



SALMONELLA CONTAMINATION AND ANTIMICROBIAL RESISTANCE IN FARMED *BANDICOTA INDICA*

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Abstract

The consumption of farmed Greater bandicoot rats (*Bandicota indica*) is increasingly popular in Thailand, yet food safety data remain limited. This preliminary study assessed the prevalence of *Salmonella* spp. contamination and antimicrobial resistance patterns in farmed *B. indica* in Mahasarakham Province, northeastern Thailand. The study comprised three components: (1) determination of *Salmonella* spp. prevalence using two sampling methods (carcass wash water and meat wash (homogenate of muscle tissue in buffered peptone water)) from 60 rats across 6 farms; (2) comparison of detection rates between the two methods; and (3) antimicrobial susceptibility testing of isolates against seven antibiotics using the disk diffusion method following CLSI guidelines. *Salmonella* spp. contamination was detected in 100% of farms (6/6), with sample-level prevalence of 70% (42/60) for carcass wash and 58.3% (35/60) for meat wash methods. Antimicrobial resistance testing of 42 isolates revealed high resistance to tetracycline (52.38%), followed by ampicillin (19.05%), cefazolin (14.29%), streptomycin (7.14%), ciprofloxacin (4.76%), and nalidixic acid (2.38%), with no resistance to sulfamethoxazole/trimethoprim. The universal farm-level contamination and high antimicrobial resistance rates, particularly to tetracycline, indicate significant public health concerns. These baseline data highlight the need for improved hygiene practices in rat farming, processing, and consumption, as well as surveillance programs to monitor antimicrobial resistance patterns in this emerging food animal sector.

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Introduction

Greater bandicoot rats (*Bandicota indica*) have historically been captured as agricultural pests in Thailand but have increasingly become a source of protein, particularly in rural northeastern regions [1]. This shift from pest control to livestock production reflects both traditional consumption practices and emerging commercial opportunities. In Mahasarakham Province and surrounding areas, rat meat is consumed in fresh, grilled, and processed forms and is sold at local fresh markets and by roadside vendors; comparable patterns of hunting, preparation, and consumption have been documented elsewhere in the Lower Mekong region [2]. The primary species farmed for consumption, *B. indica*, is preferred for its relatively large body size and meat yield, and its growth performance and carcass characteristics under farmed conditions have been documented [3].

Despite the growing economic importance of rat farming, the food safety profile of farmed *B. indica* remains poorly characterized. Rodents, including *B. indica*, are recognized reservoirs for numerous zoonotic pathogens capable of transmission to humans through direct contact or consumption of contaminated meat [4,5]. Among these pathogens, *Salmonella* spp. represents a critical public health concern as one of the most common causes of foodborne illness worldwide [6]. The World Health Organization estimates that non-typhoidal *Salmonella* causes approximately

95 million cases of gastroenteritis annually, with the majority originating from contaminated food sources [7].

Salmonella spp. are Gram-negative, rod-shaped bacteria belonging to the family Enterobacteriaceae, comprising over 2,500 serovars distributed across multiple species and subspecies [8]. These facultative anaerobes can survive for extended periods in various environmental conditions and are transmitted primarily through the fecal-oral route [9]. In humans, salmonellosis typically manifests 6–72 hours post-exposure with symptoms including diarrhea, fever, abdominal cramps, nausea, and vomiting, with illness duration of 4–7 days in uncomplicated cases [10]. However, severe infections may result in bacteremia, particularly in immunocompromised individuals, young children, and the elderly [11].

The emergence and dissemination of antimicrobial-resistant (AMR) *Salmonella* strains represent an escalating global health crisis [12]. Antimicrobial resistance complicates treatment of invasive salmonellosis, prolongs illness duration, increases hospitalization rates, and elevates mortality risks [13,14]. The development of multidrug-resistant (MDR) *Salmonella*, defined as resistance to three or more antimicrobial classes, further limits therapeutic options [15]. In Southeast Asia, including Thailand, studies have documented increasing trends in AMR among *Salmonella* isolates from various animal sources, with resistance to tetracycline, ampicillin, and sulfonamides frequently reported [16,17].

Previous research on rodent meat safety in Thailand has identified *Salmonella* contamination in rats purchased from roadside markets in central Thailand, with isolated strains exhibiting resistance to multiple antibiotics [17]. Saengthongpinit et al. reported *Salmonella* prevalence in *Rattus tanezumi* and *B. indica* meat samples, with 19 different serovars identified and all strains resistant or partially resistant to at least two of the antimicrobial agents tested [17]. However, comprehensive data on *Salmonella* prevalence and AMR patterns specifically in farmed *B. indica* from northeastern Thailand remain absent from the scientific literature.

Furthermore, standardized microbiological sampling methods for rat carcasses have not been established. While carcass rinsing and surface swabbing techniques are well-documented for conventional livestock species, their applicability and relative sensitivity for detecting *Salmonella* contamination in small rodent carcasses require empirical validation. Understanding the performance characteristics of different sampling methods is essential for developing practical surveillance protocols suitable for implementation in rat processing facilities and markets.

The present study was designed as a preliminary investigation to address these knowledge gaps by establishing baseline data on *Salmonella* spp. prevalence and phenotypic antimicrobial resistance patterns in farmed *B. indica* in Mahasarakham Province. Additionally, this study compared two sampling methods — whole carcass wash versus meat wash — to inform future surveillance strategies. The findings provide essential evidence for risk assessment and inform the development of targeted interventions to enhance food safety in this emerging livestock sector.

Objects and methods

Study design and sampling strategy

This cross-sectional study was conducted from February to September 2024 in Mahasarakham Province, northeastern Thailand. Six commercial rat farms (Farm A, Farm B, Farm C, Farm D, Farm E, Farm F) were purposively selected based on accessibility and willingness of farmers to participate. All farms practiced intensive indoor housing systems with concrete pens and provided commercial feed supplemented with local agricultural by-products. No information on antimicrobial usage was systematically collected in this preliminary study, representing a limitation addressed in the Discussion section.

From each farm, 10 adult *B. indica* rats (5 males and 5 females) were randomly selected for sampling, yielding a total sample size of 60 animals. Carcasses were obtained from the farmers' routine commercial slaughter and processing operations. Researchers were not involved in any stage of animal husbandry, health management, or slaughter. Sample collection was performed post-mortem on carcasses prepared for commercial sale. Two sampling methods were employed on each carcass: (1) whole carcass wash method and (2) meat wash method, allowing paired comparison of bacterial recovery rates.

Ethical considerations

All samples were collected post-mortem from carcasses generated by the farms' routine commercial slaughter operations. The researchers took no part in the housing, handling, health management, transport, or slaughter of any animal, and no procedure was performed on live animals for the purposes of this study. Institutional animal ethics approval was therefore not required under the regulations applicable at the time the study was conducted. The owners of all participating farms gave informed consent for sample collection and for the use of the resulting data.

Sample collection procedures

Carcass Wash Method: Immediately after slaughter by farm staff and prior to evisceration, each rat carcass, following complete removal of the hair, was placed in a sterile plastic bag containing 200 mL of sterile buffered peptone water (BPW; Merck KGaA, Darmstadt, Germany). The carcass was manually massaged through the bag exterior for 2 minutes to dislodge surface bacteria. The rinsate was collected and designated as the carcass wash sample.

Meat Wash Method: Following evisceration and removal of skin, a 25 g portion of skeletal muscle tissue (primarily from hindlimb and back regions) was aseptically collected from each carcass. The meat sample was placed in a stomacher bag with 225 mL of sterile BPW (Merck KGaA, Darmstadt, Germany), representing a single 1:10 (25 g in 225 mL) dilution with no further serial dilutions, and homogenized in a paddle blender (Nissei AM-8 Ace Homogenizer, Japan) for 5 minutes at 3,000 rpm. The homogenate was designated as the meat wash sample. Both sample types from each animal were processed immediately for *Salmonella* isolation following the ISO 6579-1:2017 standard method.

Salmonella isolation and identification

Salmonella detection followed the ISO 6579-1:2017¹ standard method with modifications suitable for the sample types. The isolation procedure comprised four main stages.

Pre-enrichment: In accordance with ISO 6579-1:2017, the sample suspensions in buffered peptone water (BPW; Merck KGaA, Darmstadt, Germany) served directly as the non-selective pre-enrichment. These were the carcass wash rinsate and the meat wash homogenate (25 g in 225 mL BPW, a 1:10 suspension). Both were incubated at 37°C for 18 ± 2 h to resuscitate stressed cells, with no further dilution before incubation.

Selective Enrichment: Following pre-enrichment, 0.1 mL was transferred to 10 mL Rappaport-Vassiliadis Soya (RVS) broth (Merck KGaA, Darmstadt, Germany) and incubated at 42°C for 24 hours. Simultaneously, 1 mL was inoculated into 10 mL Muller-Kauffmann tetrathionate-novobiocin (MKTn) broth (Merck KGaA, Darmstadt, Germany) and incubated at 37°C for 24 hours.

¹ ISO 6579-1:2017: Microbiology of the food chain — Horizontal method for the detection, enumeration and serotyping of *Salmonella* -Part 1: Detection of *Salmonella* spp. Technical Committee: ISO/TC 34/SC 9, 2017.

Selective Plating: From each selective enrichment broth, loopfuls were streaked onto multiple selective and differential agar media: xylose lysine deoxycholate (XLD) agar, Hektoen enteric (HE) agar, bismuth sulfite (BSA) agar, brilliant green (BGA) agar, and MacConkey agar (all from HiMedia Laboratories Pvt. Ltd., Mumbai, India). Plates were incubated at 37 °C for 24–48 hours and examined for presumptive *Salmonella* colonies based on characteristic morphology and color on each medium.

Biochemical Confirmation: Presumptive colonies were subcultured onto Nutrient Agar (HiMedia Laboratories Pvt. Ltd., Mumbai, India) and subjected to biochemical testing using triple sugar iron (TSI) agar, motility-indole-lysine (MIL) medium, and urease tests (all from HiMedia Laboratories Pvt. Ltd., Mumbai, India). Kovac's reagent (HiMedia Laboratories Pvt. Ltd., Mumbai, India) was used for the indole test. Isolates demonstrating the typical *Salmonella* biochemical profile (TSI: alkaline slant/acid butt with H₂S production and gas; MIL: motility-positive, indole-negative, lysine decarboxylase-positive; urease-negative) were confirmed as *Salmonella* spp. [18]. This preliminary study employed phenotypic identification methods; molecular confirmation and serotyping were not performed due to resource constraints.

Antimicrobial susceptibility testing

All confirmed *Salmonella* isolates were subjected to antimicrobial susceptibility testing using the Kirby-Bauer disk diffusion method following Clinical and Laboratory Standards Institute (CLSI) guidelines [19]. Seven antimicrobial agents commonly used in human and veterinary medicine were tested: tetracycline (30 µg), ampicillin (10 µg), cefazolin (30 µg), streptomycin (10 µg), ciprofloxacin (5 µg), nalidixic acid (30 µg), and sulfamethoxazole/trimethoprim (1.25/23.75 µg) (all discs from HiMedia Laboratories Pvt. Ltd., Mumbai, India). Bacterial suspensions adjusted to 0.5 McFarland standard were inoculated onto Mueller-Hinton agar (MHA; HiMedia Laboratories Pvt. Ltd., Mumbai, India) plates using sterile swabs. Antimicrobial discs were applied to the inoculated surfaces and plates were incubated at 37 °C for 16–18 hours. Inhibition zone diameters were measured to the nearest millimeter using vernier calipers and interpreted as susceptible (S), intermediate (I), or resistant (R) according to CLSI breakpoints for *Salmonella* spp. [19]. *Escherichia coli* ATCC 25922 was used as the quality control strain in each testing batch. Resistance percentages reported in this study refer to the resistant category only; intermediate isolates are reported separately (Table 3). Differences between CLSI and EUCAST in the definition and reporting of the intermediate category have been reviewed elsewhere [20].

Quality control and assurance

All culture media were quality-tested with appropriate positive and negative control strains before use. *Salmonella enterica* subsp. *enterica* serovar Typhimurium ATCC 14028 served as the positive control for isolation procedures and antimicrobial susceptibility testing. Aseptic techniques were

maintained throughout all procedures, and laboratory personnel followed established aseptic protocols to minimize contamination and ensure reproducibility.

Statistical analysis

Prevalence estimates were calculated with 95 % confidence intervals using the Wilson score method. Comparison of *Salmonella* detection rates between sampling methods was performed using McNemar's test for paired proportions. Statistical significance was set at $p < 0.05$. All statistical analyses were performed using R software version 4.3.2 (R Foundation for Statistical Computing, Vienna, Austria) [21].

Results and discussion

Prevalence of *Salmonella* spp. contamination

The investigation revealed widespread *Salmonella* spp. contamination across all surveyed rat farms in Maharashtra Province. At the farm level, *Salmonella* was detected in 100 % (6/6) of participating farms, indicating universal contamination at the production source. At the individual animal level, the carcass wash method detected *Salmonella* in 70 % (42/60, 95 % CI: 57.5–80.1 %) of sampled rats, while the meat wash method yielded positive results in 58.3 % (35/60, 95 % CI: 45.7–69.9 %) of samples (Table 1).

Table 1. Prevalence of *Salmonella* spp. contamination by detection level and sampling method

Detection Level	Method	Positive/Total	Prevalence, %	95 % CI	p-value
Farm-level	Both methods	6/6	100	61.0–100	N/A
Sample-level	Carcass wash	42/60	70.0	57.5–80.1	0.12
	Meat wash	35/60	58.3	45.7–69.9	

The sample-level prevalence observed in this study (70% by carcass wash and 58.3% by meat wash) is notably higher than the 32% (67/208) reported by Saengthongpinit et al. for rectal swab and meat samples from two rodent species purchased at roadside markets in central Thailand [17]. This discrepancy likely reflects differences in study design: our farm-based investigation captured contamination at the source of production, whereas market-based sampling represents a mixture of animals from multiple sources with variable handling and processing conditions. The universal farm contamination suggests endemic *Salmonella* colonization within the surveyed rat farming operations, potentially related to environmental contamination, feed sources, or insufficient biosecurity measures.

Comparison with published data reveals variable *Salmonella* prevalence in rodent populations. Rodents sampled in traditional wet markets in Thailand showed a high prevalence of 49.1 % [22], while investigations of commensal rats in urban environments have documented prevalence rates

ranging from 0 % to 33 % depending on geographic location and rodent species [23,24]. The substantially higher prevalence observed in our farmed population (70 % by carcass wash) may reflect differences between wild and farmed populations, with confined farming conditions potentially facilitating fecal-oral transmission and environmental contamination.

Farm-specific prevalence varied considerably (Table 2), with positive sample proportions ranging from 30 % to 100 % by the carcass wash method and 40 % to 80 % by the meat wash method. This heterogeneity suggests that farm management practices, hygiene standards, and environmental factors influence contamination levels, although detailed farm characterization data were not collected in this preliminary study.

Table 2. Farm-specific *Salmonella* spp. prevalence by sampling method

Farm	Carcass wash	Meat wash
ID	Positive, %	Positive, %
Farm A	8/10 (80)	4/10 (40)
Farm B	10/10 (100)	7/10 (70)
Farm C	9/10 (90)	8/10 (80)
Farm D	5/10 (50)	4/10 (40)
Farm E	7/10 (70)	8/10 (80)
Farm F	3/10 (30)	4/10 (40)
Overall	42/60 (70)	35/60 (58.3)

Comparison of sampling methods

Statistical comparison of the two sampling techniques revealed that the carcass wash method yielded a numerically higher but statistically non-significant *Salmonella* detection rate than the meat wash method (70 % vs. 58.3 %; McNemar's test, $p = 0.12$).

The higher surface contamination detected by the carcass wash method is consistent with established principles of carcass microbiology; wherein surface contamination typically exceeds internal muscle contamination in properly eviscerated animals [25]. During slaughter and processing, bacterial transfer from hide, feet, and gastrointestinal contents to carcass surfaces is well-documented in conventional livestock [26]. In the case of rats, the small body size and thin skin may facilitate more extensive surface contamination during handling and processing. The carcass wash method samples the entire external surface area, capturing bacteria from skin, extremities, and body cavities, whereas the meat wash method samples only internal muscle tissue, which experiences lower contamination levels unless cross-contamination occurs during cutting and deboning.

The recovery of contamination by both sampling methods is consistent with cross-contamination during processing, whereby surface bacteria are transferred to meat, a phenomenon extensively documented in poultry and meat processing facilities [27,28].

From a practical surveillance perspective, these findings suggest that the carcass wash method may offer practical advantages for detecting *Salmonella* contamination in rat car-

casses and may be more suitable for monitoring programs at slaughter or processing facilities. However, the meat wash method more accurately represents consumer exposure through consumption of processed meat products. Ideally, comprehensive surveillance programs should incorporate both methods to capture contamination at different stages of the production-to-consumption continuum.

Antimicrobial resistance patterns

Antimicrobial susceptibility testing of 42 *Salmonella* isolates revealed widespread resistance to multiple antibiotic classes (Table 3). One presumptive colony was selected from each culture-positive animal for confirmation and susceptibility testing; the 42 isolates were distributed across the six farms as follows: Farm A, 8; Farm B, 8; Farm C, 10; Farm D, 4; Farm E, 8; Farm F, 4. Isolates were not retained from every culture-positive animal, so the number of isolates tested is smaller than the number of culture-positive animals shown in Table 2. No duplicate isolates were taken from the same animal. Because most animals were culture-positive by both sampling methods, a single representative isolate was retained per animal without preferential assignment to a sampling method. The sample type of origin was documented only for Farm F (three isolates from meat wash and one from carcass wash), so a complete carcass-versus-meat attribution for all 42 isolates could not be reconstructed from the records (see Study limitations). Tetracycline resistance was most prevalent, observed in 52.38 % (22/42) of isolates, followed by ampicillin resistance at 19.05 % (8/42), cefazolin resistance at 14.29 % (6/42), streptomycin resistance at 7.14 % (3/42), ciprofloxacin resistance at 4.76 % (2/42), and nalidixic acid resistance at 2.38 % (1/42). No isolates exhibited resistance to sulfamethoxazole/trimethoprim, with all 42 isolates classified as susceptible to this combination antibiotic.

Table 3. Antimicrobial resistance patterns of *Salmonella* spp. isolates from farmed *Bandicota indica* (n = 42)

Antimicrobial agent	Conc. (μg)	R, n (%)	I, n (%)	S, n (%)
Tetracycline	30	22 (52.38)	0 (0.00)	20 (47.62)
Ampicillin	10	8 (19.05)	3 (7.14)	31 (73.81)
Cefazolin	30	6 (14.29)	3 (7.14)	33 (78.57)
Streptomycin	10	3 (7.14)	2 (4.76)	37 (88.10)
Ciprofloxacin	5	2 (4.76)	3 (7.14)	37 (88.10)
Nalidixic acid	30	1 (2.38)	0 (0.00)	41 (97.62)
Sulfamethoxazole/Trimethoprim	1.25/23.75	0 (0.00)	0 (0.00)	42 (100.00)

Conc., concentration; R, resistant; I, intermediate; S, susceptible; n, number of isolates.

Multidrug resistance (MDR), defined as resistance to three or more antimicrobial classes, was observed in 2.38 % (1/42) of isolates. This isolate exhibited resistance to tetracycline (tetracyclines), ampicillin (β-lactam), and streptomycin (aminoglycosides), representing a pattern that limits therapeutic options for invasive infections.

The seven antimicrobial agents evaluated in this study were selected to represent the major drug classes relevant to both the clinical management of human salmonellosis and antimicrobial use in food-animal production, in line with the One Health approach. Tetracycline, ampicillin, streptomycin, and sulfamethoxazole/trimethoprim were included because they are among the most widely used agents in livestock and correspond to the classic resistance markers historically associated with multidrug-resistant *Salmonella* [10,15]. Ampicillin (a penicillin), cefazolin (a first-generation cephalosporin), ciprofloxacin (a fluoroquinolone), and the quinolone nalidixic acid were chosen because they represent antimicrobial categories of direct clinical importance, since β -lactams, fluoroquinolones, and extended-spectrum cephalosporins are the principal options for treating invasive non-typhoidal salmonellosis in humans. Nalidixic acid was tested alongside ciprofloxacin specifically to screen for reduced fluoroquinolone susceptibility, as nalidixic acid resistance can signal emerging quinolone resistance mechanisms even when ciprofloxacin appears susceptible *in vitro*. Cefazolin was additionally included as a phenotypic indicator of β -lactamase activity within the cephalosporin class. This panel also reflects the antimicrobials commonly monitored in Thai and regional *Salmonella* surveillance programs, facilitating comparison with existing resistance data from food animals and their products.

The high prevalence of tetracycline resistance (52.38 %) observed in this study aligns with regional and global trends. A meta-analysis of *Salmonella* antimicrobial resistance in Iran reported a high tetracycline resistance rate of 60 % [29]. In Thailand specifically, previous studies have documented tetracycline resistance rates ranging from 20 % to 80 % in *Salmonella* isolates from various animal sources [30,31]. The extensive use of tetracyclines in livestock production, including as growth promoters and for disease prevention, has been implicated in the selection and dissemination of tetracycline resistance genes [32].

Direct comparison with the survey of market-sourced rodent meat from central Thailand is limited, because that study tested oxytetracycline and doxycycline rather than tetracycline and reported agent-specific resistance frequencies only in supplementary material [17]. The high tetracycline resistance observed here is nevertheless consistent with the multiresistance described in that survey, in which every isolate was resistant or partially resistant to at least two of the agents tested [17]. This discrepancy may reflect differences between farmed and wild-caught populations, regional variation in antimicrobial usage patterns, or temporal trends of increasing resistance. Unfortunately, the absence of antimicrobial usage data in our study precludes definitive conclusions regarding the drivers of resistance in these populations.

Ampicillin resistance (19.05 %) was the second most prevalent resistance phenotype detected. Ampicillin, a β -lactam antibiotic, remains an important first-line treatment for salmonellosis in some settings, although fluoro-

quinolones and third-generation cephalosporins are increasingly preferred for severe infections [33]. Resistance to β -lactam antibiotics in *Salmonella* typically results from β -lactamase production encoded by plasmid-borne genes such as blaTEM and blaCTX-M [34]. The detection of ceftazolin resistance in 14.29 % of isolates is noteworthy; ceftazolin is a first-generation cephalosporin, and resistance to it commonly reflects β -lactamase production that may co-select for resistance to higher-generation cephalosporins, which represent critically important antimicrobials for treating invasive salmonellosis in humans [35].

Ciprofloxacin resistance remained low (4.76 %), and all isolates were susceptible to sulfamethoxazole/trimethoprim. These findings are encouraging, as fluoroquinolones and trimethoprim-sulfamethoxazole combinations serve as important therapeutic options for complicated salmonellosis [36]. However, vigilant monitoring is essential, as fluoroquinolone resistance in *Salmonella* has been increasing globally and antimicrobial-resistant infections carry a substantial global mortality burden [13].

The antimicrobial resistance patterns observed in this study likely reflect the selective pressures exerted by antimicrobial use in animal agriculture, although direct evidence is lacking from our data. In Thailand, antimicrobials are widely available and used in livestock production, often without veterinary oversight [38]. The National Antimicrobial Resistance Surveillance Center Thailand (NARST) has documented increasing resistance trends in foodborne pathogens, emphasizing the need for strengthened antimicrobial stewardship in the agricultural sector [39].

Public health implications and risk assessment

The findings of this preliminary investigation reveal critical food safety concerns with direct public health implications. The universal farm-level contamination (100 % of farms) combined with high individual-animal prevalence (70 % by carcass wash method) indicates that consumers of farmed rat meat face substantial exposure risks to *Salmonella* spp. This contamination level substantially exceeds those reported for conventional livestock species in Thailand, where *Salmonella* prevalence in chicken and pork typically ranges from 10–40 % at retail markets [30,40]. Notably, *Salmonella* Rissen and *Salmonella* Weltevreden have been recovered from both retail meat and human clinical cases in Thailand, with molecular typing indicating shared clones between food and patients [40].

The epidemiological significance of these findings must be contextualized within consumption patterns in north-eastern Thailand. Rat meat consumption is deeply embedded in local food culture, with community surveys in the Lower Mekong region reporting rodent consumption prevalences as high as 86 % among rural populations [2]. Traditional preparation methods often involve grilling or brief cooking, which may not achieve sufficient internal temperatures to eliminate *Salmonella* throughout the meat [41]. The combination of high prevalence, traditional consumption

practices, and limited cold chain infrastructure in rural markets creates conditions conducive to foodborne disease transmission.

The detection of antimicrobial-resistant *Salmonella*, including one isolate resistant to three antimicrobial classes, represents a particularly concerning dimension of risk. The high tetracycline resistance rate (52.38%) mirrors patterns observed in other livestock sectors in Thailand and across Southeast Asia, reflecting decades of agricultural antimicrobial use [29,31]. When consumers ingest resistant bacteria through undercooked meat, two public health consequences may follow: (1) direct infection with resistant strains, limiting treatment options if invasive disease develops; and (2) intestinal colonization with resistant bacteria or mobile genetic elements, contributing to the human resistome and enabling horizontal gene transfer to human-associated pathogens [42].

Of particular concern is the emergence of cefazolin resistance (14.29% of isolates). Although cefazolin itself is a first-generation cephalosporin, resistance to β -lactam agents in *Salmonella* may signal the potential for co-selection of resistance to third-generation cephalosporins, which represent critically important antimicrobials for treating severe human salmonellosis, especially in children and immunocompromised patients [35]. The presence of such resistance in a food animal population suggests selective pressure from antimicrobial use, although the specific drivers remain uncharacterized in this preliminary study.

Comparison with international data reveals that *Salmonella* prevalence in farmed rodents substantially exceeds that in wild rodent populations. Studies of wild animals in Brazil and of urban rats in the Democratic Republic of the Congo have reported comparatively low prevalence in free-living rodent populations [23,24], suggesting that farming conditions — including confinement, high stocking densities, and potential antimicrobial exposure — may amplify contamination risks relative to wild populations. This observation has implications for other countries where rodent farming is practiced or emerging, including China, Vietnam, and other Southeast Asian nations.

The economic implications warrant consideration as well. While rat farming provides supplemental income for rural households and serves local markets, the food safety risks identified in this study could undermine consumer confidence and market development if not adequately addressed. Moreover, foodborne illness outbreaks attributable to contaminated rat meat could generate significant public health costs through medical treatment, productivity losses, and surveillance responses.

Implications for sampling and surveillance strategies

The methodological comparison conducted in this study has practical implications for surveillance program design. The numerically higher detection rate of the carcass wash method (70% vs. 58.3%), although not statistically significant ($p = 0.12$), suggests that this technique may be pre-

ferable for monitoring programs at slaughter facilities or processing points. The co-occurrence of carcass and meat contamination indicates that surface contamination is associated with internal contamination, likely through cross-contamination during processing.

From a regulatory perspective, these findings suggest that interventions targeting surface hygiene during slaughter and processing may reduce downstream contamination in meat products. Critical control points likely include: (1) prevention of fecal contamination during evisceration, (2) minimization of cross-contamination from skin to muscle during skinning and butchering, and (3) implementation of effective carcass washing or decontamination procedures. The small body size of rats presents unique challenges compared to conventional livestock, as manual processing predominates and standardized mechanical processing systems do not exist.

Study limitations and future research priorities

As a preliminary investigation, this study has several inherent limitations. The use of phenotypic identification methods without molecular serotyping limits epidemiological comparison with human clinical isolates. Antimicrobial resistance was assessed phenotypically without genotypic characterization of resistance determinants. The absence of farm-level antimicrobial usage data precludes analysis of use-resistance relationships. The cross-sectional design captures prevalence at a single timepoint without addressing temporal dynamics. The purposive sampling of six farms limits generalizability to the broader industry. Isolate origin is a further limitation. Because most animals were culture-positive by both methods and one isolate was retained per animal, the sample type of origin (carcass wash versus meat wash) could not be fully attributed for the 42 tested isolates, except for Farm F. This prevented a matrix-specific comparison of resistance patterns. Susceptibility testing was also performed on fewer isolates (42) than the number of animals that were culture-positive by at least one sampling method (Table 2), because isolates were not retained from every culture-positive animal; the resistance estimates therefore relate to the subset of isolates tested. In addition, detection followed the qualitative (presence/absence) method of ISO 6579-1:2017; enumeration of *Salmonella* was not undertaken, and only detection frequency is reported. Quantitative estimation of contamination levels would require a dedicated enumeration approach, such as the most probable number (MPN) technique of ISO/TS 6579-2:2012², which is recommended for future work. Biochemical confirmation of presumptive isolates was limited to phenotypic tests owing to resource and time constraints.

Despite these constraints, this study establishes the first systematic baseline data on *Salmonella* contamination and antimicrobial resistance in farmed *B. indica* in northeastern Thailand. Future research priorities include:

² ISO/TS 6579-2:2012: Microbiology of food and animal feed - Horizontal method for the detection, enumeration and serotyping of *Salmonella* - Part 2: Enumeration by a miniaturized most probable number technique. Technical Committee: ISO/TC 34/SC 9, 2012.

(1) molecular characterization of isolates through serotyping and whole-genome sequencing to enable source attribution and resistance gene identification [37]; (2) longitudinal surveillance incorporating farm management practices and antimicrobial usage patterns; (3) assessment of contamination at retail markets and evaluation of consumer handling practices; (4) intervention trials testing hygiene improvements, processing modifications, and antimicrobial stewardship strategies; and (5) multi-provincial surveys to characterize regional variation and inform national surveillance frameworks.

Conclusion

This study demonstrates that *Salmonella* spp. contamination is widespread in commercially farmed *Bandicota*

indica in Mahasarakham Province, with 100 % farm-level and 70 % individual-level prevalence detected by carcass wash sampling. The carcass wash method detected contamination numerically more frequently than the meat wash method, although this difference did not reach statistical significance ($p = 0.12$); this may reflect greater recovery of surface contamination. Antimicrobial resistance was detected in the majority of isolates, with *B. indica* being a meaningful reservoir of antimicrobial-resistant *Salmonella* spp., which may represent a potential public health concern for consumers in northeastern Thailand. Improved farm hygiene, standardized slaughter practices, and responsible antimicrobial use are warranted to mitigate contamination risks in this emerging food sector.

REFERENCES

- Lin, S., Yao, D., Jiang, H., Qin, J., Feng, Z. (2024). Predicting current and future potential distributions of the greater bandicoot rat (*Bandicota indica*) under climate change conditions. *Pest Management Science*, 80(2), 734–743. <https://doi.org/10.1002/ps.7804>
- Suwannarong, K., Chapman, R. S., Lantican, C., Michaelides, T., Zimicki, S. (2015). Hunting, food preparation, and consumption of rodents in Lao PDR. *PLOS ONE*, 10(7), Article e0133150. <https://doi.org/10.1371/journal.pone.0133150>
- Thip-uten, S., Jitjak, T., Saensri, P., Kaewsena, T., Muangkhot, W., Thip-uten, T. et al. (2025). Effect of different diets on growth performance and carcass characteristics of Nu Phuk (*Bandicota indica*) raised under a circle cement pond. *International Journal of Agricultural Technology*, 21(4), 1535–1544. <https://doi.org/10.63369/ijat.2025.21.4.1535-1544>
- Sabour, S., Azimi, T., Nasser, A., Hadi, N., Mohsenzadeh, A., Shariati, A. (2022). A global overview of the most important zoonotic bacteria pathogens transmitted from *Rattus norvegicus* to humans in urban environments. *Infectious Medicine*, 1(3), 192–207. <https://doi.org/10.1016/j.imj.2022.07.002>
- Blasdel, K. R., Morand, S., Laurance, S. G. W., Doggett, S. L., Hahs, A., Trinh, K. et al. (2022). Rats and the city: Implications of urbanization on zoonotic disease risk in Southeast Asia. *Proceedings of the National Academy of Sciences*, 119(39), Article e2112341119. <https://doi.org/10.1073/pnas.2112341119>
- Lamichhane, B., Mawad, A. M. M., Saleh, M., Kelley, W. G., Harrington, P. J., Lovestad, C. W. et al. (2024). Salmonellosis: An overview of epidemiology, pathogenesis, and innovative approaches to mitigate the antimicrobial resistant infections. *Antibiotics*, 13(1), Article 76. <https://doi.org/10.3390/antibiotics13010076>
- Stanaway, J. D., Parisi, A., Sarkar, K., Blacker, B. F., Reiner, R. C., Hay, S. I. et al. (2019). The global burden of non-typhoidal salmonella invasive disease: A systematic analysis for the Global Burden of Disease Study 2017. *The Lancet Infectious Diseases*, 19(12), 1312–1324. [https://doi.org/10.1016/S1473-3099\(19\)30418-9](https://doi.org/10.1016/S1473-3099(19)30418-9)
- Kumar, G., Kumar, S., Jangid, H., Dutta, J., Shidiki, A. (2025). The rise of non-typhoidal *Salmonella*: An emerging global public health concern. *Frontiers in Microbiology*, 16, Article 1524287. <https://doi.org/10.3389/fmicb.2025.1524287>
- Chattaway, M. A., Langridge, G. C., Wain, J. (2021). *Salmonella* nomenclature in the genomic era: A time for change. *Scientific Reports*, 11(1), Article 7494. <https://doi.org/10.1038/s41598-021-86243-w>
- Jajere, S. M. (2019). A review of *Salmonella enterica* with particular focus on the pathogenicity and virulence factors, host specificity and antimicrobial resistance including multidrug resistance. *Veterinary World*, 12(4), 504–521. <https://doi.org/10.14202/vetworld.2019.504-521>
- Marchello, C. S., Birkhold, M., Crump, J. A., Martin, L. B., Ansah, M. O., Breggi, G. et al. (2022). Complications and mortality of non-typhoidal salmonella invasive disease: A global systematic review and meta-analysis. *The Lancet Infectious Diseases*, 22(5), 692–705. [https://doi.org/10.1016/S1473-3099\(21\)00615-0](https://doi.org/10.1016/S1473-3099(21)00615-0)
- Murray, C. J. L., Ikuta, K. S., Sharara, F., Swetschinski, L., Robles Aguilar, G., Gray, A. et al. (2022). Global burden of bacterial antimicrobial resistance in 2019: A systematic analysis. *The Lancet*, 399(10325), 629–655. [https://doi.org/10.1016/S0140-6736\(21\)02724-0](https://doi.org/10.1016/S0140-6736(21)02724-0)
- Naghavi, M., Vollset, S. E., Ikuta, K. S., Swetschinski, L. R., Gray, A. P., Wool, E. E. et al. (2024). Global burden of bacterial antimicrobial resistance 1990–2021: A systematic analysis with forecasts to 2050. *The Lancet*, 404(10459), 1199–1226. [https://doi.org/10.1016/S0140-6736\(24\)01867-1](https://doi.org/10.1016/S0140-6736(24)01867-1)
- Tack, B., Vanaenrode, J., Verbakel, J. Y., Toelen, J., Jacobs, J. (2020). Invasive non-typhoidal *Salmonella* infections in sub-Saharan Africa: A systematic review on antimicrobial resistance and treatment. *BMC Medicine*, 18(1), Article 212. <https://doi.org/10.1186/s12916-020-01652-4>
- Magiorakos, A.-P., Srinivasan, A., Carey, R. B., Carmeli, Y., Falagas, M. E., Giske, C. G. et al. (2012). Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: An international expert proposal for interim standard definitions for acquired resistance. *Clinical Microbiology and Infection*, 18(3), 268–281. <https://doi.org/10.1111/j.1469-0691.2011.03570.x>
- Tadee, P., Patchanee, P., Pascoe, B., Sheppard, S. K., Meunsene, D., Buawiratert, T. et al. (2021). Occurrence and sequence type of antimicrobial resistant *Salmonella* spp. circulating in antibiotic-free organic pig farms of northern Thailand. *Thai Journal of Veterinary Medicine*, 51(2), 311–319. <https://doi.org/10.56808/2985-1130.3123>
- Saengthongpinit, C., Sratongno, K., Phimpraphai, W., Tulayakul, P., Morand, S., de Garine-Wichatitsky, M. (2019). Antimicrobial resistance of *Salmonella* spp. isolates and heavy metal traces from rodent meat purchased from roadside markets, central Thailand. *Foodborne Pathogens and Disease*, 16(10), 687–695. <https://doi.org/10.1089/fpd.2018.2609>

18. Awang, M. S., Bustami, Y., Hamzah, H. H., Zambry, N. S., Khalid, M. F., Aziah, I. et al. (2021). Advancement in *Salmonella* detection methods: From conventional to electrochemical-based sensing detection. *Biosensors*, 11(9), Article 346. <https://doi.org/10.3390/bios11090346>
19. Clinical and Laboratory Standards Institute. (2023). Performance standards for antimicrobial susceptibility testing (33rd ed., CLSI supplement M100). Clinical and Laboratory Standards Institute, Wayne, PA, USA.
20. Kahlmeter, G., Giske, C. G., Kirn, T. J., Sharp, S. E. (2019). Point-counterpoint: Differences between the European Committee on Antimicrobial Susceptibility Testing and Clinical and Laboratory Standards Institute recommendations for reporting antimicrobial susceptibility results. *Journal of Clinical Microbiology*, 57(9), Article e01129-19. <https://doi.org/10.1128/JCM.01129-19>
21. R Core Team. (2023). R: A language and environment for statistical computing (version 4.3.2) [Computer software]. R Foundation for Statistical Computing, Vienna, Austria, 2023. Retrieved from <https://cran.r-project.org/src/base/R-4/R-4.3.2.tar.gz> Accessed December 18, 2025
22. Ribas, A., Saijuntha, W., Agatsuma, T., Prantlová, V., Poonlaphdech, S. (2016). Rodents as a source of *Salmonella* contamination in wet markets in Thailand. *Vector-Borne and Zoonotic Diseases*, 16(8), 537–540. <https://doi.org/10.1089/vbz.2015.1894>
23. Santos, E. J. E. d., Lopes, A. T. S., Fehlberg, H. F., Rocha, J. M., Brito Júnior, P. d. A., Bernardes, F. C. S. et al. (2024). Low occurrence of *Salmonella* spp. in wild animals in Bahia, Brazil — Population assessment and characterization in the Caatinga and Atlantic Forest Biomes. *Animals*, 14(1), Article 21. <https://doi.org/10.3390/ani14010021>
24. Falay, D., Hardy, L., Tanzito, J., Lunguya, O., Bonebe, E., Peeters, M. et al. (2022). Urban rats as carriers of invasive *Salmonella* Typhimurium sequence type 313, Kisangani, Democratic Republic of Congo. *PLOS Neglected Tropical Diseases*, 16(9), Article e0010740. <https://doi.org/10.1371/journal.pntd.0010740>
25. Peruzy, M. F., Houf, K., Joossens, M., Yu, Z., Proroga, Y. T. R., Murru, N. (2021). Evaluation of microbial contamination of different pork carcass areas through culture-dependent and independent methods in small-scale slaughterhouses. *International Journal of Food Microbiology*, 336, Article 108902. <https://doi.org/10.1016/j.ijfoodmicro.2020.108902>
26. Gomes-Neves, E., Abrantes, A. C., Vieira-Pinto, M., Müller, A. (2021). Wild game meat — A microbiological safety and hygiene challenge? *Current Clinical Microbiology Reports*, 8(2), 31–39. <https://doi.org/10.1007/s40588-021-00158-8>
27. Zeng, H., Rasschaert, G., De Zutter, L., Mattheus, W., De Reu, K. (2021). Identification of the source for *Salmonella* contamination of carcasses in a large pig slaughterhouse. *Pathogens*, 10(1), Article 77. <https://doi.org/10.3390/pathogens10010077>
28. Boubendir, S., Arsenault, J., Quessy, S., Thibodeau, A., Fravalo, P., Thériault, W. P. et al. (2021). *Salmonella* contamination of broiler chicken carcasses at critical steps of the slaughter process and in the environment of two slaughter plants: Prevalence, genetic profiles, and association with the final carcass status. *Journal of Food Protection*, 84(2), 321–332. <https://doi.org/10.4315/JFP-20-250>
29. Narimisa, N., Razavi, S., Jazi, F. M. (2024). Prevalence of antibiotic resistance in *Salmonella* Typhimurium isolates originating from Iran: A systematic review and meta-analysis. *Frontiers in Veterinary Science*, 11, Article 1388790. <https://doi.org/10.3389/fvets.2024.1388790>
30. Kong-Ngoen, T., Santajit, S., Tunyong, W., Pumirat, P., Sookrungs, N., Chaicumpa, W. et al. (2022). Antimicrobial resistance and virulence of non-typhoidal *Salmonella* from retail foods marketed in Bangkok, Thailand. *Foods*, 11(5), Article 661. <https://doi.org/10.3390/foods11050661>
31. Lertwatcharasarakul, P., Phatthanakunanan, S., Tulayakul, P. (2025). Retrospective analysis of antimicrobial resistance of *Salmonella* spp. isolated from livestock and its environment in Thailand. *Frontiers in Veterinary Science*, 12, Article 1584940. <https://doi.org/10.3389/fvets.2025.1584940>
32. Lekagul, A., Kirivan, S., Tansakul, N., Krisanaphan, C., Srinha, J., Laoprasert, T. et al. (2023). Antimicrobial consumption in food-producing animals in Thailand between 2017 and 2019: The analysis of national importation and production data. *PLOS ONE*, 18(4), Article e0283819. <https://doi.org/10.1371/journal.pone.0283819>
33. Tack, B., Phoba, M.-F., Barbé, B., Kalonji, L. M., Hardy, L., Van Puyvelde, S. et al. (2020). Non-typhoidal *Salmonella* bloodstream infections in Kisantu, DR Congo: Emergence of O5-negative *Salmonella* Typhimurium and extensive drug resistance. *PLOS Neglected Tropical Diseases*, 14(3), Article e0008121. <https://doi.org/10.1371/journal.pntd.0008121>
34. McMillan, E. A., Jackson, C. R., Frye, J. G. (2020). Transferable plasmids of *Salmonella enterica* associated with antibiotic resistance genes. *Frontiers in Microbiology*, 11, Article 562181. <https://doi.org/10.3389/fmicb.2020.562181>
35. Pietsch, M., Simon, S., Meinen, A., Trost, E., Banerji, S., Pfeifer, Y. et al. (2021). Third generation cephalosporin resistance in clinical non-typhoidal *Salmonella enterica* in Germany and emergence of blaCTX-M-harboring pESI plasmids. *Microbial Genomics*, 7(10), Article 000698. <https://doi.org/10.1099/mgen.0.000698>
36. Crump, J. A., Nyirenda, T. S., Kalonji, L. M., Phoba, M.-F., Tack, B., Platts-Mills, J. A. et al. (2023). Nontyphoidal *Salmonella* invasive disease: Challenges and solutions. *Open Forum Infectious Diseases*, 10(Suppl 1), S32-S37. <https://doi.org/10.1093/ofid/ofad020>
37. Brown, E. W., Bell, R., Zhang, G., Timme, R., Zheng, J., Hammack, T. S. et al. (2021). *Salmonella* genomics in public health and food safety. *EcoSal Plus*, 9(2), Article eESP-0008-2020. <https://doi.org/10.1128/ecosalplus.ESP-0008-2020>
38. Tangcharoensathien, V., Chanvatik, S., Sommanustweechai, A. (2018). Complex determinants of inappropriate use of antibiotics. *Bulletin of the World Health Organization*, 96(2), 141–144. <https://doi.org/10.2471/BLT.17.199687>
39. National Antimicrobial Resistance Surveillance Center, Thailand (NARST). (2023). Antimicrobial resistance surveillance data: Cumulative antibiograms [Online database]. National Institute of Health, Department of Medical Sciences, Ministry of Public Health, Thailand. Retrieved from <https://narst.dmsc.moph.go.th/> Accessed June 27, 2026
40. Prasertsee, T., Chokesajjawatee, N., Santiyanont, P., Chuammitri, P., Deedom, M., Tadee, P. et al. (2019). Quantification and rep-PCR characterization of *Salmonella* spp. in retail meats and hospital patients in northern Thailand. *Zoonoses and Public Health*, 66(3), 301–309. <https://doi.org/10.1111/zph.12565>
41. Tumelty, L., Fa, J. E., Coad, L., Friant, S., Mbane, J., Kamogne, C. T. et al. (2023). A systematic mapping review of links between handling wild meat and zoonotic diseases. *One Health*, 17, Article 100637. <https://doi.org/10.1016/j.onehlt.2023.100637>
42. Vinayamohan, P. G., Pellissery, A. J., Venkitanarayanan, K. (2022). Role of horizontal gene transfer in the dissemination of antimicrobial resistance in food animal production. *Current Opinion in Food Science*, 47, Article 100882. <https://doi.org/10.1016/j.cofs.2022.100882>

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