

ZOONOTIC BACTERIA AND ANTIMICROBIAL RESISTANCE IN RED FOX (*VULPES VULPES*) POPULATIONS: A MINI-REVIEW OF RECENT STUDIES

BACTERII ZOONOTICE ȘI REZISTENȚA ANTIMICROBIALĂ ÎN POPULAȚII DE VULPE ROȘCATĂ (*VULPES VULPES*): O SINTEZĂ A STUDIILOR RECENTE

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ABSTRACT | REZUMAT

The red fox (*Vulpes vulpes*) is a highly adaptable and abundant species in Europe, playing a significant role in the spread of antibiotic-resistant and zoonotic pathogens. As the most common wild canid in Europe, the red fox interacts with humans, watercourses, soils, and contaminated food, posing a risk of contamination between them and hunters. The emergence of antimicrobial resistance (AMR) is a global public health threat, as emphasized by the World Health Organization (WHO). One Health (OH) principles highlight the interconnectedness of human, animal, and environmental health, underscoring the importance of monitoring AMR in wildlife. This review aims to increase awareness of the existence of AMR bacteria in European red foxes. A comprehensive analysis of 15 studies reveals a significant prevalence of zoonotic bacterial pathogens in red foxes across Europe, with high frequencies of resistance to multiple antimicrobial classes. The findings highlight the urgent need for monitoring and mitigating antibiotic resistance in wildlife populations to prevent potential zoonotic transmission and inform public health strategies. By integrating human health, veterinary, and governmental systems, effective strategies can be developed to mitigate antibiotic resistance in red foxes and reduce the risk of zoonotic transmission to humans.

Keywords: zoonotic bacteria, antimicrobial resistance, red fox, Europe

Vulpea roșcată (*Vulpes vulpes*) este o specie sălbatică foarte adaptabilă și abundentă în Europa, care joacă un rol semnificativ în răspândirea agenților patogeni zoonotici care prezintă rezistență la antibiotice. Fiind cel mai răspândit carnivor din Europa, vulpea roșcată interacționează cu oamenii, cu cursurile de apă, cu solurile și cu resturile alimentare contaminate, ceea ce reprezintă un risc de contaminare a mediului natural. Apariția rezistenței antimicrobiene (AMR) reprezintă o amenințare globală la adresa sănătății publice, după cum subliniază Organizația Mondială a Sănătății (OMS). Principiile „One Health” evidențiază legătura dintre sănătatea umană, animală și de mediul natural, subliniind importanța monitorizării antibiotezistenței în fauna sălbatică. Acest articol de sinteză își propune să crească gradul de conștientizare a existenței bacteriilor AMR la vulpea roșcată europeană. O analiză cuprinzătoare a 15 studii relevă o prevalență semnificativă a agenților patogeni bacterieni zoonotici la speciile de vulpe roșcată din țările UE, cu frecvențe ridicate de rezistență la mai multe clase de antimicrobiene. Constatările evidențiază necesitatea urgentă de monitorizare și atenuare a rezistenței la antibiotice în populațiile de animale sălbatice pentru a preveni o potențială transmitere zoonotică și pentru a informa strategiile de sănătate publică. Prin integrarea sistemelor de sănătate publică, veterinară și sistemul guvernamental, se pot dezvolta strategii eficiente pentru a atenua rezistența la antibiotice la *Vulpes vulpes* și pentru a reduce riscul de transmitere zoonotică la oameni.

Cuvinte cheie: zoonoze, rezistența la antibiotice, vulpea roșcată, Europa

Long before antibiotics were discovered and developed to treat infectious illnesses, antibiotic resistance had existed and developed, due to the existence of environmental microorganisms, which are well known for producing natural antibiotics (29). However, the overuse of antibiotics in recent decades, in

medicinal, veterinary, and agricultural operations, has only managed to accelerate the development and spread of bacterial antibiotic resistance (6, 22).

In the present, antimicrobial resistance (AMR) is considered by the World Health Organization (WHO) as one of the most significant public health issues of the twenty-first century (28). Moreover, the link between humans, animals, and the environment has been recognized by One Health (OH), emphasizing that AMR affects the three groups collectively (8).

Although most wildlife prefers to live away from

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people, certain species, such as foxes, have evolved to coexist alongside domestic animals or humans in urban settings. Due to human population growth and natural habitat destruction, the contacts between anthropogenic source sites and wild animals will continue to rise (12).

The red fox (*Vulpes vulpes*) is a representative of the *Canidae* family, and the most numerous wild species of the canid family in Europe (15). This wild species is an opportunistic predator, that also feeds on small birds, mustelids, eggs, small rodents and, not lastly, human waste (7). By interacting with the domestic human waste, foxes could become infected with novel AMR bacteria, leading to their deaths, or potentially becoming reservoirs for those bacteria (8).

Recent studies suggest that red foxes could be used as wildlife indicators of AMR dissemination due to their capability of becoming hosts for AMR bacteria, including Extended spectrum Beta-Lactamase (ESBL) producing *Escherichia coli*, Shiga toxin-producing *E. coli* (STEC), *Salmonella* spp., *Enterococcus* spp., *Listeria monocytogenes*, and Methicillin resistant *Staphylococcus aureus* (MRSA) (6, 8, 10, 12, 13, 15). In most wildlife, AMR is associated with exposure to food, water, and land contaminated with domestic, medical, agricultural, or industrial discharges, containing faecal matter and antibiotic residues, among others.

All of the above are supported by the idea that, typically, antibiotics and veterinary care are not given to wild animals, with the exception of some very specific situations (14, 21). Given their predatory, scavenging and exploratory behaviour, and growing population in urban and peri-urban regions, foxes are considered an epidemiological connection between humans, domestic animals, and natural ecosystems (24).

The current research in the field of AMR bacteria in wild animals was mainly focused on determining the prevalence, antibiotic resistance pattern and occasionally the resistance genome for some cultivable microorganisms (E.g. *Escherichia coli*, *Enterococcus* spp., *Salmonella* spp., *Staphylococcus* spp., *Listeria monocytogenes*) (2, 6, 8, 13, 15, 27). However, when compared to the abundance of studies conducted on humans, or domestic animals, a lack of research in the wildlife field was observed (3, 5, 26).

From a One Health point of view, understanding the dynamics of antimicrobial resistance in a sentinel species is mandatory for developing strategies to control environmental contamination and disease outbreaks. Studies are crucial for gaining a deeper understanding of the dynamics of AMR in natural ecosystems. Therefore, in this study, the aim is to put together all the recent studies that used the red fox (*Vulpes vulpes*) as a sentinel species in Europe.

MATERIALS AND METHODS

To identify scientific articles relevant to the study's aim, a search was conducted in the PubMed database. This review includes data published in scientific articles from January 1, 2018, to May, 2024.

The search strategy for this review involved simultaneously using three or four specific keywords in the database search area. The specific terms included the name of the target sentinel species, "Red fox" or "*Vulpes vulpes*", combined with other keywords such as "faecal", "gut", "bacteria", "antimicrobial" or "resistance." The resulting raw data was then processed to ensure that the selected scientific articles focused on monitoring the occurrence of gut originated pathogenic microorganisms in red foxes, within an EU member state or highlighted their resistance to antimicrobials.

RESULTS AND DISCUSSIONS

The initial PubMed search yielded 31 publications, but only 15 aligned with the objectives of this mini-review and were subsequently included and analysed. Red foxes play a significant role in the transmission and spread of zoonotic diseases within the environment. As reservoirs of antimicrobial-resistant microorganisms, they pose a considerable public health threat. In this study, a total of 15 publications were analysed. Among these, 11 reported the occurrence of bacterial pathogens isolated from faecal matter or intestinal contents, while four focused on rectal or faecal swabs. Furthermore, only 11 of the 15 selected studies examined the antimicrobial susceptibility of the identified pathogens.

The analysis of the 15 publications included in this review, revealed that 2859 out of 763 red fox examined samples, between 2018 and 2024, tested positive to bacterial pathogens included in *Escherichia*, *Salmonella*, *Enterococcus*, *Staphylococcus*, *Yersinia*, *Klebsiella*, and *Campylobacter* genus, some of which also presenting multi-drug resistance (MDR) (Table 1). Ultimately, the resulting prevalence was 26.68%.

In the Northern Europe, two studies examined the prevalence of zoonotic pathogens and their antibiotic resistance from a total of 849 samples from the red fox. The first study was conducted by Mo et al. (2018) in Norway. A total of 528 samples were collected through single faecal swabbing from wild red foxes that were hunted, in order to identify the pathogen *Escherichia coli*. Afterwards, the samples were divided depending on the population density of the area that they were harvested from. Thus, out of the 528 samples in the study, 108 (20.5%), 328 (62.1%), and 92 (17.4%) were provided from areas with low, medium and high population density, respectively.

Table 1

Summary of recent studies that were conducted on *Vulpes vulpes* zoonotic bacteria prevalence and antimicrobial resistance within European Union member states

Country	Sample origin	Examined /Positive (%)	Identified species, no. (%)	AMR profile, no. of resistant strains (%)	References
Ireland	Faecal swabs	321/37 (11.53)	<i>E. coli</i> 37 (100)	AMP (100); CAZ (100); FEP (67.6); FOX (56.8); CHL (40.1); CIP (51.3); CST (2.8); CTX (100); GEN (13.5); NA (43.2); SXT (62.2); TET (64.9);	O'Hagan et al., 2021 (18)
Italy	Faeces	285/2 (0.7)	<i>Y. palearctica</i> 2 (100);	AMP+CEF+ERY 1 (50); AMP+CEF+ERY+CTX+CXM 1 (50);	Carella et al., 2022 (4)
Italy	Faeces	22/4 (18,2)	<i>Y. enterocolitia</i> 2 (9.1); <i>Y. frederikserii</i> 2 (9.1);	n.a.	Ebani et al., 2022 (9)
Italy	Intestinal contents	718/42 (6)	<i>S. enterica</i> subsp. <i>enterica</i> 36 (85.71); <i>S. enterica</i> subsp. <i>salamae</i> 3 (7.14); <i>S. enterica</i> subsp. <i>diarizonae</i> 2 (4.76); <i>S. enterica</i> subsp. <i>Houtenae</i> 1 (2.38);	n.a.	Gambi 2022 et al., 2022 (10)
Italy	Faeces	109/31 (28.4)	<i>E. coli</i> (100);	n.a.	Bertelloni et al., 2022 (1)
Italy	Faeces	3/1 (33.33)	<i>Klebsiella oxytoca</i> 1 (100)	AMP+DA;	Gambino et al., 2021 (11)
Italy	Faeces	45/14 (31.11)	<i>Campylobacter vulpis</i> sp. nov.	n.a.	Parisi et al., 2021 (20)
Norway	Faeces	528/434 (82.2)	<i>E. coli</i> (100)	TET+TGC+CHL+AMP+SXT+GEN+CIP+NA+CST;	Mo et al., 2018 (17)
Poland	Rectal + oral swabs	415/157 (37.83)	<i>S. aureus</i> 27 (17.2); <i>S. pseudintermedius</i> 104 (66.2); <i>S. sciuri</i> 7 (4.5); <i>S. succinus</i> 4 (2.54); <i>S. xylosus</i> 8 (5.1); <i>S. warneri</i> 1 (0.64); <i>S. vitulinus</i> 2 (1.27); <i>S. haemolyticus</i> 3 (1.9); <i>S. chromogenes</i> 1 (0.64);	ERY 9 (6.9); GEN 2 (1.5); RIF 1 (0.76); DA 12 (9.2); P 22 (16.8); SXT 3 (2.3); TET 40 (30.5); NI 1 (0.76);	Hahaj et al., 2024 (15)
Poland	Faecal swabs	352/37 (10.51)	<i>E. coli</i> (100)	AMP (100); CTX (100); TET (59.5); SUL (51.4); NA (48.6); CIP (24.3); STR (21.6); KAN (13.5); CHL (13.5); NFT (2.7);	Osinska et al., 2022 (19)
Poland	Intestinal content	10	<i>Salmonella</i> spp. <i>Escherichia</i> spp.	B-lactams; TET;	Skarżyńska et al., 2020 (25)
Portugal	Faeces	37/3 (8)	<i>E. coli</i> 3 (100);	CAZ+ATM+NA 1 (33.33);	Dias et al., 2022a (8)
Slovakia	Faeces	10/n.a.	<i>Enterococcus</i> spp.	TET+AMP+VAN+ERY;	Hamarova et al., 2021 (16)
Spain	Rectal swabs	3/3 (100)	<i>Enterococcus</i> spp. 3 (100)	CHL+CIP+ERY+GEN+QD+STR+TET 1 (33.33); CIP+QD+TET 2 (66.66);	Garcia et al., 2022 (13)
Spain	Faeces	1/1 (100)	<i>Psychrobacillus vulpis</i> sp. nov. 1 (100)	NA+KAN 1;	Rodriguez et al., 2020 (23)

Legend: AMP – Ampicillin; ATM – Aztreonam; CAZ – Ceftazidime; CEF – Cephalothin; CHL – Chloramphenicol; CIP/CI – Ciprofloxacin; CST – Colistin; CTX – Cefotaxime; CXM – Cefuroxime; DA – Clindamycin; ERY – Erythromycin; FEP – Cefepime; FOX – Cefoxitin; GE/GEN – Gentamicin; KAN – Kanamycin; NA – Nalidixic acid; NI/NFT – Nitrofurantoin; QD – Quinupristin-dalfopristin; RIF – Rifampicin; ST/STR – Streptomycin; SUL – Sulfamethoxazole; SXT – Sulfamethoxazole/trimethoprim; TE/TET – Tetracycline; TGC – Tigecycline; VAN – Vancomycin

The studied pathogen was successfully isolated from 434 samples, with a prevalence of 82.2%. The antimicrobial susceptibility was tested on all the isolates by broth microdilution, determining the minimum inhibitory concentrations (MIC). The occurrence of AMR was 9.2%, 6.3%, and 14.7% in the low, medium and high population density areas, respectively. Resistance towards sulfamethoxazole, ampicillin and tetracycline were the most encountered, followed by quinolones, gentamicin or tigecycline, respectively. In medium and high population density areas, resistance to ciprofloxacin and/or nalidixic acid was detected as well. Moreover, two strains showed resistance to colistin, and nine other isolates presented MDR (Table 1). The occurrence of AMR in wild foxes in this study has been proven to be related to population density (17).

The second study was realised in Ireland, by O'Hagan et al. (2021), where the presence of extended spectrum beta lactamase resistant and AmpC-type beta lactamases *Escherichia coli* (ESBL/AmpC) was screened from red fox faecal samples (n = 321). ESBL were detected in 37 out of the 321 samples (11.53 %). The MIC was determined for all 37 isolates in order to assess the antimicrobial resistance profile. In order to do this, the MICs for 20 antimicrobials were checked. As the results have shown, MDR was present in 100% of the ESBL *E. coli* isolates, with resistance frequency of 100% towards ampicillin, ceftazidime, cefotaxime, followed by a descending resistance frequency from 67.6% to 2.8%, towards cefepime, tetracycline, sulfamethoxazole, ceftiofur, ciprofloxacin, trimethoprim, nalidixic acid, chloramphenicol, gentamicin, colistin and ertapenem (18).

In Central-Eastern region of Europe, four studies that occurred in Poland (n=3) and Slovakia (n=1) were selected to be analysed in this work. A total of 787 samples were collected and screened for bacterial pathogens and potential AMR. The first Polish study was done by Skarżyńska et al. (2020), and it involved the examination of bacterial composition and quantification of antimicrobial resistance through shotgun metagenomics of DNA, that was isolated from intestinal content of different animals, including the red fox. Thus, samples were collected between 2017 and 2018 from hunted wild foxes (n = 10). The results revealed evidence of *Escherichia* spp. and *Salmonella* spp. in addition to a significant AMR to drugs important for public health, in the studied red foxes. High resistance towards the tetracyclines and beta-lactams was observed (25).

Another study conducted in Poland by Osińska et al. (2022) analysed the resistance towards antimicrobials of cephalosporin-resistant (CR) *Escherichia coli* strains, that were collected during five years from wild animals, including faecal swabs from *Vulpes vulpes*. Out of 352 red fox samples, 37 were positive to CR *E.*

coli, recording a prevalence of 10.5%. Overall, twenty-four of the isolates (64.9%) showed MDR phenotype. The predominant resistance phenotypes observed were to ampicillin (100%), tetracycline (59.5%), and sulfamethoxazole (51.4%). *E. coli* strains demonstrated significant resistance to quinolones, with 48.6% resistant to nalidixic acid and 24.3% to ciprofloxacin; all ciprofloxacin-resistant isolates also exhibited resistance to nalidixic acid. Additionally, 21.6 were resistant to streptomycin and 13.5 % towards chloramphenicol and kanamycin, while all isolates were susceptible to gentamicin (19).

Hahaj et al. (2024) analysed the presence of coagulase-positive *Staphylococcus* in swabs collected from red foxes, in the south-east region of Poland. Oral and rectal swabs were collected from a total of 209 foxes (*Vulpes vulpes*), reaching a total of 415 samples (rectal swabs, n = 206; oral swabs, n = 209). Out of the 415 samples, 37.83% (n = 157) were positive to bacterial isolation. The most frequent staphylococcal species was *Staphylococcus pseudointemedius* (n=104 66.2%), followed by *S. aureus* (n = 27; 17.2%), *S. xylosus* (n=8; 5.1%), *S. sciuri* (n=7; 4.5%), *S. succinus* (n=4; 2.54%), *S. vitulinus* (n=2; 1.27%), *S. haemolyticus* (n=3; 1.9%) and *S. chromogenes* 1 (0.64). Moreover, the strains were tested for AMR, showing the highest frequency of resistance towards tetracycline (40/157; 30.5%) and penicillin (22/157; 16.8%), followed by clindamycin (12/157; 9.2%), erythromycin (9/157; 6.9%), gentamycin (2/157; 1.5%), sulfamethoxazole (3/157; 2.3%), rifampicin and nitrofurantoin (Table 1) (15).

In Slovakia, wildlife originated *Enterococcus* species were screened for the presence of resistance against several antimicrobial substances. Therefore, ten enterococcal species that were isolated from the red fox had shown resistance towards tetracycline, ampicillin, vancomycin and erythromycin (16).

In Southern Europe, nine studies were selected to be analysed in this work and they were located in Italy (n=6), Spain (n=2) and Portugal (n=1).

A study that was conducted in the southern region of Italy, provided valuable insights into the prevalence of antibiotic-resistant bacteria in wild animals in Sicily. Through a comprehensive analysis of bacterial isolates from 368 wild animals, including three red foxes, the research revealed a high frequency of antibiotic resistance among the isolated strains. Notably, a single strain of *Klebsiella oxytoca* was identified in a red fox (1/3; 33.33%), which exhibited resistance to ampicillin and clindamycin, as determined by biochemical tests and 16S rRNA sequencing (11).

Parisi et al. (2021) analysed in their work the caecal contents of 45 wild red foxes collected in 2013 and discovered a novel taxon, *Campylobacter vulpis* sp. nov. Initially identified as *C. upsaliensis* through PCR, the

isolates were later confirmed to be distinct through multi-locus sequence typing (MLST) and polyphasic analysis (20). The findings highlight the importance of rigorous phylogenetic analysis in microbiology, underscoring the potential for unexpected diversity within bacterial populations and emphasizing the need for continued research into the evolution and ecology of these organisms.

Another study investigated *Yersinia enterocolitica* strains in wildlife in the northwestern Italian Alps, analysing 285 red fox faecal samples that were collected between 2015 and 2018. Two samples from red foxes (285/2; 07%) were found to be positive for *Yersinia palearctica*, and were further tested by Kirby-Bauer technique for antibiotic resistance. Results showed that one strain was resistant to ampicillin, cephalothin, and erythromycin, and the other presented resistance to five antibiotics, these being ampicillin, cephalothin, erythromycin, cefotaxime and cefuroxime (Table 1) (4). These findings highlight the importance of monitoring antimicrobial resistance in wildlife populations and potential for *Yersinia* spp. to spread to humans.

A study conducted in Italy investigated the presence of various bacterial pathogens in *Vulpes vulpes*, a common species of red fox. The pathogens of interest included *Salmonella* spp., *Yersinia* spp., *Listeria monocytogenes*, *Brucella* spp., *Ehrlichia canis*, *Anaplasma phagocytophilum*, *Coxiella burnetii*, and *Leptospira* spp. The analysis revealed that two (9.1%) strains of *Yersinia enterocolitica* biotype 1 and two (9.1%) strains of *Yersinia frederiksenii* were isolated from a total of 22 red fox fecal samples (9). Unfortunately, antibiotic resistance profiles were not determined as part of this study.

In a recent study, researchers Gambi et al. (2022) set out to explore the prevalence of various *Salmonella* subspecies and serotypes in wild carnivores in the Emilia-Romagna Region, Italy, over a six-year period from 2016 to 2022. A comprehensive analysis of 718 fox (*Vulpes vulpes*) carcasses was conducted, with samples taken from the large intestine contents of each animal. The results showed that 42 foxes (approximately 6%) tested positive for *Salmonella*. Further analysis revealed a diverse range of subspecies, including *S. enterica* subsp. *Enterica*, which accounted for the majority of isolates (85.71%), followed by *S. enterica* subsp. *Salamae* (7.14%), *S. enterica* subsp. *Diarizonae* (4.76%), and *S. enterica* subsp. *Houtenae* (2.38%) (Table 1) (10).

A recent study analysed the DNA of 109 faecal samples collected from red foxes in central Italy between 2016-2018 (n=109). The samples were obtained from regularly hunted animals, whose faeces were previously collected for other research purposes. The molecular analysis revealed that 31 (28.4%) of the strains could be classified into one of three distinct

pathotypes of *Escherichia coli*: enteropathogenic *E. coli* (n = 18), Shiga toxin-producing *E. coli* (n = 7), and enterohemorrhagic *E. coli* (n=3). The findings suggest that wildlife may play a role in the transmission of *E. coli* infections, as they may both harbour and shed these pathotypes, thereby posing a potential risk to human and animal health (1).

A groundbreaking discovery has shed new light on the microbial world of the red fox. In 2015, a team of researchers isolated a unique bacterial strain from the faeces of a red fox in Spain's Tablas de Daimiel National Park. Using a comprehensive array of techniques, including 16S rRNA phylogenetic analysis, MLSA, phylogenomic, chemotaxonomic, and phenotypic studies, scientists have confirmed that this strain, designated Z8T, represents a novel species within the genus *Psychrobacillus*. The proposed name for this remarkable microbe is *Psychrobacillus vulpis* sp. nov., a finding that expands our understanding of the microbial diversity of the red fox and its ecological niche (23).

In a comprehensive study, researchers in Aragón, Spain aimed to investigate the antibiotic resistance patterns of *Enterococcus* spp. in wild mammals. Rectal samples were collected from 103 wild animals, including three red foxes, using a swabbing technique. The results showed that all samples were positive for *Enterococcus* spp., and a thorough assessment of antibiotic resistance was conducted using the Kirby-Bauer disc diffusion (DD) test. The findings revealed a concerning trend of multi-drug resistance among the isolates, with one strain exhibiting resistance to seven antimicrobial agents, including chloramphenicol, ciprofloxacin, erythromycin, gentamicin, quinupristin-dalfopristin, streptomycin, and tetracycline. The remaining two strains demonstrated resistance to ciprofloxacin, quinupristin-dalfopristin, and tetracycline. This study highlights the urgent need for monitoring and mitigating antibiotic resistance in wildlife populations to prevent potential zoonotic transmission and inform public health strategies (13).

In a recent study conducted in Portugal, Dias et al. (2022) isolated three Shiga toxin-producing *E. coli* (STEC) strains from fresh faecal samples collected from 37 red foxes. Antimicrobial susceptibility tests done using disk diffusion susceptibility assays, revealed a resistance profile, with one strain exhibiting resistance to ceftazidime, aztreonam, and nalidixic acid, highlighting the potential for zoonotic transmission and emphasizing the need for continued surveillance and mitigation of antibiotic resistance in wildlife populations (8).

CONCLUSIONS

A comprehensive analysis of 15 relevant publications retrieved from the PubMed database has re-

vealed a concerning prevalence of 26.68% for zoonotic bacterial pathogens in wild European Red foxes (*Vulpes vulpes*). Specifically, a total of 763 out of 2859 examined samples tested positive for species belonging to eight genera, including *Escherichia*, *Salmonella*, *Yersinia*, *Campylobacter*, *Staphylococcus*, *Klebsiella*, *Enterococcus*, and *Psychrobacillus*. These pathogens are known to be capable of transmission between animals and humans, highlighting the potential risk of zoonotic transmission.

The results of antimicrobial resistance testing were particularly alarming, with high frequencies of resistance observed to multiple antimicrobial classes in Ireland, Poland, Spain, and Italy. Notably, some strains exhibited multi-drug resistance profiles, which can significantly complicate treatment options for infected individuals. These findings underscore the urgent need for monitoring and mitigating antibiotic resistance in wildlife populations to prevent potential zoonotic transmission and inform public health strategies.

To address this critical issue, a collaborative effort is required among human health, veterinary, and governmental systems. This integrated approach must be informed by the principles of the One Health concept, which recognizes that human health is inextricably linked to the health of animals and the environment.

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