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Prevalence, Antibiotic Resistance, and Implications for Public Health Due to *Salmonella* Contamination in Food Products

Fatima Sayed [a], Rupinder Kaur [a], Vikas Jha [b*] and Umme Atiya Quraishi [c]

[a] Department of Zoology, Guru Nanak Khalsa College, Mumbai-400019, India.
[b] National Facility for Biopharmaceuticals, Guru Nanak Khalsa College, Mumbai-400019, India.
[c] Department of Bioinformatics, Guru Nanak Khalsa College, Mumbai-400019, India.

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

This research investigated the prevalence of *Salmonella* species in meat, chicken, fish, prawn, and milk samples, and their resistance to antibiotics was examined. The study findings demonstrated varying levels of *Salmonella* contamination in different food types, including meat and chicken samples showing higher prevalence rates compared to fish, prawn, and milk. Notably, the isolated *Salmonella* strains exhibited resistance to multiple antibiotics, raising concerns about the potential dissemination of antibiotic-resistant strains through the food chain and its implications for public health. The study underscores the critical importance of continuous surveillance in monitoring *Salmonella* prevalence and antibiotic resistance in food products. It also highlights the significance

**Corresponding author: Email: vikasjjha7@gmail.com;*

of promoting responsible antibiotic usage in both human and veterinary medicine to safeguard food safety and public health.

Keywords: Enterobacteriaceae; oxygen tolerance; Salmonella enterica; Salmonella bongori; Serogroups, serovars; S. pullorum; S. gallinarum; Salmonellosis*; Bacteraemia; pmqr elements;* drug efflux systems*;* multi-drug resistant *Salmonella.*

1. INTRODUCTION

Salmonella a member of the family *Enterobacteriaceae* is a gram-negative, rod-shaped motile bacterium. *Salmonella* is capable of surviving with or without oxygen. *Salmonella* is comprised of two known species: *Salmonella enterica* and *Salmonella bongori*. *Salmonella enterica* consists of six subspecies: *enterica, salamae, arizonae, diarizonae, houtenae,* and *indica*. The subspecies are categorized into serogroups and serovars. Serogroups are based on O antigens while serovars are based on H antigens. Different strains identification depends on O and H antigens [1,2]. *Salmonella enterica* is the most common infection reported in warm-blooded animals [2].

Salmonella as a source of infection poses a significant threat to food-producing animals, poultry in particular, and has direct implications for their global market and food products derived from them. *Salmonella* serovars like *S.pullorum* and *S.gallinarum* cause high mortality in young and older birds. Poultry carries serovars of *Salmonella* in their gastrointestinal tracts without showing any signs of illness, increasing the risk of contamination in raw products from animals during slaughtering and processing [3].

Salmonellosis can be classified as a minor or major disease. Minor Salmonellosis arises from non-typhoidal strains of *Salmonella* and is characterised by self-limiting diarrhoea and rarely progresses to bacteraemia. Whereas Major Salmonellosis causes typhoid fever [1]. The bloodstream is primarily affected by typhoid fever. Non-typhoidal strains of *Salmonella* cause gastroenteritis in individuals with healthy immune systems [2].

Salmonella enters poultry flocks by various means such as from environment, feed, vectors or primarily due to inadequate biosecurity measures [4]. The *Salmonella* problem has intensified due to the enormous animal and human food production and the rapid international trade of livestock. Detecting *Salmonella* in live animals, animal-derived food and environment is crucial for developing effective control and prevention strategies [5,4].

Antibiotic resistance in *Salmonella* is a global concern. The prevalence of antibiotic-resistant *Salmonella* species is largely attributed to the use of antibiotics in animal farms [4]. The Centres for Disease Control and Prevention (CDC) has classified antibiotic-resistant *S.typhi* as a serious disease and stresses the importance of monitoring and preventive measures to control the spread of resistant strains [6].

The increased utilization of fluoroquinolone antibiotics, like ciprofloxacin, has led to resistant *Salmonella* strains or less susceptible strains for this antibiotic [7,6]. The various mechanisms like PMQR elements, mutations in target genes and drug efflux systems, contribute to the development of fluoroquinolone resistance in *Salmonella* [7]. The emergence of resistant strains is not only limited to humans but to animals as well. Reports indicate that extensive use of antibiotics in treating animal diseases or as growth promoters have led to drug-resistant bacteria dissemination and occurrence [6].

This study aimed to assess the prevalence of multi-drug resistant *Salmonella* strains from various sources including meat, milk, fish, and eggs. This study aimed to determine drug resistance patterns and the extent of spread of multi-drug resistant strain of *Salmonella*.

2. MATERIALS AND METHODS

2.1 Isolation of *Salmonella* from Chicken Samples

A random collection of 17 swab samples was obtained from the surface of chilled broiler chicken meat sourced from various retail poultry shops across Mumbai. Tetrathionate brilliant green bile broth was prepared, and each swab sample was mixed with 20 *mL* of the prepared broth. Subsequently, the samples were incubated at 37°C for 24 hours to for *Salmonella* enrichment [8]. After incubation, the enriched broth was streaked onto selective agar plates

(XLD agar) suitable for *Salmonella* isolation. These plates were then incubated at 37°C for 24-48 hours under aerobic conditions. Following incubation, the plates were examined for the presence of *Salmonella* colonies, and biochemical tests were conducted to confirm the presence of *Salmonella*. This comprehensive approach was crucial for the identification and confirmation of *Salmonella* presence in the swab samples [8].

2.2 Isolation of *Salmonella* from Meat Samples

Total 28 Meat samples were collected from various sources in the Mumbai region. Sterile cotton throat swabs (CTS) were utilized, and each CTS was moistened with 10 *mL* of sterile saline peptone water (SPW) [9]. To ensure comprehensive coverage, a 100 cm^2 area on each meat sample surface was swabbed at four main points: brisket, flank, ramp, and neck. Strict measures were implemented to prevent cross-contamination during the sample collection. Within 24 hours of collection, the swabs were inoculated in nutrient broth and then incubated for 24 hours at 37 ± 0.5°C. Following the incubation, the nutrient broth was streaked onto Hektoen Enteric agar medium. Subsequently, the plates were incubated for an additional 24 hours at 37 ± 0.5°C for negative plates, while presumptive single colonies with green or blue colouration and a black centre on Hektoen Enteric agar, indicative of *Salmonella* growth, were selected. Biochemical tests including Catalase, Citrate, Lysine, Ornithine, ONPG, Mannitol, and Gelatin tests were performed on the selected colonies [9]. These steps were crucial in the comprehensive identification and confirmation of *Salmonella* presence in the meat samples.

2.3 Isolation of *Salmonella* from Milk Samples

1 *mL* of each milk sample (aseptically measured) was homogenized into 9 *mL* of buffered peptone water and incubated at 37°C for 24 hours for primary enrichment. (RVS) Rappaport-Vassiliadis with soya was adjusted to room temperature, and a 0.1 *mL* aliquot from the primary enrichment sample was transferred into 10 *mL* of RVS and incubated at 41.5°C for 24 hours. Secondary enrichment tubes were vortexed before plating on XLD agar, streaked using a 10 µL loop, and incubated at 35°C for 24 hours. After the recommended incubation time, suspected *Salmonella* colonies were identified on selective-differential agar plates, appearing as pink colonies with or without black centres on XLD agar. Three to five typical *Salmonella* colonies were then picked and streaked onto Trypton soya agar, followed by further biochemical identification through incubation at 37°C for 18–24 hours [10].

2.4 Isolation of *Salmonella* from Prawn Samples

Prawn samples from the Mumbai region were processed to detect the presence of *Salmonella* using the 3-step technique outlined by Wallace and Hammack [11,12]. This involved enrichment with Rappaport-Vassiliadis broth and Tetrathionate broth, followed by plating onto selective media, including Hektoen enteric agar and MacConkey agar. Suspicious *Salmonella* colonies were identified on the plating media and then transferred to trypticase soy agar (TSA). Isolates that demonstrated typical reactions were subjected to bio-typing for the identification of *Salmonella* species and subspecies, following the guidelines outlined by Le Minor and Popoff [13]. This comprehensive process was employed to ensure the accurate detection and identification of *Salmonella* in prawn samples.

2.5 Isolation of *Salmonella* from fish Samples

Total 29 fish samples were collected in the Mumbai region for isolating *Salmonella* by following ISO 6579-1:2017 standards (International Organization for Standardization, 2017). 25 g of each sample was initially homogenized in sterile bags with buffer peptone water (BPW) using the Stomacher method and then placed in the incubator at 37°C for 18 ± 2 hours for bacterial enrichment [14]. Subsequently, the enriched cultures were spread onto selective Rappaport Vassiliadis medium with soya (RV) and Kauffmann Tetrathionate Novobiocin (MKTTn) and incubated at 41.5°C and 37°C, respectively, for 24 ± 3 hours. Pure colonies were plated on Xylose Lysine Deoxycholate (XLD) agar and Mannitol Lysine Crystal Violet Brilliant Green agar (*ML*CB) and incubated at 37°C for 24 ± 3 hours [14].

2.6 Biochemical Characterisation

Biochemical tests were carried out for preliminary identification (17). Catalase test to determine presence of catalase enzyme activity; Citrate test

to assess the ability of bacteria to utilize citrate as sole carbon source; Lysine decarboxylase and Ornithine decarboxylase tests to evaluate the ability of the bacteria to decarboxylate lysine and ornithine, respectively; Motility test to observe the movement of bacterial cells; ONPG (ortho-Nitrophenyl-β-galactoside) test to detect the presence of β-galactosidase enzyme activity; Mannitol test to determine the fermentation of mannitol sugar; Gelatin test to assess the ability of bacteria to hydrolyse gelatin; Slant and Butt tests to observe the production of acid and gas in triple sugar iron agar (TSI); Hydrogen sulfide (H2S) production test to detect the production of hydrogen sulfide gas; and Gas production test to observe the production of gas within the medium [15,16].

2.7 Antibiotic Susceptibility Testing

The antibiotic resistance screening method employed involved disk diffusion assay. Isolates of *Salmonella* obtained from various sources, including prawn, milk, meat, chicken, and fish samples, were cultured on Mueller Hinton agar plates. Sterile disks with antibiotics, including Gentamycin, Nalidixic acid, trimethoprim, tetracycline, Ciprofloxacin, Chloramphenicol, Erythromycin, ampicillin, ofloxacin, and Cefoperazone, at a concentration of 10µg/mL, were evenly placed on the agar surface. The plates were incubated at 37°C for 24 hours. Following incubation, the zones of inhibition around each disk were measured to determine the susceptibility of the *Salmonella* isolates to the antibiotics [17]. Growth was indicated by the absence of a zone of inhibition, while susceptibility was indicated by the presence of a zone of inhibition.

2.8 16S rRNA Identification

The 16S rRNA Polymerase Chain Reaction (PCR) was conducted to amplify the 16S rRNA gene of the isolated *Salmonella* samples using a PCR Thermocycler (Applied Biosystems) [18]. The amplification utilized specific primers, namely 8F and 907R. The PCR setup involved the preparation of a reaction buffer, followed by amplification under specified conditions. After amplification, the products were qualitatively assessed using 1.5% agarose gel electrophoresis to confirm successful amplification [19]. Subsequently, the samples were sent for sequencing. For DNA sequencing and species identification, cycle sequencing reactions were conducted using Universal primers 8F and 907R. The obtained 16S rRNA sequences were aligned and analyzed using the BLASTn search tool to identify the isolates, allowing for direct comparisons with database sequences available at the National Centre for Biotechnology Information (NCBI). This comprehensive approach facilitated the accurate characterization and identification of bacterial species in the study. Total of 82 sequences were submitted to the GenBank database under the assigned accession numbers (PP647610 to PP647691), representing 7 strains from prawn samples, 4 strains from milk samples, 28 strains from meat samples, 14 strains from chicken samples, and 29 strains from fish samples.

3. RESULTS AND DISCUSSION

Salmonella is often found in contaminated food, particularly in raw or undercooked meat, poultry, eggs, and unpasteurized dairy products. Screening in food production facilities plays a vital role in identifying tainted products, thus preventing widespread foodborne illnesses. *Salmonella* infections can lead to gastroenteritis, manifesting as symptoms like diarrhoea, cramps, and fever, which poses significant risks to vulnerable populations. Outbreaks can be detected and controlled, safeguarding public health and lessening the burden on healthcare systems by conducting screenings. Additionally, the screening process yields essential data that allows health authorities to track trends, pinpoint potential contamination sources, and develop targeted interventions. Adhering to food safety regulations is imperative for businesses to ensure consumer safety and uphold their reputation. Regular screening serves as a preventive measure, averting economic losses resulting from outbreaks, which may include recalls and damage to brand reputation.

The primary objective of the study was to identify *Salmonella* as the predominant bacterium and comprehend its prevalence in Mumbai. However, the study did not focus on identifying individual *Salmonella* species; instead, it categorized 82 confirmed *Salmonella* isolates into 5 groups based on variations in the samples. The identification process adhered to Bergey's Manual of Determinative Bacteriology, specifically utilizing Group 5: Family *Enterobacteriaceae* Lactose negative flowchart. Among the 82 *Salmonella* isolates, 28(34.14%) were obtained from meat, 29 (35.36%) from fish, 14 (17.07%) from chicken, 7 (8.53%) from prawn, and 4 (4.87%) from milk samples.

Table 1. The colony characteristics and bifurcation of *Salmonella* isolates obtained from meat, chicken, fish, prawn and milk samples.

	Number of Samples	Colony characteristic
Isolates from meat	28	Rod
Isolates from fish	29	Rod
Isolates from chicken	14	Rod
Isolates from prawn	7	Rod
Isolates from milk	4	Rod

Biochemical tests were utilized to verify the identity of the isolates as *Salmonella*. Each *Salmonella* isolate was then subjected to antibiotic sensitivity screening, where 10 different antibiotics were tested, including Gentamycin, Nalidixic acid, trimethoprim, tetracycline, Ciprofloxacin, Chloramphenicol, Erythromycin, ampicillin, ofloxacin, and Cefoperazone. The micro broth dilution technique was employed for this screening. To ensure consistency and comparability with other research studies, a standardized concentration of 10 µg/mL was selected for all tested antibiotics. This approach aimed to promote uniformity in the research and facilitate a comprehensive understanding of the antibiotic resistance patterns exhibited by the isolates.

In the analysis of antibiotic susceptibility among the isolates (Table 2), it was found that there were varying levels of resistance and sensitivity across different antibiotics. Notably, Gentamycin and Chloramphenicol showed equal distribution between sensitivity and intermediate organisms, with no resistance observed. Nalidixic acid and Ciprofloxacin displayed relatively high levels of resistance at 42.85% and 42.85% respectively, with Nalidixic acid also showing a significant portion of intermediate organisms. Trimethoprim exhibited low resistance at 17.85% and a high sensitivity rate of 78.57%. Tetracycline showed moderate resistance at 10.71%, with a considerable portion of intermediate organisms. Erythromycin and Ampicillin displayed relatively high resistance rates of 67.85% and 57.14% respectively, with Erythromycin also showing a notable proportion of intermediate organisms. Ofloxacin and Cefoperazone exhibited low resistance rates of 7.14%, with Cefoperazone also showing a significant portion of intermediate organisms.

The antibiotic susceptibility analysis among the isolates revealed varying levels of resistance and sensitivity across different antibiotics (Table 3). Gentamycin demonstrated low resistance (3.44%) and high sensitivity (93.10%), with a small portion of intermediate organisms (3.44%). Nalidixic acid exhibited moderate resistance (41.37%) and sensitivity (31.03%), with a notable proportion of intermediate organisms (27.58%). Trimethoprim and Tetracycline showed high resistance rates (75.86% and 79.31% respectively) and low sensitivity rates (17.24% for both), with minimal intermediate organisms. Ciprofloxacin displayed low resistance (3.44%) and moderate sensitivity (68.96%), with a significant proportion of intermediate organisms (27.58%). Chloramphenicol had moderate resistance (27.58%) and sensitivity (55.17%), with a portion of intermediate organisms (17.24%). Erythromycin showed moderate resistance (34.48%) and a high proportion of intermediate organisms (65.51%), with no sensitive organisms listed. Ampicillin exhibited high resistance (75.86%) and low sensitivity (17.24%), with minimal intermediate organisms. Ofloxacin demonstrated high sensitivity (96.55%) and no resistance, with a small portion of intermediate organisms (3.44%). Cefoperazone displayed moderate resistance (13.79%) and moderate sensitivity (72.41%), with a small proportion of intermediate organisms (13.79%).

The analysis of antibiotic susceptibility among the isolates revealed varying patterns of resistance and sensitivity across different antibiotics (Table 4). Gentamycin demonstrated low resistance (14.28%) and high sensitivity (85.71%), with no intermediate organisms observed. Nalidixic acid exhibited moderate resistance (64.28%) and low sensitivity (35.71%), with no intermediate organisms reported. Trimethoprim displayed high resistance (78.57%) and low sensitivity (21.42%), with no intermediate organisms detected. Tetracycline showed high resistance (92.85%) and a small proportion of intermediate organisms (7.14%), with no sensitive organisms listed. Ciprofloxacin demonstrated moderate resistance (21.42%), moderate sensitivity (50%), and a notable proportion of intermediate organisms (28.57%). Chloramphenicol had low resistance (7.14%) and moderate sensitivity (71.42%), with a portion of

intermediate organisms (21.42%). Erythromycin showed moderate resistance (57.14%) and sensitivity (21.42%), with a proportionate distribution of intermediate organisms (21.42%). Ampicillin exhibited complete resistance (100%), with no sensitive organisms reported. Ofloxacin demonstrated low resistance (14.28%) and high sensitivity (85.71%), with no intermediate organisms observed. Cefoperazone showed no resistance, moderate sensitivity (50%), and a balanced distribution of intermediate organisms (50%).

Table 2. The efficacy of individual antibiotics against 28 *Salmonella* isolates from meat samples

Antibiotics	Number of resistant organisms	Number of sensitive organisms	Number of intermediate organisms
Gentamycin	-	14(50%)	14(50%)
Nalidixic acid	12(42.85%)	7(25%)	9(32.14%)
Trimethoprim	5(17.85%)	22(78.57%)	1(3.57%)
Tetracycline	3(10.71%)	13(46.42%)	12(42.85%)
Ciprofloxacin	12(42.85%)	1(3.57%)	15(53.57%)
Chloramphenicol	-	25(89.28%)	3(10.71%)
Erythromycin	19(67.85%)	1(3.57%)	8(28.57%)
Ampicillin	16(57.14%)	4(14.28%)	8(28.57%)
Ofloxacin	2(7.14%)	26(92.85%)	-
Cefoperazone	2(7.14%)	15(53.57%)	11(39.28%)

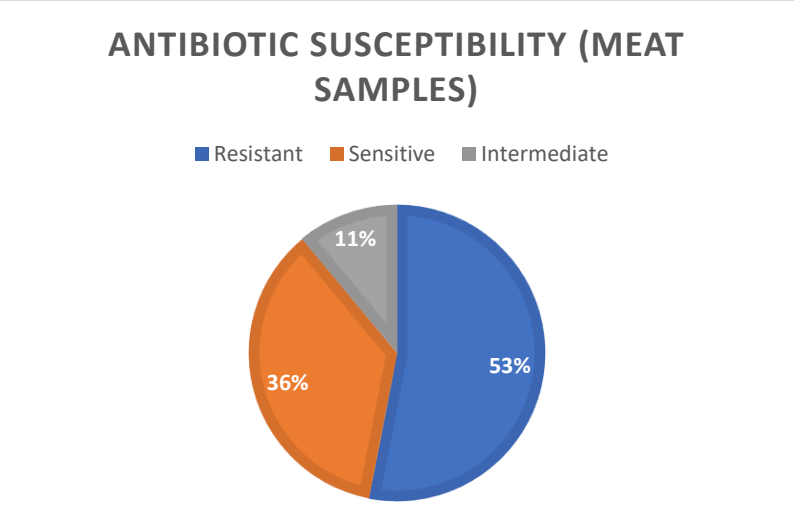

Fig. 1. Antibiotic susceptibility among the isolates

Table 3. The efficacy of individual antibiotics against 29 *Salmonella* isolates from fish samples

Antibiotics	Number of resistant organisms	Number of sensitive organisms	Number of intermediate organisms
Gentamycin	1(3.44%)	27(93.10%)	1(3.44%)
Nalidixic acid	12(41.37%)	9(31.03%)	8(27.58%)
Trimethoprim	22(75.86%)	5(17.24%)	2(6.89%)
Tetracycline	23(79.31%)	5(17.24%)	1(3.44%)
Ciprofloxacin	1(3.44%)	20(68.96%)	8(27.58%)
Chloramphenicol	8(27.58%)	16(55.17%)	5(17.24%)
Erythromycin	10(34.48%)	-	19(65.51%)
Ampicillin	22(75.86%)	5(17.24%)	2(6.89%)
Ofloxacin	-	28(96.55%)	1(3.44%)
Cefoperazone	4(13.79%)	21(72.41%)	4(13.79%)

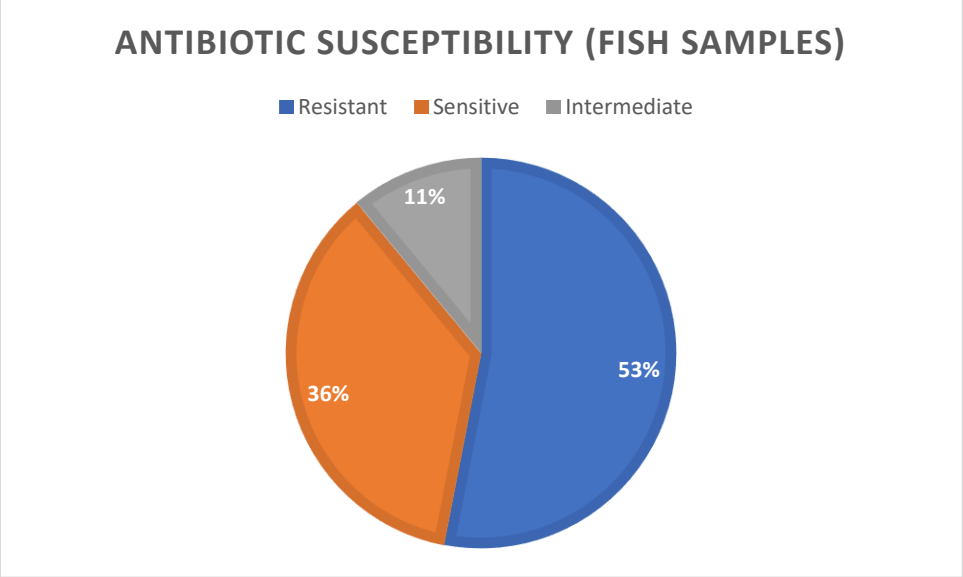

Fig. 2. Antibiotic susceptibility among the isolates

Table 4. The efficacy of individual antibiotics against 14 *Salmonella* isolates from chicken samples

Antibiotics	Number of resistant organisms	Number of sensitive organisms	Number of intermediate organisms
Gentamycin	2(14.28%)	12(85.71%)	-
Nalidixic acid	9(64.28%)	5(35.71%)	-
Trimethoprim	11(78.57%)	3(21.42%)	-
Tetracycline	13(92.85%)	-	1(7.14%)
Ciprofloxacin	3(21.42%)	7(50%)	4(28.57%)
Chloramphenicol	1(7.14%)	10(71.42%)	3(21.42%)
Erythromycin	8(57.14%)	3(21.42%)	3(21.42%)
Ampicillin	14(100%)	-	-
Ofloxacin	2(14.28%)	12(85.71%)	-
Cefoperazone	-	7(50%)	7(50%)

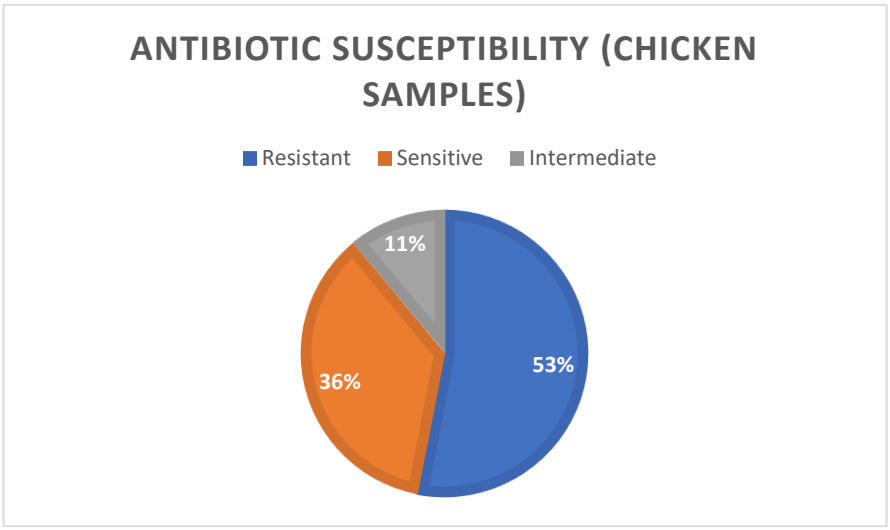

Fig. 3. Antibiotic susceptibility among the isolates

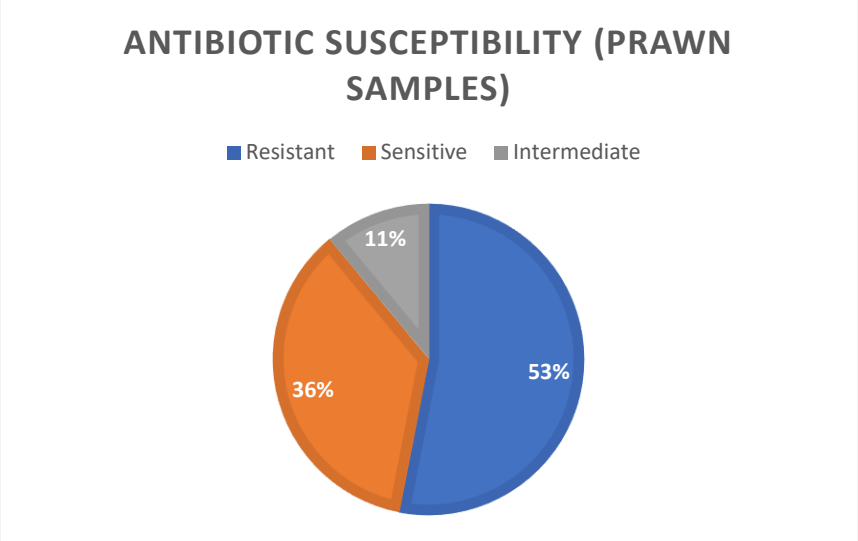

Fig. 4. Antibiotic susceptibility among the isolates

Table 5. The efficacy of individual antibiotics against 7 *Salmonella* isolates from prawn samples

Antibiotics	Number of resistant organisms	Number of sensitive organisms	Number of intermediate organisms
Gentamycin	-	7(100%)	-
Nalidixic acid	2(28.57%)	2(28.57%)	3(42.85%)
Trimethoprim	7(100%)	-	-
Tetracycline	7(100%)	-	-
Ciprofloxacin	1(14.28%)	3(42.85%)	3(42.85%)
Chloramphenicol	-	3(42.85%)	4(57.14%)
Erythromycin	2(28.57%)	-	5(71.42%)
Ampicillin	7(100%)	-	-
Ofloxacin	1(14.28%)	6(85.71%)	-
Cefoperazone	7(100%)	-	-

The analysis of antibiotic susceptibility among the isolates revealed diverse resistance and sensitivity profiles across different antibiotics (Table 5). Gentamycin exhibited complete sensitivity (100%), with no resistance or intermediate organisms observed. Nalidixic acid displayed moderate resistance (28.57%) and sensitivity (28.57%), with a notable proportion of intermediate organisms (42.85%). Trimethoprim and Tetracycline both showed complete resistance (100%), with no sensitive organisms detected. Ciprofloxacin demonstrated low resistance (14.28%), moderate sensitivity (42.85%), and a notable proportion of intermediate organisms (42.85%). Chloramphenicol exhibited moderate sensitivity (42.85%) and a significant proportion of intermediate organisms (57.14%), with no resistance observed. Erythromycin showed moderate resistance (28.57%) and a notable proportion of intermediate organisms (71.42%), with no sensitive organisms reported. Ampicillin and Cefoperazone both displayed complete resistance (100%), with no sensitive organisms observed. Ofloxacin demonstrated low resistance (14.28%), high sensitivity (85.71%), and no intermediate organisms reported.

The analysis of antibiotic susceptibility among the isolates revealed varying resistance and sensitivity patterns across different antibiotics (Table 6). Gentamycin exhibited complete sensitivity (100%), with no resistance observed. Nalidixic acid and Trimethoprim both showed equal proportions of resistance (50%) and sensitivity (50%), with no intermediate organisms reported. Tetracycline demonstrated complete resistance (100%), with no sensitive organisms detected.

Table 6. The efficacy of individual antibiotics against 4 *Salmonella* isolates from milk samples

Antibiotics	Number of resistant organisms	Number of sensitive organisms	Number of intermediate organisms
Gentamycin	-	4(100%)	-
Nalidixic acid	2(50%)	2(50%)	-
Trimethoprim	2(50%)	2(50%)	-
Tetracycline	4(100%)	-	-
Ciprofloxacin	-	4(100%)	-
Chloramphenicol	2(50%)	2(50%)	-
Erythromycin	1(25%)	3(75%)	-
Ampicillin	4(100%)	-	-
Ofloxacin	-	4(100%)	-
Cefoperazone	-	-	4(100%)

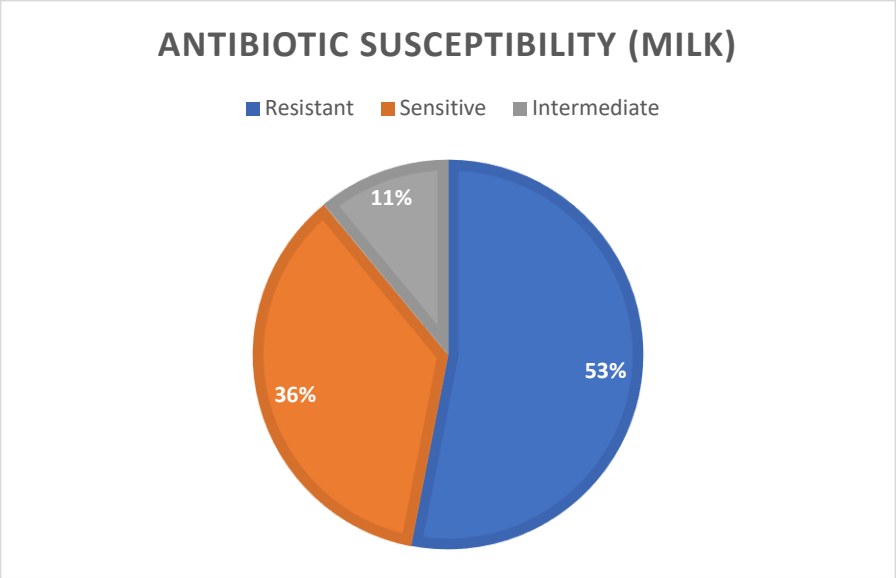

Fig. 5. Antibiotic susceptibility among the isolates

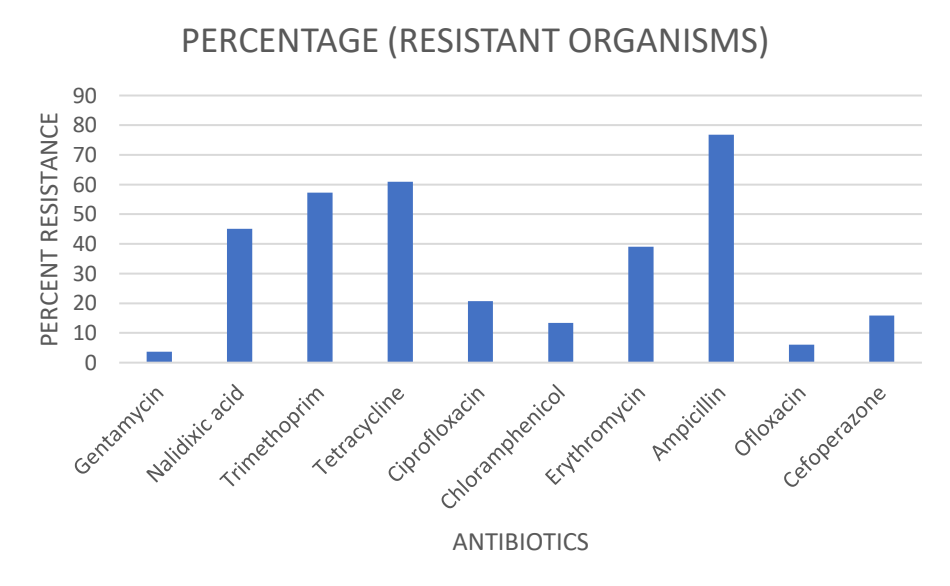

Fig. 6. Resistant organisms against Antibiotics

Ciprofloxacin, Chloramphenicol, Ofloxacin, and Ampicillin all displayed complete sensitivity (100%), with no resistant organisms observed. Erythromycin exhibited partial resistance (25%) and partial sensitivity (75%), with no intermediate organisms reported. Cefoperazone showed complete resistance (100%), with no sensitive or intermediate organisms observed.

Salmonella species have earned a reputation for their capacity to develop resistance to a diverse range of antibiotics. This resistance can emerge through various mechanisms, including genetic mutations within bacterial genes and the acquisition of resistance genes from other bacteria through a process known as horizontal gene transfer. The rise of antibiotic resistance in *Salmonella* presents substantial challenges in managing *Salmonella* infections in both human and animal populations. It can result in more severe and prolonged illnesses, escalate healthcare expenditures, and lead to higher mortality rates. The excessive and improper use of antibiotics in human medicine, agriculture, and animal husbandry plays a pivotal role in fostering the development of antibiotic resistance not only in *Salmonella* but also in other bacterial species. When antibiotics are utilized inappropriately or discontinued prematurely, bacteria can adapt and develop resistance, rendering infections harder to treat effectively. To address antibiotic resistance in *Salmonella* species and other infectious agents, it is imperative to promote responsible antibiotic usage in both human and veterinary medical settings. Additionally, implementing robust surveillance programs becomes crucial to closely monitor the prevalence and dissemination of antibiotic-resistant *Salmonella* strains. Such vigilance enables timely intervention and the deployment of effective control measures to mitigate the spread of resistance [20,21].

4. CONCLUSION

Salmonella, a gram-negative bacterium, was prevalent across meat, fish, chicken, prawn, and milk samples in Mumbai, highlighting widespread food contamination. Alarmingly, many *Salmonella* strains showed resistance to multiple antibiotics, emphasizing the urgent global issue of antimicrobial resistance. The indiscriminate use of antibiotics in animal farming and possibly human medicine is a significant contributing factor. This resistance compromises treatment efficacy, elevates healthcare costs, and poses a severe public health threat. Enhanced surveillance and responsible antibiotic stewardship are essential to address this growing challenge and protect public health.

CONFLICT OF INTEREST

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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