes, followed by denaturation for 1 minute at 96°C. The product amplification was separated on agarose gel 2% and stained with gel-red.UV light used for visualized stained gel, *blaTEM* gene was considered positive when a band was observed at 867bp on gel, as seen in the positive control, *E. coli* ATCC 35218, control negative PCR is master PCR without DNA target. Results from PCR sequencing were obtained at Genetic Science Indonesia. We used sequencing data from GenBank OQ096423.1 isolate from human Filipina, MH744562.1 Isolate human Malaysia, OP999009 isolate human Thailand, and OR680712.1 isolate pig Thailand to provide a data analysis section.

RESULTS AND DISCUSSION

A total of 85 bats were captured using mist nets from Saung Pengembur Cave, Central Lombok District. Identification results showed 77 bats were *Rhinolophus* spp. (Figure 2.A) and 8 bats were *H. diadema* (Figure 2.B), as shown in Table 1.

We isolated 63 *E. coli* from 85 bat guano individuals living in Saung Pengembur Cave, Central Lombok District, West Nusa Tenggara. Colonies that grow on EMBA showing metallic sheen phenomena (Figure 3.A) morphology showed gram negative coccobacilli (Figure 3.B), from biochemical test positive *E. coli* indole ring showed pink color on Sulfide Indole Motility (SIM) media and looks motile (positive), MR is red (positive) and VP is yellow (negative), and citrate green (negative). Our research results showed that *E. coli* isolates from bat guano in Saung Pengembur Cave, Central Lombok District, were resistant to antibiotics (Table 2, Figure 5). The highest resistance occurred to the antibiotic azithromycin 46% (29/63), tetracycline 23.8% (15/63), amoxicillin 20.6% (13/63), sulfamethoxazole/trimethoprim 19% (12/63), ciprofloxacin 16.7% (6/63), gentamicin 1.5% (1/63), and cefotaxime had no resistance 0% (0/63) (Figure 4).

We succeeded in isolating nine (9) *E. coli* ESBL *bla*TEM genes carried by bats from Saung Pengembur

Cave, West Nusa Tenggara, Indonesia (Figure 6). From the PCR result, we carried out a sequencing test to determine the genetic closeness between our isolate and the isolate *bla*TEM *E. coli* from GenBank. Result of sequencing our isolate with OQ096423.1, OR095844.1, ON221404.1, MH744563.1, and JN037848.1, with samples 2.31, 2.33, 2.35, and 2.70 had a genetic relationship with a bootstrap 99% that indicates a strong relationship (Figure 7).



Figure 2. Bats caught from Saung Pengembur Cave, Central Lombok, West Nusa Tenggara, Indonesia. A. Morphology of *Rhinolophus* sp., B. Morphology of *Hipposideros diadema*

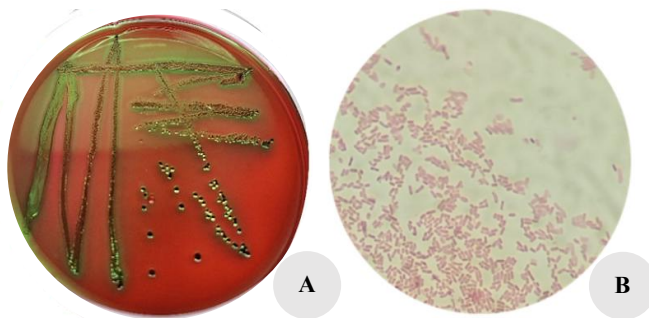


Figure 3. A. Colony of *Escherichia coli* bacteria on EMBA agar, B. Gram staining of *E. coli* (Gram-negative coccobacilli)

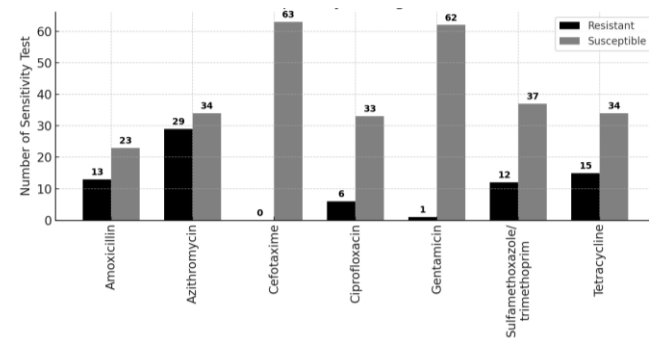


Figure 4. Antibiotic susceptibility testing using disk diffusion of *Escherichia coli* bacteria from bats in Saung Pengembur Cave, Central Lombok District, West Nusa Tenggara, Indonesia, with CLSI (2020) guidelines

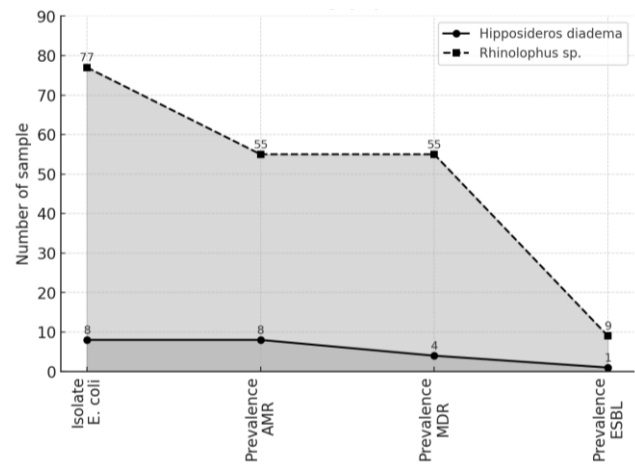


Figure 5. Interpretation resistance and ESBL profile of *Escherichia coli* bacteria from bats in Saung Pengembur Cave, Central Lombok District, West Nusa Tenggara, Indonesia

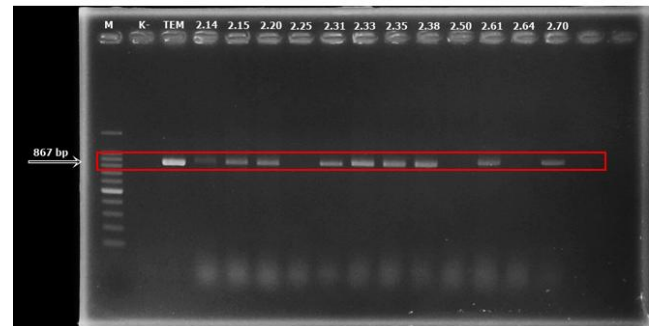


Figure 6. PCR result *bla*TEM ESBL *Escherichia coli* 867bp isolated from bats in Saung Pengembur Cave, West Nusa Tenggara, Indonesia. Note: Negative control (K-); positive control (TEM); positive results isolate *E. coli* from *Rhinolophus* sp.: 2.14, 2.15, 2.31, 2.33, 2.35, 2.38, and 2.61; positive results isolate *E. coli* from *Hipposideros diadema*: 2.20 and 2.70 negative results 2.25, and 2.64 *Rhinolophus* sp., 2.50 negative result *Hipposideros diadema*

Table 1. Body size identification bats were caught from Saung Pengembur Cave, Central Lombok, West Nusa Tenggara, Indonesia

Cave	Species of bats	Sex	Number of bats	Size of bats (cm)	
				Body length	Wingspan
Saung Pengembur Cave	<i>Rhinolophus</i> sp.	Male	29	3-5.3	8.3-12.3
		Female	48	3.1-5.7	8.5-14.8
	<i>Hipposideros diadema</i>	Male	5	7-10.1	22.3-26.4
		Female	3	8.2-10.2	22.1-29.8

Table 2. Resistance and ESBL profile of *Escherichia coli* bacteria from bats in Saung Pengembur Cave, Central Lombok District, West Nusa Tenggara, Indonesia

Cave	Species of bats	Number of samples	Number of positive isolates <i>E. coli</i>	Prevalence AMR	Prevalence MDR	Prevalence ESBL blaTEM from PCR
Saung	<i>Rhinolophus</i> sp.	77	55 (55/77, 71.4%)	55 (55/55, 100%)	9 (9/55, 16.3%)	7 (7/9, 77.8%)
Pengembur Cave	<i>Hipposideros diadema</i>	8	8 (8/8, 100%)	8 (8/8, 100%)	3 (3/8, 37.5%)	2 (2/3, 66.7%)

Discussion

There are no differences in wing size, shape, or other functional parameters between male and female bats. However, wing morphology in females suggests that maternal reproductive advantages may influence aerodynamic performance during pregnancy or migration (O'Mara et al. 2016). Although bats encompass a wide variety of species with similar external appearances, morphological traits such as body size, fur color, facial structure, tail shape, and tail length are often used for species identification (Morgan et al. 2019; Cao et al. 2023). The bat species *Rhinolophus* sp. is distinguished by the presence of a noseleaf and a horseshoe-shaped facial structure (Zhou et al. 2009), while *H. diadema* is similarly characterized by a horseshoe-shaped nose and face (Srinivasulu et al. 2010).

Both *Rhinolophus* sp. and *H. diadema* are insectivorous species that hunt by flying parallel to vegetation, particularly near forest edges, at approximately 50 cm above ground. Occasionally, they perch to observe their prey. *Rhinolophus* species have been documented to travel at least 4.2 km from their roosts during foraging (Goiti et al. 2003). Their primary diet includes insect orders such as Hymenoptera, Coleoptera, Hemiptera, Diptera, and Lepidoptera (Sin et al. 2020; Mohamed et al. 2023). Many insects on farms, particularly Diptera, are known to carry pathogenic bacteria such as *E. coli*, *Salmonella*, and *Campylobacter* (Retamales et al. 2011), which can be ingested by wildlife during feeding (Riwu et al. 2022b). *Escherichia* spp. has been isolated from Diptera (*Musca domestica*) with a prevalence of 21.45% were collected from the Malabe Medical Officer of Health (MOH) (Ranasinghe et al. 2023).

Wing morphology, including wing width and length, is closely associated with the bat's habitat and foraging behavior, and is also utilized in echolocation (Salsamendi et al. 2005). Female *Rhinolophus* bats tend to have broader

wings than males, although both sexes emit high-frequency echolocation calls (Győrössy et al. 2020).

In this study, biochemical identification using SIM, MR, VP, and citrate tests confirmed the presence of *E. coli* through positive indicators: a pink ring in SIM, red MR, yellow VP, and green citrate results (Prayudi et al. 2023). Since bats are untamed animals that can travel around and interact with different habitats without supervision, the existence of antibiotic-resistant bacteria in bat guano could be harmful to public health. While no direct cases of bat-to-human transmission of resistant bacteria have been reported, the possibility of zoonotic transmission must be considered, especially due to increasing human-wildlife conflict driven by habitat loss and fragmentation (Gerbáčová et al. 2020).

In this study, 63 isolates from insectivorous bats were successfully obtained from 85 samples. The results will be different in fruit bats, isolating *E. coli* from fruit bats will obtain lower numbers than insectivorous because of environmental and diet factors, fruit bat species that rarely touch the ground are thus less to come into contact with *E. coli* (McDougall et al. 2021). All 63 isolates (100%) were resistant to the antibiotics used in this study. Consistent with Mustika et al. (2024), this study found that *E. coli* isolates from bats in East Lombok District, Indonesia, showed the highest resistance to azithromycin (46%). Kartasmita et al. (2020) also reported that macrolide antibiotics showed the highest resistance rates in a study conducted across Asia by the Asian Network for Surveillance of Resistant Pathogens (2008-2009). In Indonesia, macrolides are the second-line treatment for pneumonia after penicillin (Kurniawati et al. 2021). Antibiotic consumption and population are closely related to the level of resistance that occurs; in addition, environmental conditions that have a humid and warm climate promote the spread of bacteria (Sun et al. 2024).

been shown to carry AMR *E. coli*, such as in Peru (Benavides et al. 2018), Poland (Nowakiewicz et al. 2020), Portugal (Sabença et al. 2021), and Australia (McDougall et al. 2021). Guano from insectivorous bats in Malaysia showed that it contains not only bacterial pathogens, but contain viruses that can affect to humans and animals (Mahyudin et al. 2021). Species, sex, and acting habits are factors that contribute to pathogens and resistant bacteria found in bats (Ferreira et al. 2024). Increased frequent wildlife-human interactions, sharing environments, and contact with guano can transfer ARG when entering through the digestive tract or respiratory tract via water, food, or water and contact with skin (Huang et al. 2025).

Data from the World's Best Award in 2020, Bali and Lombok are the 10 best Asia's islands in Asia (Alamsyah et al. 2021). The close genetic relationship of bats to humans from Malaysia could occur because Lombok is a famous destination, and tourists come to Lombok to explore the beaches, mountains, waterfalls, and caves (Jaya et al. 2021). Travelers increase global dissemination and emergence of AMR bacteria in other organisms (El Ghany et al. 2020). Genetic closeness between blaTEM from bats in this research with poultry blaTEM *E. coli* from Australia not far distance between Lombok and Australia, some species of bats migrate seasonally because they have been observed flying across the sea (Solick and Newman 2021). From reported by Vasenkov et al. (2023) bats can migrate 2515 km. The report showed that wildlife can be a reservoir of bacteria with high levels of AMR and spread the bacteria to humans (Devnath et al. 2022). New data from Australia, post-fire in Australis, many injured/ill bats enter wildlife hospitals and some individuals received antimicrobial therapy blaTEM gene was detected in 25.2% (39/155) of bats. This data showed that not significant difference in fire-affected bats pre-fire bats ($P > 0.05$) (McDougall et al. 2024). A longitudinal study by Benavides et al. (2022) showed that isolates *E. coli* from bats same with livestock, with high similar plasmid profiles across samples from up to 100 km apart, in suggest that long-term circulation of resistance in bat population. Anthropogenic activities are closely related to the presence of antibiotic resistance in bats. In Brazil, bats residing protected natural park showed that isolates low resistance level in bacteria (Cláudio et al. 2018). The One Health approach can be applied to overcome this problem of antibiotic resistance. The One Health approach is essential to address AMR across human, animal, and environmental interfaces, including wildlife (Ramandinianto et al. 2020; Adesoji et al. 2024). While *E. coli* is typically a commensal bacterium in the gastrointestinal tract, certain strains can cause opportunistic infections such as pneumonia, urinary tract infections, and septicemia (McDougall et al. 2022). The absence or lack data of resistance antibiotic in Southeast Asian countries makes it difficult to estimate the spread of antibiotic resistance carried by bats (Assefa et al. 2025).

The detection of antibiotic-resistant *E. coli* in bats from Saung Pengembur Cave, Central Lombok, indicates environmental contamination in the areas where bats live, feed, and drink. Monitoring, regulating, and reducing

antibiotic use is crucial to control the spread of antimicrobial resistance (Khairullah et al. 2019, et al. 2023). The discovery of the blaTEM *E. coli* from bats captured from Saung Pengembur Cave implies that transmission can occur when bat guano is used as fertilizer, guano excreted by bats when they search for food and drink which contaminates the human living, livestock, environment, and water environment. Socialization regarding maintaining the natural habitat of bats or not using guano as fertilizer is necessary to increase conservation in order to ensure that there in No. horizontal transfer of resistance between bats, humans, livestock, and environmental in order to improve One Health. In this research we did not use comparative data from another host, so for future studies need to comparing isolate *E. coli* or other bacteria from livestock and environment near from Saung Pengembur Cave, Central Lombok District, West Nusa Tenggara, Indonesia.

In conclusion, a total of 85 bats were successfully identified, consisting of two species: *Rhinolophus* sp. and *H. diadema*. Morphological analysis showed no significant difference in wing length between male and female individuals. From the samples collected, 63 *Escherichia coli* isolates were successfully cultured. Antibiotic resistance testing revealed the following resistance rates: azithromycin (46%), tetracycline (23.8%), amoxicillin (20.6%), sulfamethoxazole/trimethoprim (19%), ciprofloxacin (16.7%), gentamicin (1.5%), and cefotaxime (0%), indicating no resistance to cefotaxime. Among the 63 *E. coli* isolates, nine were found to carry the Extended Spectrum Beta-Lactamase (ESBL) gene bla_{TEM}. Phylogenetic analysis indicated that *E. coli* strains isolated from bats in Saung Pengembur Cave shared a close genetic relationship with GenBank sequence MH744563.1 from a human isolate in Malaysia and JN037848.1 from a poultry isolate in Australia. The risk of spreading AMR from bats can be reduced by not fertilizing plants with bat guano, consuming water only after ensuring it's not contaminated with bacteria, and limiting interaction with bats, especially from caves and where bats roost. Therefore, ongoing monitoring and scientific investigation are crucial to comprehend the patterns of Antimicrobial Resistance (AMR) within bat populations and their implications for public health. This involves examining the origins of contamination and evaluating the ecological role of bats in the spread and maintenance of AMR.

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