

First Report on the Isolation of *Salmonella enterica* subsp. *enterica* Serovar Hofit in Wild Boars (*Sus scrofa*) in Türkiye

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Abstract

The aim of this study was to isolate potential bacterial pathogens, such as *Salmonella* spp., from wild boars (*Sus scrofa*) inhabiting the Southern Marmara Region of Türkiye and to evaluate the *in vitro* antibiotic susceptibility of the isolates. Samples, including feces and internal organs (lymph nodes, liver, lungs, kidneys, and spleen), were collected from a total of 34 legally hunted wild boars. *Salmonella enterica* subsp. *enterica* serovar Hofit was isolated from 6 (17.6%) animals. Ciprofloxacin, streptomycin, ampicillin, tetracycline, chloramphenicol, enrofloxacin, gentamicin, ceftiofur, cefoxitin, nalidixic acid, amoxicillin/clavulanic acid, and trimethoprim/sulfamethoxazole discs were used to determine the *in vitro* antimicrobial susceptibility of *S. Hofit* isolates. All *S. Hofit* isolates had 100% sensitivity to 11 of the antibiotics tested, and three isolates were resistant only to streptomycin. As a result, this study is the first to report the isolation of *S. Hofit* from wild boars worldwide. The high isolation rate (17.6%) suggests a potential adaptation of this serovar to swine hosts. The apparent prevalence of *S. Hofit* in wild boars raises concerns not only for wildlife but also for potential public health implications.

Keywords: isolation, serotyping, *S. Hofit*, antimicrobial susceptibility testing, wild boar

Introduction

The increase in wild boar populations worldwide in recent years is explained by natural and environmental changes as well as biological and ecological factors (Jori et al., 2021). Wild boars can easily adapt to different environments, such as mixed forests of oak and beech trees, often surrounding swamps and meadows (Tack, 2018). Due to their omnivorous diet, wild boars can easily harbor zoonotic and other bacterial pathogens, especially *Salmonella* spp., in their intestines and lymphatic tissues, and can easily spread them to the environment (Chiari et al., 2013). *Salmonella* species, one of the most common zoonotic pathogens, remains a serious public health threat worldwide. The most important of these is *Salmonella enterica*, which is one of the most important species in the genus *Salmonella* and is the most pathogenic among the species (Teklemariam et al., 2023).

It is reported that wild boars (*Sus scrofa*) are among the most significant reservoirs of pathogens at the wildlife/livestock interface in Europe, and that they may be a highly effective host for *Salmonella* spp. excretion rates when compared to other wild ruminants (Hilbert et al., 2012). However, little is known about the role of wild boar in *Salmonella* spp. epidemiology at the boar-livestock interface, although high *Salmonella* spp. seroprevalence has been

reported in wild ungulates sharing the same habitats as cattle (Navarro-Gonzalez et al., 2012). Wild boars play an important role in the spread of *Salmonella* spp. over a wide area, including urban and peri-urban areas, due to their interaction with both farm animals and human waste litter (Gil-Molino et al., 2022). In the period of the global pandemic of the virus SARS-CoV-2 (Covid-19) that occurred in 2020–2021, wild boars were observed to be entering residential areas, despite the implementation of quarantine measures on the human population. Although wild boars live in forested areas in our country, they can contaminate these environments with their feces by raiding agricultural areas (corn, wheat, and orchards) in the summer and autumn seasons (Jemeršić et al., 2021).

The adaptation of *S. enterica*, particularly *S. Typhimurium*, to pigs has been well documented through phylogenetic analyses conducted in pig production systems in Thailand, Laos, and Brazil (Prathan et al., 2019; Seribelli et al., 2021). Similar phylogenetic investigations are essential for assessing the host adaptation potential of other serovars, including *Salmonella enterica* subsp. *enterica* serovar Hofit, which has been only rarely reported in the literature. Notably, *S. Hofit* was isolated from the feces and pus of a patient with perforating appendicitis, with possible exposure sources including turtles and sewage water (Scheidegger and Frei, 1990).

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Today, antimicrobial resistance (AMR) in microorganisms is increasingly causing serious public health concerns, and controlling this situation is of great importance in terms of the effectiveness of antibiotics (Gil-Molino et al., 2022). It is evident that wildlife has the capacity to function as a reservoir and distributor for AMR at the human–wildlife interface (Dhama et al., 2013). However, the current literature on AMR bacteria circulating in wildlife is limited. In contrast, wild boars have been observed to play a more significant role as reservoirs, carriers, and distributors of AMR bacteria (Torres et al., 2020). The presence of AMR in zoonotic bacteria, such as *Salmonella* spp., poses a significant threat to the effective treatment of diseases in both animals and humans (Newell et al., 2010). A literature search was conducted to ascertain the prevalence of *Salmonella* spp. in wild boar in our country. However, no relevant studies were identified. Wild boars can act as carriers of various bacteria, viruses, and parasites that can be transmitted to humans and domestic animals through direct contact with the boars, consumption of contaminated food, or indirectly via a contaminated environment. The objective of this study was to identify potential bacterial pathogens, such as *Salmonella* spp., from wild boars in the Southern Marmara Region of Türkiye and to evaluate the *in vitro* antibiotic susceptibility of these isolates.

Materials and Methods

Samples

In this study, samples were collected from a total of 34 wild boars (*S. scrofa*) that were legally hunted during the August 2024–February 2025 hunting season in the Southern Marmara Region of Türkiye. Fecal samples were obtained from all animals (n : 34), while tissue samples—including lymph nodes, liver, lungs, kidneys, and spleen—were collected from six animals (n : 6) that underwent necropsy. The necropsies were performed by experts from the Department of Pathology, Faculty of Veterinary Medicine, Balıkesir University. No macroscopic lesions were observed during the examinations. Approximately 6–8 g of fecal samples were collected from the rectum of wild boars using sterile swabs and placed in sterile Falcon tubes, while approximately 8–10 g of tissue samples were collected in sterile Stomacher bags. The samples were transported under cold chain conditions and analyzed shortly after collection.

Isolation of *Salmonella* spp.

One gram of fecal samples was collected and transferred into test tubes containing 9 mL of 1% buffered peptone water (BPW, Oxoid CM1049). The samples were then homogenized using a vortex. In addition, 1 g of tissue samples was collected, crushed with a sterile scalpel in a sterile petri dish, and then added to the tubes containing 1% BPW. The samples were homogenized using a vortex. Then, both groups of samples were incubated at 37°C for 24 h. 0.1 mL of the pre-enrichment medium from each sample was inoculated into tubes containing 10 mL of Rappaport Vassiliadis broth (1.07700, Merck, Darmstadt, Germany) and incubated at 41.5°C for 24 h. Then, a core of the selective enrichment medium was taken from each sample and plated on Xylose

LysineDeoxycholate agar (Oxoid, CM0469, Basingstoke, UK). The plates were incubated at 37°C for 24 h (ISO 6579, 2002). Following the end of the incubation period, three to five suspect colonies were selected from the petri dishes that had shown growth with a black center and a pink halo. These were then purified on brain heart infusion agar (LB.BL.4012352, Biolife, Italiana). The purified isolates were then examined for their macroscopic and microscopic morphology. An isolated colony was harvested in 10 μ L of sterile water, and 1 μ L of this mixture was deposited on a target plate in two replicates and allowed to dry at room temperature. One microliter of absolute ethanol was then added to each well and dried. One microliter of matrix solution (α' -cyano-4-hydroxycinnamic acid) (bioMérieux, France) was then added and allowed to co-crystallize with the sample. Samples were processed using a MALDI-TOF-MS spectrometer (VITEK[®] MS, bioMérieux, France) and analyzed with MYLA[®] software v3.2 (bioMérieux, France). Identification was based on spectral fingerprints, with the presence or absence of specific peaks serving as unique identifiers for each isolate. The resulting profiles were compared against a comprehensive reference database integrated into the system library. Isolates with an identification confidence level above 90% were considered to be *Salmonella* spp. The reliability and accuracy of this method for identifying *Salmonella* at the species level have been demonstrated in previous validation studies (Kuhns et al., 2012; Kang et al., 2017).

Serotyping

Serotyping was performed by seroagglutination using commercial specific antisera (SSI Diagnostica, Denmark) according to the Kauffmann–White–Le Minor Scheme (Grimont and Weill, 2007). Briefly, *Salmonella* isolates were streaked onto nutrient agar (CM0003, Oxoid, Basingstoke, UK) and grown overnight at 37°C. A single colony was mixed with a drop (20 μ L) of antiserum for each different serum. Agglutination observed within the first 10 s after mixing was considered a positive result.

Antimicrobial susceptibility testing

Kirby-Bauer disc diffusion method (Bauer et al., 1966) was employed for the detection of antimicrobial susceptibility of *S. Hofit* isolates according to the standards of the Clinical Laboratory Standards Institute (CLSI, 2018; CLSI, 2020). Briefly, *S. Hofit* isolates were incubated in Mueller Hinton broth (211443, BD, Sparks, MD, USA) for 18–24 h at 37°C. The turbidity of the bacterial cultures grown in suitable liquid media was visually adjusted to the 0.5 McFarland standard (1.5×10^8 cfu/mL) with sterile saline solution (pH 7.2). The test was performed on Mueller Hinton agar (1.103872, Merck), and the diameters of the inhibition zones were measured in millimeters. Ciprofloxacin (10 μ g, Oxoid), streptomycin (10 μ g, Oxoid), ampicillin (25 μ g, Oxoid), tetracycline (30 μ g, Oxoid), chloramphenicol (30 μ g, Oxoid), nalidixic acid (30 μ g, Oxoid), enrofloxacin (5 μ g, Oxoid), gentamicin (10 μ g, Oxoid), ceftiofur (30 μ g, Oxoid), cefoxitin (30 μ g, Oxoid), amoxicillin/clavulanic acid (2/1, 30 μ g, Oxoid) and trimethoprim/sulfamethoxale (25 μ g, Oxoid) discs were used in antimicrobial susceptibility test. The selection of these antibiotics tested in the study was influenced by their

widespread use in both human and veterinary medicine (Hinson et al., 2025; Lertwatcharasarakul et al., 2025).

Statistical analysis

According to the *in vitro* antimicrobial susceptibility test results, Fisher's exact test was performed using SPSS software (Version 30) to determine the statistical significance between the numbers of antibiotic-resistant and -susceptible *S. Hofit* isolates.

Results

Isolation and serotyping

A total of 34 wild boar samples (comprising feces, lymph nodes, liver, lung, kidney, and spleen) were examined, and *S. Hofit* was isolated from 6 (17.6%) animals. Five (83.3%) serovars were isolated from fecal samples, and 1 (16.7%) from internal organs.

Antimicrobial susceptibility testing

All *S. Hofit* isolates were found to be 100% sensitive to 11 of the tested antibiotics, while three isolates showed resistance only to streptomycin. The results of the antimicrobial susceptibility test are presented in Table 1 and Figure 1.

Statistical analysis

According to the evaluation using Fisher's exact test, no statistically significant difference was observed in the number of *S. Hofit* isolates with respect to *in vitro* susceptibility or resistance to the tested antibiotics ($p > 0.05$).

Discussion

The natural habitats of wild boars are predominantly forests and shrublands; however, they also inhabit agricultural lands and pastures where small cattle and livestock are

grazed. It is important to note that wild boars in the wild act as a reservoir for both livestock and humans due to the pathogenic microorganisms they carry. The genus *Salmonella*, belonging to the family *Enterobacteriaceae*, is a facultative anaerobic, Gram-negative, motile, and entero-invasive bacillus. Two closely related major species primarily exist for *Salmonella*: *S. bongori* and *S. enterica*. Of these two, *S. enterica*, which has over 2,700 serovars, is accountable for over 99% of all human infections. Different serovars of *Salmonella*, a pathogenic bacterium, can cause infections by settling in the digestive system and intestinal lymphoid tissues of boars (Ellermeier and Schlauch, 2006; Stevens and Gray, 2013; Sahu et al., 2025). The dissemination of *Salmonella* spp. to the environment is predominantly facilitated by the feces of animals. Both contaminated foods of animal origin and green vegetables irrigated with contaminated water have been identified as contributing factors in the transmission of the agent to humans (WHO, 2023). The most predominant species responsible for salmonellosis cases in humans is *S. enterica* (Gaffuri and Holmes, 2012).

In previous studies investigating the prevalence of *Salmonella* spp. in wild boars, detection rates ranged from 9.5% to 38%, depending on the geographic region and sampling conditions (Fredriksson-Ahomaa et al., 2020; Carraro et al., 2022). Although the presence of *Salmonella* spp. in wild boars is well documented, specific data on individual serovars remain limited. In the present study, *S. Hofit* was isolated from 17.6% of fecal and tissue samples collected from wild boars in the Southern Marmara Region of Türkiye, with 83.3% of the isolates obtained from feces and 16.7% from tissue. This is the first global report of the isolation of *S. Hofit* from wild boars, representing a significant contribution to the current knowledge of wildlife reservoirs of zoonotic pathogens. *S. Hofit* is a rarely reported serovar, previously identified only sporadically in birds (Mansour et al., 2020) and from an unspecified source in a feed processing plant (Boqvist et al., 2003). Its detection in wild boars raises

TABLE 1. ANTIMICROBIAL SUSCEPTIBILITY OF *S. HOFIT* ISOLATES

Antibiotics	Reference values (mm)			Serovars					
	S	I	R	Isolate 1	Isolate 2	Isolate 3	Isolate 4	Isolate 5	Isolate 6
				Inhibition zone diameter (mm)					
CIP	≥31	21–30	≤20	32	31	35	35	34	36
S	≥15	12–14	≤11	13	11*	11	14	13	11
AMP	≥17	14–16	≤13	21	20	22	22	21	22
TE	≥15	12–14	≤11	23	21	25	25	23	27
CHL	≥18	13–17	≤12	26	27	30	27	26	28
NAL	≥19	14–18	≤13	25	22	24	23	24	25
ENR	≥21	18–20	≤16	27	28	26	31	29	29
GEN	≥15	12–14	≤11	25	25	26	25	24	25
EFT	≥21	18–20	≤17	25	22	24	23	24	25
FOX	≥18	15–17	≤14	24	26	27	26	26	27
AMC	≥18	14–17	≤13	26	26	26	25	26	26
SXT	≥16	11–15	≤10	29	23	26	26	28	28

AMC, Amoxicillin/clavulanic acid (2/1, 30 µg, Oxoid); AMP, Ampicillin (25 µg, Oxoid); CHL, Chloramphenicol (30 µg, Oxoid); CIP, Ciprofloxacin (10 µg, Oxoid); EFT, Ceftiofur (30 µg, Oxoid); ENR, Enrofloxacin (5 µg, Oxoid); FOX, Cefoxitin (30 µg, Oxoid); GEN, Gentamicin (10 µg, Oxoid); I, Intermediate; NAL, Nalidixic acid (30 µg, Oxoid); R, Resistant; S, Sensitive; S, Streptomycin (10 µg, Oxoid); SXT, Trimethoprim/sulfamethoxale (25 µg, Oxoid); TE, Tetracycline (30 µg, Oxoid).

*Values in bold indicate resistance to the corresponding antibiotic.

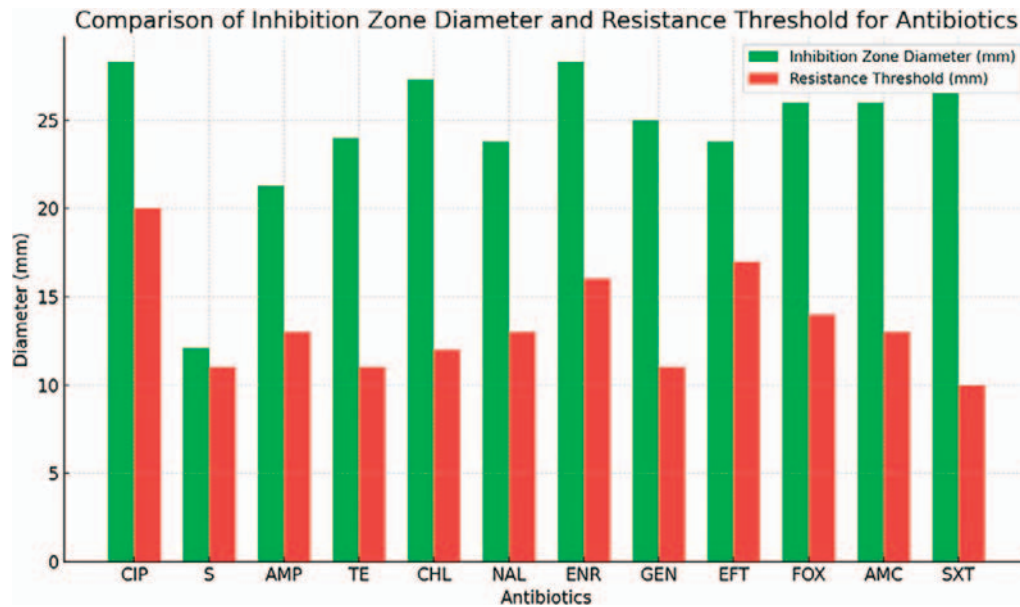


FIG. 1. A bar chart illustrating the mean inhibition zone diameters (green bars) and the corresponding resistance thresholds (red bars) of *S. Hofit* isolates for each tested antibiotic. The visualization was created using the Python programming language with the matplotlib library (version 3.0 or higher). Antibiotics with inhibition zones above the threshold are considered effective, while those at or below the threshold indicate potential resistance and reduced efficacy. CIP, Ciprofloxacin (10 μg , Oxoid); S, Streptomycin (10 μg , Oxoid); AMP, Ampicillin (25 μg , Oxoid); TE, Tetracycline (30 μg , Oxoid); CHL, Chloramphenicol (30 μg , Oxoid); NAL, Nalidixic acid (30 μg , Oxoid); ENR, Enrofloxacin (5 μg , Oxoid); GEN, Gentamicin (10 μg , Oxoid); EFT, Ceftiofur (30 μg , Oxoid); FOX, Cefoxitin (30 μg , Oxoid); AMC, Amoxicillin/clavulanic acid (2/1, 30 μg , Oxoid); SXT, Trimethoprim/sulfamethoxazole (25 μg , Oxoid).

concern due to the zoonotic potential of many *Salmonella* serovars and the increasing interface between wildlife, livestock, and humans (Hilbert et al., 2012). The identification of this uncommon serovar in free-ranging wild boars highlights the need for further epidemiological surveillance and molecular studies to better understand its transmission dynamics. This is especially important considering that *S. enterica* subsp. *enterica*—the subspecies to which *S. Hofit* belongs, comprises numerous serovars known to cause foodborne illness (Mansour et al., 2020; Teklemariam et al., 2023). As wild boars are increasingly recognized as reservoirs of foodborne pathogens, and given that *Salmonella* spp. account for nearly 18% of all foodborne outbreaks in the European Union (ECDC, 2019), our findings underscore the potential public health risk associated with this serovar. Additionally, the growing threat of antimicrobial-resistant *Salmonella* strains, driven in part by subtherapeutic and improper antibiotic use, particularly in veterinary medicine, requires urgent attention (Gullberg et al., 2011). This study provides novel data that are crucial for risk assessment and highlight the importance of targeted surveillance in both wildlife and domestic animal populations.

Although AMR is increasingly recognized as a global public health concern, data on AMR in wildlife, particularly in wild boars, remain limited. Recent studies have suggested that wild boars may serve as reservoirs and environmental disseminators of resistant bacteria (Torres et al., 2020).

In the present study, all *S. Hofit* isolates showed complete susceptibility (100%) to 11 of the 12 antibiotics tested. Resistance was observed only to streptomycin, detected in three out of six isolates. The inhibition zone diameters for all antibiotics—except streptomycin—exceeded their respective

resistance thresholds, as illustrated in Figure 1, indicating a generally low level of resistance among the isolates. Furthermore, descriptive analysis showed that the majority of the antibiotics tested—trimethoprim-sulfamethoxazole, gentamicin, chloramphenicol, tetracycline, and amoxicillin/clavulanic acid—had mean inhibition zones well above the established clinical breakpoints, reflecting strong antimicrobial efficacy. Streptomycin was the only antibiotic for which resistance was detected, with several isolates exhibiting inhibition zones at or below the resistance threshold (≤ 11 mm) (Table 1, Fig. 1). These findings contrast with reports from livestock and poultry, where multidrug-resistant strains are commonly observed (Rau et al., 2021; Chea et al., 2025; Di Taranto et al., 2025). The high susceptibility observed in wild boar isolates may be due to their limited or nonexistent exposure to antibiotics and the small sample size analyzed. Nevertheless, the detection of even low-level resistance to streptomycin highlights the importance of continued AMR surveillance across various environmental and wildlife settings.

Although human infections with *S. Hofit* are extremely rare, isolated cases—such as perforating appendicitis (Scheidegger and Frei, 1990)—suggest that it can cause severe disease, particularly in immunocompromised individuals. While its zoonotic potential remains poorly understood, the detection of *S. Hofit* in wild boars raises concerns. As noted by Galán-Relaño et al. (2023) and Pal et al. (2024), transmission of non-typhoidal *Salmonella* serovars to humans can occur through environmental contamination and direct or indirect contact with wildlife, especially via hunting activities or shared habitats.

To mitigate this potential risk, we recommend targeted surveillance of wild boar populations, particularly in areas close to farms and human settlements. This should include environmental sampling (e.g., water sources, feeding sites), testing of hunted carcasses, and molecular typing to track possible transmission routes. Ecologically, wild boars often inhabit fragmented landscapes where forested areas intersect with agricultural land, increasing the likelihood of contact with domestic pigs through shared water sources, damaged fences, or contaminated feed (Bonardi et al., 2019; Makovska et al., 2023). These interface zones represent critical control points and should be prioritized for surveillance and enhanced biosecurity measures.

S. enterica includes more than 2,700 serovars with varying host ranges and pathogenicity (Sahu et al., 2025). While research has traditionally focused on well-characterized serovars such as *S. Typhimurium* (Zhao et al., 2025), emerging strains like *S. Hofit* are expected to gain increasing attention. Based on its detection in wild boars, and considering the established link between swine and human health in *Salmonella* transmission (Soliani et al., 2023), phylogenetic analyses—particularly those conducted on *S. Hofit* isolates from pigs—may reveal genetic similarities with porcine-adapted serovars such as *S. Typhimurium* and *S. Derby*. These findings underscore the importance of investigating lesser-known serovars in animal reservoirs and their implications for food safety.

S. Hofit has been taxonomically classified and listed in the NCBI Taxonomy Browser; however, it remains poorly characterized in the scientific literature, with no published reports describing its epidemiology or pathogenic potential (NCBI, 2025). To the best of our knowledge, this study represents the first documented isolation of *S. Hofit* from wild boars globally. Notably, the relatively high isolation rate (17.6%) observed in this population suggests a potential adaptation of this serovar to swine hosts. These findings underscore the need for further epidemiological and genomic studies to elucidate its ecological niche, transmission dynamics, and potential implications for public and animal health.

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Authors' Contributions

Z.I. took a leading role in revising the article based on the reviewers' comments and preparing detailed responses to their feedback and also contributed significantly to statistical analyses, methodology development, data collection, conceptualization, and resource acquisition. H.H. contributed to writing—review and editing. M.G. contributed to conceptualization, methodology development, data collection, writing—original draft, and writing—review and editing.

Ethics Statement

This work was approved by the Republic of Türkiye, Ministry of Agriculture and Forestry, General Director of Nature Conservation and National Parks (228685).

Data Availability Statement

The data presented are contained within the article.

Author Disclosure Statement

The authors declare no conflicts of interest.

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References

- Bauer AW, Kirby WMM, Sherris JC, et al. Antibiotic susceptibility testing by a standardized single disk method. *Am J Clin Pathol* 1966;45(4_ts):493–496; doi: 10.1093/ajcp/45.4_ts.493
- Bonardi S, Bolzoni L, Zanoni RG, et al. Limited exchange of *Salmonella* among domestic pigs and wild boars in Italy. *Ecohealth* 2019;16(3):420–428; doi: 10.1007/s10393-019-01418-2
- Boqvist S, Hansson I, Nord Bjerselius U, et al. *Salmonella* isolated from animals and feed production in Sweden between 1993 and 1997. *Acta Vet Scand* 2003;44(3–4):181–197; doi: 10.1186/1751-0147-44-181
- Carraro PE, Barbosa FDO, Benevides VP, et al. Prevalence and antimicrobial resistance of *Salmonella* spp. isolated from free-ranging wild boars in the State of São Paulo, Brazil. *Cienc Rural* 2022;52(8); doi: 10.1590/0103-8478cr20210263
- Chea B, Kong S, Thim S, et al. Prevalence and antimicrobial resistance of *Salmonella* spp. isolated from swine and poultry farms in Cambodia. *Vet World* 2025;18(4):918–926; doi: 10.14202/vetworld.2025.918-926
- Chiari M, Zanoni M, Tagliabue S, et al. *Salmonella* serotypes in wild boars (*Sus scrofa*) hunted in northern Italy. *Acta Vet Scand* 2013;55(1):42; doi: 10.1186/1751-0147-55-42
- CLSI. Performance Standards for Antimicrobial Disk Susceptibility Tests, 13th ed. Clinical and Laboratory Standards Institute supplemented M02. CLSI: Wayne, PA; 2018, p. 4.
- CLSI. Performance Standards for Antimicrobial Susceptibility Testing, 30th ed. Clinical and Laboratory Standards Institute supplement M100, CLSI: Wayne, PA; 2020.
- Dhama K, Chakraborty S, Kapoor S, et al. One world, one health—veterinary perspectives. *Adv Anim Vet Sci* 2013;1(1):5–13.
- Di Taranto P, Petrucci P, Normanno F, et al. Prevalence and antimicrobial resistance of *Salmonella* strains isolated from chicken samples in Southern Italy. *Microorganisms* 2025; 13(2):270; doi: 10.3390/microorganisms13020270
- ECDC. *Salmonella* the Most Common Cause of Foodborne Outbreaks in the European Union. European Centre for Disease Prevention and Control. 2019. Available from: <https://www.ecdc.europa.eu/en/news-events/salmonella-most-commoncause-foodborne-outbreaks-european-union> [Last accessed: April 4, 2023].
- Ellermeier C, Slauch J. (eds). *The Genus Salmonella*. The Prokaryotes: Gamma Subclass. Springer. New York, 2006, pp. 124–158.
- Fredriksson-Ahomaa M, London L, Skrzypczak T, et al. Foodborne zoonoses common in hunted wild boars. *Ecohealth* 2020;17(4):512–522; doi: 10.1007/s10393-020-01509-5
- Gaffuri A, Holmes JP. *Salmonella* Infections. In: *Infectious Diseases of Wild Mammals and Birds in Europe*. John Wiley & Sons, Ltd.: Hoboken, USA, 2012, pp. 386–397.
- Galán-Relaño Á, Valero Díaz A, Huerta Lorenzo B, et al. *Salmonella* and salmonellosis: An update on public health

- implications and control strategies. *Animals* 2023;13(23):3666; doi: 10.3390/ani13233666
- Gil-Molino M, Gonçalves P, Risco D, et al. Dissemination of antimicrobial-resistant isolates of *Salmonella* spp. in wild boars and its relationship with management practices. *Trans-bound Emerg Dis* 2022;69(5):e1488–e1502; doi: 10.1111/tbed.14480
- Grimont PAD, Weill FX. (eds). *Antigenic Formulae of the Salmonella Serovars*. WHO Collaborating Centre for Reference and Research on *Salmonella*. 9th ed. WHO: Paris; 2007, pp.17–154.
- Gullberg E, Cao S, Berg OG, et al. Selection of resistant bacteria at very low antibiotic concentrations. *PLoS Pathog* 2011; 7(7):e1002158; doi: 10.1371/journal.ppat.1002158
- Hilbert F, Smulders FJM, Chopra-Dewasthaly R, et al. *Salmonella* in the wildlife-human interface. *Food Res Int* 2012; 45(2):603–608; doi: 10.1016/j.foodres.2011.08.015
- Hinson C, Tonouhewa A, Azokpota P, et al. Global prevalence and antibiotic resistance profiles of bacterial pathogens in table eggs: A systematic review and meta-analysis. *Vet World* 2025; 18(4):939–954; doi: 10.14202/vetworld.2025.939-954
- Jemeršić L, Lojkić I, Krešić N, et al. Investigating the presence of SARS CoV-2 in free-living and captive animals. *Pathogens* 2021;10(6):635; doi: 10.3390/pathogens10060635
- Jori F, Massei G, Licoppe A, et al. 8. Management of wild boar populations in the European Union before and during the ASF crisis. In: *Understanding and combatting African Swine Fever*. Wageningen Academic. Leiden, The Netherlands, 2021; doi:10.3920/978-90-8686-910-7_8
- Kang L, Li N, Li P, et al. MALDI-TOF mass spectrometry provides high accuracy in identification of *Salmonella* at species level but is limited to type or subtype *Salmonella* serovars. *Eur J Mass Spectrom (Chichester)* 2017;23(2):70–82; doi: 10.1177/1469066717699216
- Kuhns M, Zautner AE, Rabsch W, et al. Rapid discrimination of *Salmonella enterica* serovar Typhi from other serovars by MALDI-TOF mass spectrometry. *PLoS One* 2012;7(6):e40004; doi: 10.1371/journal.pone.0040004
- Lertwatcharasarakul P, Phatthanakunanan S, Tulayakul P. Retrospective analysis of antimicrobial resistance of *Salmonella* spp. isolated from livestock and its environment in Thailand. *Front Vet Sci* 2025;12:1584940; doi: 10.3389/fvets.2025.1584940
- Makovska I, Dhaka P, Chantziaras I, et al. The role of wildlife and pests in the transmission of pathogenic agents to domestic pigs: A systematic review. *Animals* 2023;13(11):1830; doi: 10.3390/ani13111830
- Mansour MN, Yaghi J, El Khoury A, et al. Prediction of *Salmonella* serovars isolated from clinical and food matrices in Lebanon and genomic-based investigation focusing on Enteritidis serovar. *Int J Food Microbiol* 2020;333(16):108831; doi: 10.1016/j.ijfoodmicro.2020.108831
- Navarro-Gonzalez N, Mentaberre G, Porrero CM, et al. Effect of cattle on *Salmonella* carriage, diversity and antimicrobial resistance in free-ranging wild boar (*Sus scrofa*) in Northeastern Spain. *PLoS One* 2012;7(12):e51614; doi: 10.1371/journal.pone.0051614
- NCBI. National Center for Biotechnology Information (n.d.). *Salmonella enterica* subsp. *enterica* serovar Hofit (Taxonomy ID: 2564537). NCBI Taxonomy Browser. 2025. Available from: <https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=2564537> [Last accessed: June 28, 2025].
- Newell DG, Koopmans M, Verhoef L, et al. Food-borne diseases - the challenges of 20 years ago still persist while new ones continue to emerge. *Int J Food Microbiol* 2010;139 (Suppl 1):S3–S15; doi: 10.1016/j.ijfoodmicro.2010.01.021
- Pal M, Gutama KP, de Avila Botton S, et al. Zoonotic salmonellosis: A comprehensive review. *IJVPH* 2024;10(1):31–38; doi: 10.62418/ijvph.10.1.2024.31-38
- Prathan R, Bitrus AA, Sinwat N, et al. Phylogenetic characterization of *Salmonella enterica* from pig production and humans in Thailand and Laos border provinces. *Vet World* 2019;12(1):79–84; doi: 10.14202/vetworld.2019.79-84
- Rau RB, Ribeiro AR, dos Santos A, et al. Antimicrobial resistance of *Salmonella* from poultry meat in Brazil: Results of a nationwide survey. *Epidemiol Infect* 2021;149(149); doi: 10.1017/S0950268821002156
- Sahu AA, Sephalika S, Mohakud NK, et al. Prevalence and multi-drug resistance in non-typhoidal *Salmonella* in India: A 20-year outlook. *AMH* 2025;70(1):6; doi: 10.3390/amh70010006
- Scheidegger C, Frei R. Perforating appendicitis due to *Salmonella* Hofit. *Lancet* 1990;335(8680):59–60; doi: 10.1016/0140-6736(90)90196-C
- Seribelli AA, da Silva P, Frazão MR, et al. Phylogenetic relationship and genomic characterization of *Salmonella* Typhimurium strains isolated from swine in Brazil. *Infect Genet Evol* 2021;93:104977; doi: 10.1016/j.meegid.2021.104977();
- Soliani L, Rugna G, Prosperi A, et al. *Salmonella* infection in pigs: Disease, prevalence, and a link between swine and human health. *Pathogens* 2023;12(10):1267; doi: 10.3390/pathogens12101267
- Stevens MP, Gray JT. *Salmonella* infections in pigs. In: *Salmonella in Domestic Animals*. 2nd ed. (Barrow PA, Methner U. eds.) CABI International: Wallingford: 2013, pp. 263–294.
- Tack J. Wild Boar (*Sus scrofa*) Populations in Europe: A Scientific Review of Population Trends and Implications for Management. European Landowners' Organization: Brussels; 2018, pp. 1–56.
- Teklemariam AD, Al-Hindi RR, Albiheyri RS, et al. Human salmonellosis: A continuous global threat in the farm-to-fork food safety continuum. *Foods* 2023;12(9):1756; doi: 10.3390/foods12091756
- Torres RT, Fernandes J, Carvalho J, et al. Wild boar as a reservoir of antimicrobial resistance. *Sci Total Environ* 2020; 717(717):135001; doi: 10.1016/j.scitotenv.2019.135001
- WHO. World Health Organization. *Salmonella* (non-Typhoidal); 2023. Available from: [https://www.who.int/news-room/fact-sheets/detail/salmonella-\(non-typhoidal\)](https://www.who.int/news-room/fact-sheets/detail/salmonella-(non-typhoidal)) [Last accessed: May 15, 2023].
- Zhao H, Zhang X, Zhang N, et al. The interplay between *Salmonella* and host: Mechanisms and strategies for bacterial survival. *Cell Insight* 2025;4(2):100237; doi: 10.1016/j.cellin.2025.100237.

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