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CAVE-DWELLING BATS CARRY ANTIBIOTIC-RESISTANT *BACTERIA SALMONELLA SPP*. THAT POSE A PUBLIC HEALTH THREAT IN WEST NUSA TENGGARA, INDONESIA

NETOPIRJI, KI ŽIVIJO V JAMAH, PRENAŠAJO BAKTERIJE *SALMONELLA* SPP., ODPORNE PROTI ANTIBIOTIKOM, KI OGROŽAJO JAVNO ZDRAVJE V PROVINCI ZAHODNA NUSA TENGGARA, INDONEZIJA

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Abstract UDC 599.4: 579.842.1/.2(24)(594)

Alfiana Laili Dwi Agustin, Mustofa Helmi Effendi, Wiwiek Tyasningsih & Hani Plumeriastuti: Cave-dwelling Bats Carry Antibiotic-Resistant Bacteria* Salmonella spp. *That Pose a Public Health Threat in West Nusa Tenggara, Indonesia

Salmonella spp. is a bacteria that can be transmitted between humans and bats through feces, food, and water contamination in the environment, causing foodborne illness. This bacterial infection will be more hazardous if the bacteria become resistant to antibiotics. Bats are wild animals that have the potential to spread resistant germs into the human environment because the habitat where they live and forage is shrinking, forcing bats to migrate from their natural habitat to the human environment. Although bats do not receive antibiotics, they can be contaminated by bacteria that are resistant to antibiotics because they have close contact with humans, animals, and the environment. They are contaminated with resistant bacteria when they look for food and drink. Our research focuses on identifying the antibiotic resistance that exists in *Salmonella* spp. in bats in caves because it can endanger public health. The mist net is set at the cave's mouth between 4 to 10 pm and the mist net is checked periodically. If a bat is caught, it is swabbed with a sterile cotton bud and then examined for Gram staining and biochemistry to identify bacteria. *Salmonella* spp. isolates were evaluated for antibiotic sensitivity with tetracycline, azithromycin, cefotaxime, amoxicillin, gentamicin, sulfamethoxazole/trimethoprim, and ciprofloxacin. We

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Alfiana Laili Dwi Agustin, Mustofa Helmi Effendi, Wiwiek Tyasningsih & Hani Plumeriastuti: Netopirji, ki živijo v jamah, prenašajo bakterije* Salmonella spp.*, odporne proti antibiotikom, ki ogrožajo javno zdravje v provinci Zahodna Nusa Tenggara, Indonezija

Salmonella spp. so bakterije, ki se lahko prenašajo med ljudmi in netopirji z iztrebki, hrano in onesnaženo vodo v okolju ter povzročajo bolezni, ki se prenašajo z živili. Bakterijska okužba bo še nevarnejša, če bodo bakterije postale odporne proti antibiotikom. Netopirji so prostoživeče živali, ki lahko v človekovo okolje širijo odporne mikrobe, saj se njihov življenjski prostor, v katerem živijo in se prehranjujejo, krči, zaradi česar se netopirji iz svojega naravnega okolja selijo v človekovo okolje. Netopirji ne prejemajo antibiotikov, a se lahko okužijo z bakterijami, ki so odporne proti antibiotikom, saj so v tesnem stiku z ljudmi, drugimi živalmi in okoljem. Ko iščejo hrano in vodo, se okužijo z odpornimi bakterijami. Naša raziskava se osredotoča na ugotavljanje odpornosti bakterij *Salmonella* spp., s katerimi so okuženi netopirji v jamah, proti antibiotikom, saj lahko to pomeni grožnjo za javno zdravje. Mreža, ki se uporablja za ujetje ptic, je bila na vhodu v jamo nameščena med 16. in 22. uro in se je redno preverjala. Ko se netopir ujame, s sterilno vatirano palčko odvzamemo vzorec, nato pa se z barvanjem po Gramu in biokemično analizo identificirajo bakterije. Izolati bakterij *Salmonella* spp. so bili ocenjeni glede občutljivosti za antibiotike s tetraciklinom, azitromicinom, cefotaksimom, amoksicilinom, gentamicinom,

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successfully isolated nine isolates *Salmonella* spp. bacteria from 135 samples.The sensitivity test results showed that *Salmonella* spp. bacteria from cave bats in West Nusa Tenggara, Indonesia, were resistant to the antibiotics azithromycin 77.7%, amoxicillin 22.2%, and tetracycline 11.1%.

Keywords: *Salmonella* spp., bats, public health, antibiotic resistance.

sulfametoksazolom/trimetoprimom in ciprofloksacinom. Iz 135 vzorcev smo uspešno izolirali devet izolatov bakterij *Salmonella* spp. Rezultati testa občutljivosti so pokazali, da so bakterije *Salmonella* spp., s katerimi so okuženi jamski netopirji v provinci West Nusa Tenggara v Indoneziji, odporne proti antibiotikom azitromicin: 77,7 %, amoksicilin: 22,2 % in tetraciklin: 11,1 %.

Ključne besede: *Salmonella* spp., netopirji, javno zdravje, odpornost proti antibiotikom.

1. INTRODUCTION

Bats (order *Chiroptera*) are natural creatures that are extensively investigated to detect dangerous infectious agents like viruses, parasites, and bacteria (Szentivanyi et al., 2023). Bats are considered to spread pathogens because they live in different environments such as caves, human buildings, ravines, trees, and bridges. They move from rural areas to urban areas (Lima et al., 2018). The diversity of species, good adaptability, wide distribution, ability to survive against pathogens without showing pathology, and ability to fly to move long distances allow bats to become reservoirs of infectious agents (Ferreira et al., 2024). Guano is an excrement excreted by bats that is often used by farmers to fertilize plants, as it contains a lot of magnesium phosphate and calcium (Mozdzer, 2024). Apart from being rich in minerals that farmers need for crops, bat guano contains also many zoonotic bacterial pathogens such as *Salmonella* spp. (Dimkic et al., 2021). *Salmonella* spp. are bacteria that can be transmitted between humans and bats through feces, food, and water contamination in the environment (McDougal et al., 2023). In several countries in Africa and Asia, an estimated 33 million cases of salmonellosis threaten public health every year (Ugbo et al., 2023a). Foodborne disease infection caused by bacterial infection is transmitted through the food production chain (Ansharieta et al., 2021a; Wibisono et al., 2023). The food industry has used biological, chemical and physical methods of *Salmonella* decontamination of food products, but these methods can have a negative impact on food products (Sun et al., 2024).

Salmonella spp. family Enterobacteriaceae is associated with foodborne illness that causes Salmonellosis, the ability of *Salmonella* to enter M cells causing gastrointestinal disease (Alenazy, 2022). Manifestations of salmonellosis depend on virulence factors, serotype involved, host immunity, and infective dose (Castro-Vargas et al., 2020). Salmonellosis generally causes two diseases: Typhoid fever and non-typhoidal salmonellosis (NTS), *Salmonella* can cause symptomatic or asymptomatic infections, a bacterial infection of 10^6-10^8 CFU NTS is required to cause disease in an adult human (Xu et al., 2021). *Salmonella enteritidis* and *Salmonella typhimurium* are the most common serotype isolated from humans and animals (Roasto et al., 2023). Generally, *Salmonella* in wild animals is asymptomatic and latent, the bacteria come out with feces so that wild animals can act as a natural reservoir, *Salmonella* contamination in livestock and humans can occur, especially on farms and human environments close to the area where they live (dos Santos et al., 2022). *Salmonella* spp. can survive in a variety of environments including mud and soil that has minimal nutrients for years with Salmonella can survive for years in a variety of environments, including mud and nutrient-poor soils (Mafizur et al., 2024). Salmonellosis is estimated to cause 93.8 million cases of gastroenteritis worldwide annually with a death rate of 155,000 per year (Galan-Relano et al., 2023). According to the World Health Organization, 60% of zoonotic infectious diseases worldwide are caused by wild animals. From 1979 to 2019, antibiotic resistance in wild animals increased by 7% each year (Smoglica et al., 2024).

Misuse of antibiotics to control *Salmonella* infections as treatment and prophylaxis can result in antibiotic resistance (AMR). Poorly controlled use of antibiotics can result in multi-drug resistance (MDR) (Chu et al., 2024). *Salmonella* bacteria are pathogenic bacteria identified in bats in Lombok, West Nusa Tenggara, Indonesia (Agustin et al., 2019). The emergence of resistance requires special attention if the Extended Spectrum Beta-lactamase (ESBL) enzyme produced by bacteria is detected (Wibisono et al., 2021). ESBL is an enzyme that causes resistance to a broader spectrum of antibiotics, monobactams except cephamycin and carbapenems, third generation cephalosporins which make these antibiotics no longer effective (Wibisono et al., 2020a). Antibiotic resistance was found in *Escherichia coli* (*E. coli*) isolates from bats in West Nusa Tenggara, Indonesia (Mustika et al., 2024b), in *Klebsiella pneumoniae* (*K. pneumoniae*) from Tanjung Ringgit Cave (Kinasih et al., 2024) and in *E. coli* isolates from bats from Lawah Cave and Saung Pengembur Cave (Agustin et al., 2024). Human anthropogenic activities trigger the presence of antibiotic residues in the environment, wild animals that do not come into direct contact with antibiotics can carry resistant bacteria when they look for food and drink (Riwu et al., 2024). Human activities such as making forests into tourist attractions, deforestation, bat hunting have increased interactions between humans and bats (Esposito et al., 2023). Bats are assumed to acquire bacteria that are resistant to antibiotics when they forage for food and drink in human environments and livestock (Ingala, 2024). Bats can act as sentinels for environmental pollution due to human activities as the existence of antibiotic resistance in bats is due to contamination from humans and livestock (Rojas-Sereno et al., 2023).

Antibiotic resistance arises due to the disruption of bacterial life due to antibiotics. Antibiotic resistance can have long-term impacts on humans (Effendi et al., 2021). The presence of antibiotic-resistant bacteria in bat guano increases the potential for the spread of antibiotic resistance in humans, livestock, and the environment (Castelo-Branco et al., 2023). *Salmonella* bacteria have been resistant to the antibiotics tetracycline (82%), trimethoprim-sulfamethoxazole (59%), chloramphenicol (29%), ciprofloxacin (11,8%) and aztreonam (5,8%) on chickens sold in the traditional market in Surabaya, Indonesia (Fanissa et al., 2022). *Salmonella* bacteria in bats in several countries have shown resistance to antibiotics amoxicillin (Islam, 2014), tetracycline, Sulphamethoxazol-Trimethoprim, Azithromycin, Chloramphenicol, Amoxicillin-Clavulanic acid, Cefotaxime (Uddin et al., 2021), augmentin, cefuroxime, and ceftazidime (Aladejana et al., 2024). One Health is a concept used to solve the problems human, animal, and environmental health (Horefti, 2023). Although *E. coli* and *K. pneumoniae* in bats in West Nusa Tenggara have been detected to be resistant to several antibiotics, there has been no comprehensive research regarding the sensitivity of *Salmonella* bacteria in bats in West Nusa Tenggara. The risk of zoonotic disease is higher with the transmission of *Salmonella* spp. which is resistant to antibiotics, the presence of transposons, integrons, plasmids, and insertion sequences which all contributes to increasing antibiotic resistance (Mlangeni et al., 2024). Data on the sensitivity of *Salmonella* spp. bacterial isolates from bats from West Nusa Tenggara is important to know in relation to the description of the distribution of antibiotic resistance in wildlife, which can have an impact on human, animal, and environmental health.

2. MATERIALS AND METHODS

ETHICAL APPROVAL

In our study, we performed rectal swabs from bats approved by the Ethics Committee of the Faculty of Veterinary Medicine of Airlangga University under the number 1.KEH.046.03.2023.

STUDY PERIOD AND LOCATION

This research was conducted from December 2023 until May 2024. Samples were obtained from live bats caught from Lawah cave and Saung Pengembur cave in West Nusa Tenggara, Indonesia. Isolation, identification and sensitivity testing of *Salmonella* spp. bacteria were carried out in the Bacteriology laboratory, Faculty of Veterinary Medicine, Airlangga University, Surabaya.

STUDY AREA AND SAMPLE COLLECTION

A total of 135 bats (50 samples from Lawah cave and 85 samples from Saung Pengembur cave) were caught to collect guano using rectal swabs used as a sample, bats were caught using 20x20 mm mist nets, catching was carried out from 4 pm to 10 pm (McDougal et al., 2021). Samples were obtained by swabbing the bat's rectum by cleaning the fur around the anus using 70% isopropyl alcohol to avoid contamination of bacteria on the fur. The cotton swab was inserted into the rectum and rotated for a few moments to ensure the bacteria stuck to the cotton swab (Adesiyun et al., 2009). The swab results are placed on a Blair carry transport medium (Oxoid, UK) and distributed to the laboratory using a coller box.

ISOLATION AND IDENTIFICATION *SALMONELLA* SPP.

Bat guano resulting from rectal swabs was inoculated in tetrathionate broth (Merck®) as a fertilizer and incubated overnight. The growing organisms were inoculated on Salmonella-Shigella agar (Merck®) media and incubated at 37 ^{0}C for 18 to 24 hours. Colonies that do not ferment lactose with a round black center on Salmonella-Shigella agar media are suspected of *Salmonella* spp. and separate colonies of suspected salmonella were replanted on SSA media to obtain pure suspects.

Gram staining is used to determine the Gram characteristics and morphology of bacteria. Individual colonies of bacteria were taken using a tube and placed on a glass object plus sterile physiological NaCl, allowed to dry, then fixed in a Bunsen flame. Crystal violet was

Figure 1: Sampling locations in Lawah cave -8.539453, 116.276576 in West Lombok and Saung Pengembur cave -8.812872, 116.273968 in Central Lombok, Indonesia.

dropped and left for two minutes then washed with running water, the second stage was dripped with Lugol for 1 minute, washed with 95% alcohol, the third stage, safranin was added, left for 30 seconds and washed thoroughly using running water. Finally dried with paper, the dried glass object was supplemented with emersion oil and was observed using a microscope with a magnification of 1000 (Mustika et al., 2024a). Biochemical tests were carried out using Triple Sugar Iron Agar (TSIA) (Merck®), Sulfide Indole Motility (SIM) (Merck®), citrate (Merck®), urea (Merck®) and sugars (glucose, lactose and sucrose) (Merck®) (Hanifa et al., 2022).

ANTIMICROBIAL SENSITIVITY TEST OF ANTIBIOTIC

Antimicrobial susceptibility testing of *Salmonella* spp. isolates was carried out using the Kirby-Bauer disk diffusion test. The antibiotics used were amoxicillin 25μg (AML) (Oxoid, UK), azithromycin 15μg (AZM) (Oxoid, UK), cefotaxime 30μg (CTX) (Oxoid, UK), ciprofloxacin 5μg (CIP) (Oxoid, UK), gentamicin 10μg (CN) (Oxoid, UK), sulfamethoxazole/trimethoprim 25μg (SXT) (Oxoid, UK), tetracycline 30μg (TE) (Oxoid, UK). Mueler Hinton Agar (MHA) (Merck®) was used as a medium, *Salmonella* spp. isolates were smeared on MHA medium with a concentration equivalent to 0.5 McFarland using a sterile cotton swab. Seven (7) different antibiotic discs were carefully placed in the MHA media on the Petri dish, the Petri dish was left for 10 minutes before being turned over and incubated for 24 hours at 37 ^{0}C (Dameanti et al., 2023). The diameter of the inhibition zone formed was measured and interpreted according to the guidelines of Clinical and Laboratory Standards (CLSI) (CLSI, 2020).

3. RESULTS

Salmonella spp. bacteria which was successful isolated from bats *Rhinolophus* sp. on SSA media showed round colonies with a black dot in the middle and clear surroundings, the black color on the colony shows H_2S produced by *Salmonella* spp. (Figure 2A). Identify gram staining bacteria with microscopic examination showed red color and rod-shaped bacteria (Figure 2B). The results of the biochemical test showed that the bacteria on the TSIA media were red on the slanted side (basic) which indicated that the bacteria did not ferment lactose,

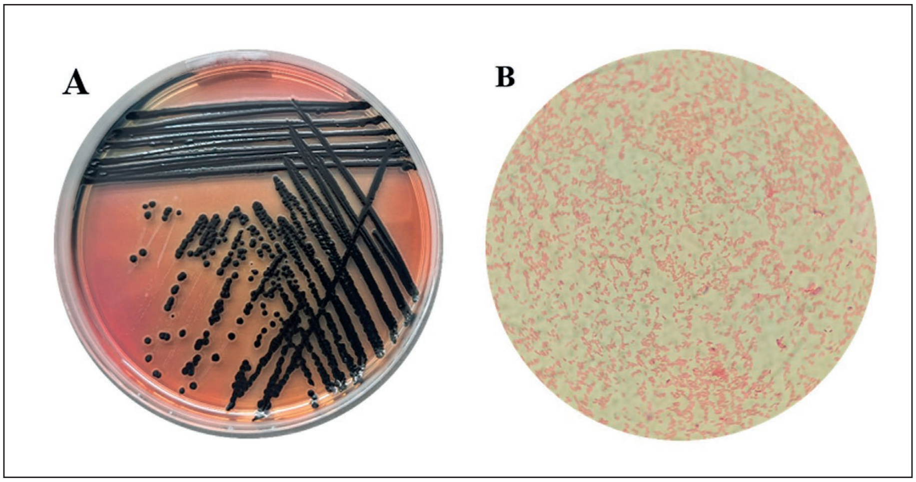

Figure 2: A) Salmonella spp. bacterial colonies on Salmonella Shigella Agar media; B) the morphology of the Gram test bacteria is red.

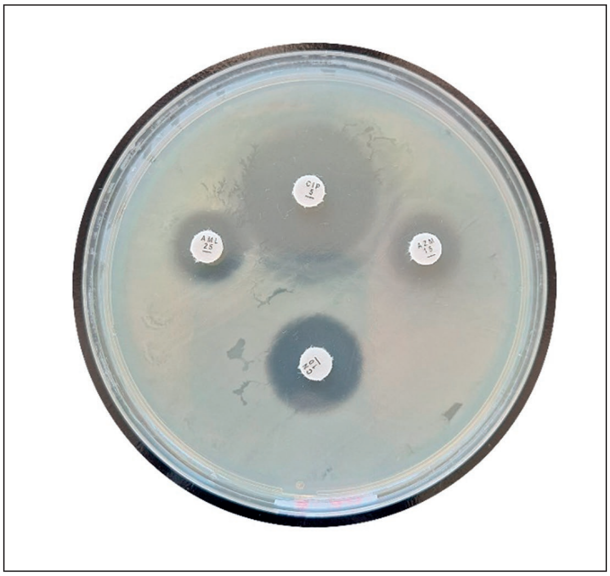

Figure 3: Antibiotic sensitivity test Salmonella spp. bacteria.

while the bottom of the media was black which indicated H_2S production. A positive SCA test result shows that the bacteria use citrate as carbon, where the media changes color to blue. The SIM test results show that motile bacteria do not form indole rings (red rings) and produce H_2S. The MRVP test results showed that the MR media remained red after being dropped using methyl red reagent and the VP media remained yellowish after being dropped using alpha napthol + 40% KOH. Negative urease test results are indicated by a yellowish colored medium.

Based on morphological tests, Gram staining and biochemical tests, the results showed that from 135 samples (50 samples from Lawah cave and 85 samples from Saung Pengembur cave) *Salmonella* spp. isolates were obtained in 6.66% (9/135) of the samples (Table 1).

Table 1: Prevalence of Salmonella spp. isolates from bats West Nusa Tenggara, Indonesia.

Lokation	Number of samples	*Salmonella spp.* Positive samples
Gua Lawah	50	7
Gua Saung Pengembur	85	2
Total sample	135	9

The sensitivity test (Figure 3) results we obtained from *Salmonella* spp. isolates from West Nusa Tenggara cave bats from 9 isolates (Table 2) had resistance to the antibiotic azithromycin (77.7%), amoxicillin (22.2%) and tetracycline (11.1%) and from Table 3 we can know that azithromycin that the antibiotic dominant resistance in bats caught from Lawah cave and Saung Pengembur cave.

Table 2: Antibiotic susceptibility profile Salmonella spp. bacteria from cave bats in West Nusa Tenggara, Indonesia.

Antibiotic	Susceptibility test profile		
	Resistant	Intermediate (%)	Susceptible (%)
Amoxicillin	22.2% (2)	11.1% (1)	66.6% (6)
Azithromycin	77.7% (7)	-	22.2% (2)
Cefotaxime	0 %	0	100% (9)
Ciprofloxacin	0 %	66.6% (6)	33.3% (3)
Gentamicin	0 %	11.1% (1)	88.8% (8)
Sulfamethoxazole/ trimethoprim	0 %	0 %	100% (9)
Tetracycline	11.1% (1)	0%	88.8% (8)

4. DISCUSSION

Bacterial cultivation is the "gold standard" for detecting *Salmonella*, but it takes quite a long time if it is used to detect this bacteria in food sources, significant losses will impact the transportation of food to market (Yang et al., 2024). The identification results in our research are in line with research by Wibisono et al., (2023) on biochemical tests to differentiate bacteria *Salmonella* and *Proteus* are urease tests, *Salmonella* bacteria show negative results in the urease test because *Salmonella* cannot convert urea into ammonia. The Polymerase Chain Reaction (PCR) test method can be used as another option to detect complex sample substances in food (Yanestria et al., 2019).

We succeeded in identifying nine sample *Salmonella* spp. bacteria from 135 samples. According to Altissimi et al., (2024) in a study, the number of *Salmonella* spp. samples that are successfully isolated depends on the sample matrix, the proximity of livestock and human settlements, and the geographical area where the samples are taken. Feces are the samples most often used as research objects because *Salmonella* spp. predilection is in the digestive tract (Yada, 2023). Updating *Salmonella* spp. prevalence data is necessary in relation to the incidence of salmonellosis from wild animals that are hunted (Oludairo et al., 2023). Reports on the identification of *Salmonella* spp. isolates from bats are quite scarce, one of 302 *Salmonella* spp. isolates from bats in Bangladesh (Islam et al, 2013), 4 of 400 (3.5 %) *Salmonella* spp. isolates from bats in Benin (Armelle et al., 2021), one of 254 (0.39 %) *Salmonella* isolates from bats in Australia (McDougal and Power, 2021) and 9 of 45 (20 %) *Salmonella* spp. isolates from bat guano samples from Thailand (Nicolas, 2024). Results of our research are in agreement with previuos researches showing 9 of 135 (6,66%) *Salmonella* spp. isolates, isolated from bats in West Nusa Tenggara, Indonesia. Bats do not make special dwellings as a place to live, they live in caves as a place to rest and hibernate, but food shortages and deforestation force them to move to villages or cities such as empty buildings, under bridges, and on farms allowing direct and indirect contact with bacteria between humans, animals, and wildlife which allows zoonotic infections to occur (Skarzynska et al., 2020).

At the Sukahaji market in Bandung, Java, Indonesia, mammals are sold live and only killed if there is a buyer. The mammals that are mostly sold are bats and squirrels. The trade in wild animals not only results in outbreaks in humans but also affects livestock, rural livelihoods, ecosystem health, and wildlife populations (Nijman et al., 2023). Food sources that are not handled and processed properly can endanger consumers due to bacterial contamination (Peratasari et al., 2022; Ugbo et al., 2023b). A total of 16 million cases of fever due to salmonellosis resulted in deaths of up to 3 million worldwide (Wibisono et al., 2020b), 3-5% of patients who recover from *Salmonella* infection will become carriers with chronic bladder infections and the bacteria will be excreted periodically through feces and urine throughout the patient's life (Li, 2020), If bacteria that are resistant to antibiotics contaminate the environment, it can have a negative impact on human and animal health (Ansharieta et al., 2021b).

Bats are order Chiroptera which consists of 1482 species and have different eating habits (Simons and Cirranello, 2024) Half of these bat species spend part of their lives in caves. The presence of AMR bacteria in bats indicates anthropogenic contamination such as exposure to human waste, livestock waste, hospital or factory wastewater treatment drugs and antimicrobial residues (Devnath et al., 2022). Antibiotic therapy is widely recognized as the most successful therapy, the golden age of antibiotics began in 1940 with more than 40 antibiotics discovered, excessive use resulted in the emergence of bacterial resistance to antibiotics, this impact was seen in the early 1990s, since then AMR is considered a global problem impact on environmental, animal, and human health (Smoglica et al., 2023). The existence of antibiotic resistance in wild animals that have never received antibiotic therapy needs to be considered carefully because it is a sign of AMR contamination in the environment due to the close relationship between wild animals, the human environment, and livestock (Ramey *et al*., 2020). In Asia, in 2019 *Salmonella* antibiotic resistance increased not only in humans but also in poultry (Takaichi et al., 2022).

In our research (Table 2), *Salmonella* spp. was resistance to azithromycin (77.7%), amoxicillin (22.2%), and tetracycline (11.1%). In line with our research, *Salmonella* isolates from Bangladesh were resistant to the antibiotics tetracycline (93%), sulfamethoxazole-trimethoprime (80%), azithromycin (76%), chloramphenicol (62%) and amoxicillin-clavulanic acid (42%) (Uddin et al., 2020). In contrast to the results of research from bats in Nigeria, antibiotic resistance to *Salmonella* spp. was high in the antibiotics third generation of cephalosporins ceftazidime (68.42%), cefuroxime (83.84%) and amoxicillin/clavulanic acid (93.37%), low resistance occurred in the antibiotics gentamicin, meropenem, ertapenem, ofloxacin, tetracycline, sulfamethoxazole and nitrofurantoin (Aladejana et al., 2024). It's also different from research by Eugen (2019) *Salmonella mikawasima* and *Salmonella bochum* isolates from bats in Côte d'Ivoire were still susceptible to all tested antibiotics. The horizontal spread of antibiotic resistance in Enterobactericeae is initiated by mobile genetic elements that are often found in livestock (Witaningrum et al., 2022).

In our study, the antibiotic resistance was the highest among azithromycin. Treatment of the antibiotic azithromycin in obese patients accumulated a lot in adipose tissue (Yu *et al*., 2022). In America, 86.2% of *Salmonella* spp. bacteria isolated from animals have experienced MDR including the antibiotics azithromycin and ceftriaxone, but antibiotic azithromycin is not recommended as a treatment in animals because if there is an allergy to this drug, the antibiotic azithromycin is metabolized in the liver so the use of this antibiotic requires caution in patients who have liver problems (Ge et al., 2024). WHO categorizes macrolides as high priority antibiotics, macrolides are used as beta-lactam support in patients allergic to β-lactam antibiotics (Trott et al., 2021). Inappropriate use of antibiotics hydroxychloroquine and azithromycin, weak supervision of buying and selling antibiotics, regulations, and policies for controlling AMR are not yet in sync between district and central governments, knowledge, habits and behavior of Indonesians regarding the use of antibiotics are still not which result increasing the incidence of AMR in Indonesia, increasing the incidence of AMR in Indonesia (Siahaan et al., 2022). The use of the antibiotic azithromycin increased during the COVID-19 pandemic, this antibiotic is used as an adjuvant antibiotic therapy to treat upper respiratory tract infections even though WHO does not include azithromycin as the main therapy for COVID-19 infection because this antibiotic has a lower artimogenic potential than other macrolides (Andanalusi et al., 2022).

Salmonella spp. is a normal flora in pigs and poultry; the source of microbial contamination comes from soil, water, and insects (Tenaya et al., 2024). In the abdomen of insects, *Salmonella* bacteria can survive for 45 days (Fazion et al., 2023). *Musca domestica* is an insect that has been shown to carry *Salmonella* bacteria which are resistant to ampicillin and tetracycline (31.21%) (Bertelloni et al., 2023). *Salmonella* spp. bacteria from laying hens in West Lombok Regency, West Nusa Tenggara are known to be resistant to the antibiotics streptomycin, tetracycline and ciprofloxacin (Ramdani et al., 2024). *Salmonella enterica, Salmonella livingstone,* and *Salmonella infantis* detected on insects *Alphitobius diaperinus* on a chicken farm in Chile (Donoso et al., 2020). *Salmonella ser. typhimurium* dan *S. ser. derby* isolated from pigs in Tuscany, the bacteria were resistant to the antibiotics sulfonamide, tetracycline, and streptomycin (Nguyen Thi et al., 2020). Reducing the use of antibiotics due to discussions between veterinarians, breeders and facilitators who have knowledge about antibiotic management can have an impact on reducing antibiotic resistance. Reducing the number of antibiotic resistance can also be achieved through research that focuses on resistance genes in agricultural wastewater and animal waste (Jimenez et al., 2023). Low awareness and limited number of veterinarians in low- and middle-income countries regarding AMR can have an impact on increasing the number of worldwide AMR (Coyne et al., 2020). In Indonesia, as many as 12.7% of deaths occurred in patients with bloodstream infections who had experienced resistant bacteria (Taruna et al., 2022). *Salmonella* spp. isolates from camel meat in Egypt are known to have experienced MDR, from PCR test results it is known that *bla*$_{\mathrm{OXA}}$ is a gene that is always present in ampicillin-resistant isolates (Sallam *et al*., 2024). The results of our research show that there is a potential risk for humans and animals who come into contact with bat guano, guano contamination of water and soil which will have an impact on public health.

5. CONCLUSION

From 135 samples we isolated 9 *Salmonella* spp. Bacteria. The susceptibility of all isolated from bats from West Nusa Tenggara, showed resistance to the antibiotic, tetracycline 11.1% (1/9), amoxicillin 22.2% (2/9) and azithromycin 77.7% (7/9). Samples still showed sensitivity to the antibiotics ciprofloxacin, cefotaxime, gentamicin, and sulfamethoxazole/trimethoprim. The ability to travel long distances over various vegetation makes bats have the potential to spread antibiotic-resistant *Salmonella* spp. bacteria in the environment which can be dangerous for public health.

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CONFLICT OF INTEREST

There is no conflict of interest.

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