Phenotypic and genotypic drug resistance profile of *Salmonella* serovars isolated from poultry farm and processing units located in and around Mumbai city, India

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**Abstract**

**Background and Aim:** The extensive use of antimicrobials in poultry has led to an increase in bacterial multidrug resistance, and the emergence of multidrug-resistant nontyphoidal *Salmonella* is a global problem. This study was performed to detect antibiotic-resistant *Salmonella* serovars in poultry farming and processing environment.

**Materials and Methods:** A total of 956 various samples, comprising 432 farm origin, 324 poultry processing stage wise and environmental, and 154 product processing stages and environmental samples, were collected from poultry farms and processing units located in and around Mumbai city. Of a total of 71 recovered isolates, 42 randomly selected *Salmonella* isolates were subjected for antibiotic susceptibility testing by disk diffusion method and serotyping. A total of 31 serotypically confirmed isolates were characterized for the presence of tetA, tetB, blaTEM*, and CTX-M gene.

**Results:** Higher resistance was recorded against Doxycycline (100%), followed by Oxytetracycline (97.62%), Neomycin (88.10%), Erythromycin (83.33%), Tetracycline (78.57%), and Cefotaxime (35.71%). Resistance from 0.00 to 26.19 percent was found to antimicrobials, namely Norfloxacin (26.19%), Ampicillin (21.43%), Azithromycin (21.43%), Ciprofloxacin (19.05%), Colistin (16.67%), Streptomycin (14.19%), Cefotaxime (14.29%), Amoxiclav (14.29%), Gentamicin (7.14%), Chloramphenicol (4.76%), Amikacin (4.76%), and Ceftazidime (0.0%). Results demonstrate that the *Salmonella* Virchow dominated and all serotypes were found to carry Tetracycline resistance gene tetA, 5 isolates were found to be positive for blaTEM, whereas none of the isolates were carrying tetB and CTX-M gene.

**Conclusion:** This study revealed that there is a significant rise of Tetracycline resistance with the presence of tetA gene in *Salmonella* spp. which indicates selective pressure for adopting resistance against tetracycline group of antibiotics.

**Keywords:** multidrug-resistant, poultry, *Salmonella* spp., tetracycline.

**Introduction**

Foodborne risk factors for human health can be recognized from poultry which includes microbiological and chemical risks, wherein *Salmonella* spp. contamination and residues from veterinary medications are important risks [1]. Microbiological risk factors are so prevailing that they can be found in almost all systems of poultry production [2]. Poultry and poultry products are known reservoirs for these foodborne pathogens, and numerous reports described the prevalence of *Salmonella* associated with live poultry, production environments, and processing plants [3]. *Salmonella* has been a pathogen of significance and is a major cause of gastroenteritis in humans [4]. *Salmonella* illness has linked with exposure to meat; a review of the Centers for Disease Control and Prevention 2012 outbreak data indicated that 10 out of 25 outbreaks were related to live poultry, shell eggs, or further processed poultry products [5].

Salmonellosis in animal and human may occur due to the involvement of >2500 serovars [6]. In India, *Salmonella* Virchow, *Salmonella* Typhimurium, and S. Enteritidis are reported as major nontyphoidal *Salmonella* serovar from poultry [7]. Among veterinary residues, antibiotic residues in meat have been a rising issue in recent years in India. Antibiotics have been used in poultry for the treatment of infections and also to counteract the adverse consequences of stress responses [8]. The presence of antimicrobial residues in meat has several impacts on health aspects to the consumer like possible contribution to the development of antibiotic resistance bacteria [9]. Various workers reported drug resistance genes against tetracycline and broad- and extended-spectrum β-lactamase antibiotics in *Salmonella* due to selective pressure [10].

Therefore, the purpose of the present study was to examine the presence of multidrug-resistant (MDR)
Salmonella spp. in poultry farming and processing establishment. The increasing single and multiple antimicrobial-resistant Salmonella strains isolated from human cases of Salmonellosis have been associated with widespread use of antimicrobial agents in food animal production [11]. This may clearly represent a public health risk by transfer of resistant Salmonella strains to humans through the consumption of contaminated poultry products.

Materials and Methods

Ethical approval

Since no animals were used in this study, ethical approval was not needed.

Sampling and study period

In the present study, for isolation of Salmonella spp., a total of 956 various samples, comprising 432 poultry farm origin, 324 poultry processing stages and environmental samples, were collected from poultry farms and processing units located in and around Mumbai city during December 2015-December 2017. Bacterial isolates were isolated by IS 5887 (Part 3): 1999 [12]. Bacterial isolates were identified on the basis of cultural characteristics on BGSA and XLD media, Gram staining, and conventional biochemical test. The isolates were further characterized by invA gene as per the method of Rahn et al. [13], to identify pathogenic Salmonella spp. Isolates identified as Salmonellae were sent to Poultry Diagnostics and Research Center, Loni Kalbhor, Pune, for serotyping.

Antimicrobial susceptibility testing

Randomly selected 42 Salmonella spp. isolates were tested for antimicrobial susceptibility by disk diffusion method (Kirby–Bauer test) using the following randomly selected 19 antimicrobials which were commonly used in animal and humans (HiMedia Laboratories, Pvt., Ltd., Mumbai, India): Gentamicin (10 μg), Azithromycin (15 μg), Cefotaxime (30 μg), Amikacin (30 μg), Amoxiclav (30 μg), Norfloxacin (10 μg), Oxytetracycline (30 μg), Enrofloxacin (10 μg), Ciprofloxacin (5 μg), Streptomycin (10 μg), Colistin (10 μg), Chloramphenicol (30 μg), Cefotaxime (30 μg), Cefazidime (30 μg), Ampicillin (10 μg), Neomycin (30 μg), Erythromycin (15 μg), Tetracycline (30 μg), and Doxycycline (30 μg). According to the Clinical and Laboratory Standards Institute [14] guidelines and interpretative criteria and based on inhibition zone, the isolates were categorized as resistance (R), intermediate (I), and sensitive (S).

Detection of antimicrobial resistance genes

The presence of genes associated with resistance to Tetracycline (tetA and tetB), broad-spectrum β-lactamases (blaTEM), and β-lactamases with extended spectrum (CTX-M) in confirmed 31 serotypes were detected by polymerase chain reaction (PCR) as per the methods [15-17] depicted in Table-1.

Results

Occurrence of Salmonella spp.

On screening these 956 samples, 71 positive Salmonella spp. were recovered with the occurrence of 7.4%. All the isolates were further confirmed as Salmonella spp. by amplification of invA gene.

Susceptibility testing through agar disk diffusion method

Antibiotic susceptibility testing was performed for randomly selected 42 confirmed invA gene-positive isolates.

Table 1. Standardization of PCR method for genotypic characterization of Salmonella spp.

| S. No. | Gene name | Target | Primer Sequence (5′-3′) | Thermal profiles for PCR | Product Size (bp) | Reference |
|--------|-----------|--------|------------------------|-------------------------|------------------|-----------|
| 1      | invA      | Invasion-associated protein | F: GTGAAATTATCAGCAGTTGCTGAAGC<br>R: TCATCGACGGCTCAAAGGAACC | 94°C×2 m/94°C×60 s - 65°C×60 s - 72°C×120 s (30 cycles)/72°C×5 m | 284 | [13] |
| 2      | blaTEM    | Broad-spectrum β-lactamases | F: ATGAGTTCAACATTTCCG<br>R: CTGACAGTTACAAAGTTA | 95°C×5 m/95°C×60 s - 55°C×60 s - 72°C×120 s (35 cycles)/72°C×7 m | 867 | [15] |
| 3      | tetA      | Tetracycline | F: GCTACATCCGTGCTGCTTC<br>R: CATAGATCGCCGTGAAGAGG | 95°C×5 m/95°C×60 s - 64°C×30 s - 72°C×30 s (40 cycles)/72°C×10 m | 210 | [16] |
| 4      | tetB      | Tetracycline | F: TGGTGGAGGGAGGACATTG<br>R: GTAATGGGGCAATAACCAGG | 95°C×5 m/95°C×60 s - 64°C×30s - 72°C×30 s (40 cycles)/72°C×10 m | 659 | [16] |
| 5      | CTX-M     | β-lactamases with extended spectrum | F: ATGTGCAGYACCAGTAARGTKATGGC<br>R: TGGGTRAARTGTSACCAGAAYCAGCG | 95°C×5 m/94°C×30 s - 62°C×90 s - 72°C×60 s (40 cycles)/72°C×10 m | 593 | [17] |

PCR: Polymerase chain reaction

Available at www.veterinaryworld.org/Vol.11/December-2018/6.pdf
isolates (Figure-1) with 19 frequently used antibiotics stated earlier. All of the isolates from this study were found to be resistant to more than two antibiotics.

**Antimicrobial resistance pattern**

The PCR assay (invA gene) positive 42 Salmonella isolates were tested against 19 commonly used antimicrobials for resistance pattern. Higher resistance was recorded against Doxycycline (100%), followed by Oxytetracycline (97.62%), Neomycin (88.10%), Erythromycin (83.33%), Tetracycline (78.57%), and Ceftizoxime (35.71%). Resistance was also found to routinely used antimicrobials, namely Norfloxacin (26.19%), Ampicillin (21.43%), Azithromycin (21.43), Ciprofloxacin (19.05%), Streptomycin (16.67%), Cefotaxime (14.19%), Enrofloxacin (14.29%), and Amoxyclav (14.29%). All the isolates were found susceptible to Ceftazidime. The drugs found to be effective in terms of susceptibility were Colistin (83.33%), Chloramphenicol (95.24%), Gentamicin (88.10%), and Amikacin (95.24%). Results are depicted in Table-2.

**Serotyping of isolates**

Out of 42 isolates, 31 were identified as S. Virchow (20), Salmonella Newport (6), and S. Typhimurium (5), whereas 11 isolates remained untypable, this indicates the dominance of serotype S. Virchow in poultry farming and processing system under study.

**Charactering of serotypes for the presence of tetA, tetB, blaTEM and CTX-M genes**

All the tested Salmonella serotypes (n=31) were found to carry Tetracycline resistance gene tetA, whereas none of them were carrying tetB gene. Whereas 5 isolates were found positive for blaTEM indicating resistance against Broad spectrum β-lactamases, and none of the isolate was found to be carrying CTX-M gene (Table-3 and Figures 2-4). The blaTEM Gene was observed in two isolates from each of S. Typhimurium (NIWH6 and ACWH6) and S. Newport (SCDM4 and RCKS4), while one isolate of S. Virchow (RCPD4). The overall occurrence of Tetracycline resistance and broad-spectrum β-lactamases resistance in Salmonella isolates was 100 and 16.12%, respectively.

**Discussion**

Poultry and their environments are act as the major sources of foodborne salmonellosis to human beings. In the present study, an overall occurrence of Salmonella isolation from poultry samples and environment was 7.4% which is of public health significance.

Although antimicrobials have a distinct advantage in the management of infection and promotion of growth in broilers, indiscriminate and non-judicious extensive use of antimicrobials could lead to the emergence of antimicrobial resistance. This uncontrolled use of drugs may exert selective pressure and promotes the proliferation of drug-resistant strains of Salmonella in poultry production system [18]. This was coupled with poor environmental sanitation and workers personal hygiene in processing could be a

![Figure-2](image-url)  
**Figure-2:** Polymerase chain reaction assay for detection of tetA gene of Salmonella isolates. Lane 1: TrackIt™ 100bp DNA ladder. Lane 2: Positive control (NIFL1). Lane 3: Positive sample. Lane 4: Negative control. Lanes 5-10: Positive samples.

**Table-2:** Phenotypic antimicrobial resistance pattern of Salmonella spp.

| S. No. | Antimicrobial agent | Susceptibility of Salmonella isolate (%) |
|--------|---------------------|----------------------------------------|
|        |                     | Sensitive | Intermediate | Resistance |
| 1      | Gen10               | 88.10     | 4.76         | 7.14       |
| 2      | AZM15               | 52.38     | 26.19        | 21.43      |
| 3      | CFX30               | 23.81     | 40.48        | 35.71      |
| 4      | AK30                | 95.24     | 0.00         | 4.76       |
| 5      | AMC30               | 83.33     | 2.38         | 14.29      |
| 6      | NX10                | 64.29     | 9.52         | 26.19      |
| 7      | OX30                | 2.38      | 0.00         | 97.62      |
| 8      | Ex10                | 59.52     | 26.19        | 14.29      |
| 9      | CFX5                | 64.29     | 16.67        | 19.05      |
| 10     | S10                 | 66.67     | 16.67        | 16.67      |
| 11     | CL10                | 83.33     | 0.00         | 16.67      |
| 12     | C30                 | 95.24     | 0.00         | 4.76       |
| 13     | CFX30               | 54.76     | 30.95        | 14.29      |
| 14     | CFX20               | 100.00    | 0.00         | 0.00       |
| 15     | AMP10               | 78.57     | 0.00         | 21.43      |
| 16     | N30                 | 11.90     | 0.00         | 88.10      |
| 17     | E15                 | 0.00      | 16.67        | 83.33      |
| 18     | TE30                | 21.43     | 0.00         | 78.57      |
| 19     | DO30                | 0.00      | 0.00         | 100.00     |
potential threat to public health. This study demonstrated that *Salmonella* isolates could acquire resistance. Resistance pattern varied from isolates to isolates, but 100.00, 97.62, 88.10, and 83.33% isolates showed resistance to Doxycycline, Oxytetracycline, Neomycin, and Erythromycin, respectively. These resistant isolates in the poultry environment might work as a potential reservoir for transfer of resistant genes into other highly infectious Gram-negative pathogens present in the poultry environment.

Similar results were reported by Ishihara *et al.* [19] with respect to Oxytetracycline (82.0%). However, neomycin resistance pattern has comparable finding with Carramiñana *et al.* [20] who reported 53.4% resistance to neomycin, while in contrast to the findings of Poppe *et al.* [21] who observed resistance <2% in *Salmonella* isolates.

**Table-3:** Antibiotic resistance and virulence marker gene detected in different *Salmonella* serotypes.

| S. No. | Source of isolate | Sample code | Serogroup  | Antibiotic resistance marker | Virulence marker |
|--------|-------------------|-------------|------------|-------------------------------|-----------------|
|        |                   |             |            | *bla*<sub>TET</sub> | *tetA* | *tetB* | *CTX-M* | *invA* |
| 1      | Cloacal swab      | NICS9       | S. Virchow | -                             | +                 | -       | -       | +       |
| 2      | Litter            | NIFL1       | S. Newport | -                             | +                 | -       | -       | +       |
| 3      | Litter            | NIFL9       | S. Virchow | -                             | +                 | -       | +       | +       |
| 4      | Feces             | NIF8        | S. Virchow | -                             | +                 | -       | +       | +       |
| 5      | Drinker           | NIDR7       | S. Virchow | -                             | +                 | -       | +       | +       |
| 6      | Drinker           | NIDR6       | S. Typhimurium | -                           | -               | +       | +       | +       |
| 7      | Worker hand       | NIWH6       | S. Typhimurium | +                           | -               | -       | +       | +       |
| 8      | Litter            | PIL1        | S. Virchow | -                             | +                 | -       | +       | +       |
| 9      | Feces             | PIF7        | S. Virchow | -                             | -                 | -       | +       | +       |
| 10     | Drinking water    | PIDW5       | S. Typhimurium | -                           | -               | +       | +       | +       |
| 11     | Worker hand       | RCWH3       | S. Virchow | -                             | -                 | -       | +       | +       |
| 12     | Carcass contact platform | RCCP5 | *Salmonella* Newport | - | + | - | + |
| 13     | Chopping board    | RCCB1       | S. Virchow | -                             | -                 | -       | +       | +       |
| 14     | Chopping board    | RCCB3       | S. Virchow | -                             | +                 | +       | +       | +       |
| 15     | Knife             | RCKS4       | S. Newport | +                             | +                 | -       | +       | +       |
| 16     | Post defeathering | RCPD4       | S. Virchow | +                             | +                 | +       | +       | +       |
| 17     | Post defeathering | RCPD3       | S. Virchow | -                             | -                 | +       | +       | +       |
| 18     | Post evisceration | RCPE2       | S. Virchow | -                             | -                 | +       | +       | +       |
| 19     | Post evisceration | RCPE3       | S. Virchow | -                             | -                 | +       | +       | +       |
| 20     | Post evisceration | RCPWC2      | S. Virchow | -                             | -                 | -       | +       | +       |
| 21     | Neck skin of eviscerated bird carcass | RCNE2  | S. Virchow | -                             | +                 | -       | +       | +       |
| 22     | Defeathering machine | SCDM4 | S. Newport | +                             | +                 | -       | +       | +       |
| 23     | Worker hand       | SCWH4       | S. Virchow | -                             | +                 | -       | +       | +       |
| 24     | Chopping board    | SCCB5       | S. Typhimurium | -                         | +               | -       | +       | +       |
| 25     | Knife swap        | SCKS4       | S. Virchow | -                             | -                 | +       | +       | +       |
| 26     | Post defeathering | SCPD2       | S. Virchow | +                             | +                 | -       | +       | +       |
| 27     | Post evisceration | SCPE4       | S. Virchow | -                             | -                 | -       | +       | +       |
| 28     | Neck skin of eviscerated bird carcass | SCNC4  | S. Virchow | +                             | +                 | -       | -       | +       |
| 29     | Worker hand       | ACWH6*      | S. Typhimurium | +             | +               | -       | -       | +       |
| 30     | Deboning cone     | ACDC6       | S. Newport | +                             | -                 | -       | +       | +       |
| 31     | Raw meat          | FPRM1       | S. Newport | -                             | -                 | -       | +       | +       |
| Total  |                   |             |             | 31                           | 31 00 00 31       | (16.12) (100) |

*Isolate (ACWH6) received gene bank accession number NCBI GenBank MG844415. S. Virchow = *Salmonella* Virchow, S. Typhimurium = *Salmonella* Typhimurium, S. Newport = *Salmonella* Newport*

Figure-3: Polymerase chain reaction assay for the detection of *tetB* gene of *Salmonella* isolates. Lane 1: TrackIT™ 100bp DNA ladder. Lane 2: Standard positive control of *Salmonella* spp. Lane 3: Negative control. Lanes 4-16: Negative samples.

In the present study, resistance <30% was recorded to antimicrobials, namely Norfloxacin, Ampicillin,
Azithromycin, Ciprofloxacin, Colistin, Streptomycin, Cefotaxime, Enrofloxacin, Amoxyclav, Gentamicin, Chloramphenicol, Amikacin, and Cefazidime. In the study, *Salmonella* isolates were found resistant to Ampicillin (21.43%), Amoxyclav (14.29%), and Cefotaxime (14.19%) which is a rising concern for India because increased use of β-lactam antibiotics to treat enteric infection, *Salmonella* spp. might be acquiring resistance to third-generation cephalosporin antibiotic in different parts of the world and leading to clinical treatment failure [22]. Isolates were susceptible to Amikacin (95.24%), Cefazidime (100.00%), and Chloramphenicol (95.24%) suggested that limited use and effective control by farmers on these compounds are associated with high susceptibility.

Scur *et al.* [23] found approximately 55% of resistance to Amoxicillin plus Clavulanic acid, Cefotaxime, Cefazidime, Amikacin, and Norfloxacin, while Ghazaey and Mirmomeni [24] observed 70–100% resistance to Gentamicin, Cefotaxime, Streptomycin, and Amoxicillin. Abunna *et al.* [25] observed 100% sensitivity to gentamicin and ciprofloxacin, whereas Ghoddusi *et al.* [26] observed it to Ampicillin, Cefazolin, Cefotaxime, Cefixime, Ceftriaxone, Enrofloxacin, Diflucloxacin, and Gentamicin which is found not in accordance with the observations of the present study.

Various serovars such as *Salmonella* Enteritidis, *S. Typhimurium*, *S. Virchow*, and *S. Newport* are important nontyphoidal causes of human salmonellosis caused by consumption of contaminated poultry products [26]. More than 53 serovars have been reported from India, and this number is on ever increasing. Various research workers isolated similar serotypes from poultry farm and processing environment, but the occurrence of *S. Virchow* (65.66) in the current study is higher than the previously isolated report [27]. Similar findings were reported by Khanna [7] who found *S. Virchow* (48%) and *S. Typhimurium* (24%), followed by *S. Infantis* (13%), *S. Indiana* (7%), *S. Enteritidis*, and *S. Hadar* (4%) each in samples collected from retail meat shops in New Delhi. Recently, research workers isolated *S. Newport* from chicken meat [28,29]. Report of *S. Newport* in a poultry farm and processing environment is a serious issue, and rapid rise of MDR *Salmonella* serovar Newport isolates over the past decade as important causes of human Salmonellosis [30].

Several serotypes are consistently found at a higher incidence, and the distribution of *Salmonella* serotypes from poultry sources varies geographically and changes over a period of time [31]. The high rates of serogroup *S. Virchow* in our studies taken together with previous data may suggest that this serogroup may be more adapted to poultry farm and processing environments under study. A total of 11 isolates remained untypable which were positive by PCR assay for *invA* gene but negative by serotyping has been termed as untypable. This may be attributed to the presence of rough mutant strains which lack the specific side chains responsible for “O” specificity or some additional abnormalities of the core structure [28].

All the tested *Salmonella* serotypes were found to carry Tetracycline resistance gene *tetA* (100%) whereas none of them were carrying *tetB* gene. Whereas, 5 isolates were found positive for *bla<sub>TEM</sub>* (16.12%) and none of the isolate was found to carry CTX-M gene. The prevalence of broad-spectrum β-lactamases resistance (*bla<sub>TEM</sub>* in the serovars from poultry farm and processing units was not uniformly distributed in samples analyzed. For *bla<sub>TEM</sub>* gene, two isolates were positive from each of *S. Typhimurium* (NIWH6 and ACWH6) and *S. Newport* (SCDM4 and RCKS4), while one isolate was positive for *S. Virchow* (RCPD4). Uniform distribution of phenotypic Tetracycline resistance (Doxycycline and Oxytetracycline) among all the serovars along with the presence of *tetA* gene indicates selective pressure on the *Salmonella* spp. for adopting resistance against Tetracycline group of antibiotics.

The overall occurrence of Tetracycline resistance and broad-spectrum β-lactamases resistance in *Salmonella* isolates was 100 and 16.12%, respectively. The findings in the present study regarding *tetA* and *tetB* gene were in corroborations with South *et al.* [10]. On the contrary Lebdah *et al.* [32] who reported 70 and 20%, prevalence for *tetA* and *tetB*, respectively.

The *tetA* gene associated with tetracycline efflux pumps was reported to be predominant in *Salmonella*, and *Escherichia coli* isolates from livestock and food animals, and it may present in mobile elements and is acquired by bacteria through horizontal gene transfer [33,34]. Result confirms good phenotypic and genotypic correlation for Tetracycline resistance among *Salmonella* isolates.

The findings for *bla<sub>TEM</sub>* gene in the current study are supported by the results of other researchers [35]. The cefotaximases (CTX-M-type extended-spectrum beta-lactamases) have become the most widespread β-lactamases over the past few years. In the current study, none of the serotypes was found to be positive for gene encoding CTX-M. Our report is in agreement...
with Wittum et al. [36], whereas our results are contradicting with reports of Riano et al. [37], who reported Salmonella serovars with the CTX-M gene, which might be due to the influence of the genomic environment on local dissemination of resistance genes among different bacterial genera [38] and antimicrobials that could not be extensively used among poultry which may confer selective pressure to acquire resistance.

Kodimalar et al. [39] reported that occurrence of tetracycline residue in feed samples reflects the extensive use of chlortetracycline agent in chicken production systems. Van Boeckel et al. [40] reported, in Asia, that antimicrobial consumption in chicken is expected to grow by 129% by 2030, wherein currently in India the issue of overuse of these antibiotics is of particular significance with South Coast of India, while the cities of Mumbai and Delhi are becoming antimicrobial consumption hotspots.

In the present study, phenotypic resistance to Tetracycline group of antibiotics with the presence of tetA gene is in correlation. This indicates selective pressure on Salmonella isolates leading to an increase in the prevalence of Tetracycline resistance posing a risk to human and animal health. However, drug-susceptible Salmonellae can also become resistant by acquiring drug resistance plasmids from other enteric pathogens in the intestinal tract of patients [41].

Our results confirm dissemination of multidrug-resistant S. Virchow, S. Typhimurium, and S. Newport from farm to processing environment which may pose a serious risk to human health. These serotypes may affect human by causing nontyphoidal Salmonellosis. Information on daily dose, duration of treatment, number of animals treated, and consumption data may be useful to relate the simultaneous existence of antimicrobial resistance [42]. In the present study, unfortunately, supportive information regarding antimicrobial usage of various other antimicrobials was not available; therefore, it was not possible to associate the observed resistances to use of antimicrobials.

Conclusion

This study revealed a significant rise in Tetracycline resistance with presence of tetA gene in Salmonella spp. indicating selective pressure for adopting resistance against tetracycline group of antibiotics. Dissemination of multidrug-resistant S. Virchow, S. Typhimurium, and S. Newport from farm to processing environment may pose a serious risk to human health, and these serotypes may affect human by causing nontyphoidal Salmonellosis.

Authors’ Contributions

RNW designed the experiment under the supervision of AMP. RJZ and RVG supervised work. Media preparation, sample collection, and bacteriological analysis were performed by RNW and VMV. Molecular work was performed by RNW, ZND, and AD. All authors participated in the draft and revision of the manuscript. All authors read and approved the final manuscript.

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Competing Interests

No persons from Vista Processed Foods Ltd. were involved at any stage of the study.

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