A Review of Poultry Product as a Source of Spreading Multidrug Resistant Salmonella: Public Health Importance

Farah Fanissa¹

¹ Master Degree Student of Veterinary Disease Science and Public Health Faculty of Veterinary Medicine, Universitas Airlangga, Indonesia

*E-mail: farah.fanissa@gmail.com

ABSTRACT

In the last few decades, foodborne disease has become one of the world's health problems with various pathogenic bacteria that accompanies the contamination of food products of animal origin. One of the foodborne diseases that is always reported every year is related to Salmonella contamination in poultry products which can cause Salmonellosis in humans. Salmonella contamination become important not because of its virulence ability to invade humans, but also because of its increased resistance to various clinical antimicrobial classes, with various cellular genetic elements that can be spread in humans along the food chain. The purpose of this review is to provide an overview of the role of poultry product in the spread of multidrug resistance Salmonella which may have implications for public health.

Keyword: Foodborne Disease; Salmonella; Virulence Factor; Multidrug-Resistance; Mobile Genetic Element

INTRODUCTION

Foodborne disease has become one of the global public health problems lately, given its implications for health and the economy. Various kinds of pathogens play a role in foodborne disease (Ejo et al., 2016). It is estimated that 17.9% of all foodborne diseases related to poultry and 19% of foodborne diseases associated with poultry are caused by Salmonella enterica contamination and infection O'Bryan et al., 2022). Foodborne disease caused by Salmonella infection, distributed in animals and foodstuffs of animal origin (Pires and Hald, 2010) and considered as the main carrier for humans (Ejo et al, 2016). In various parts of the world, foodborne disease caused by Salmonellosis, causes an increase in invasive disease, hospitalization and death (Pires and Hald, 2010) which can have a significant effect on children, the
elderly and immunocompromised (Ding and Fu, 2016). Globally, there are 94 million cases of gastroenteritis and 155,000 deaths caused by Salmonella infection each year (Yang et al, 2019).

Salmonella contamination occurs through consumption of contaminated food such as eggs, milk and poultry meat. Twenty percent of the world’s poultry products are contaminated with Salmonella and the bacteria can persist for a long time in the environment, animal facilities and through biofilm formation. In most outbreaks of Salmonellosis due to consumption of poultry products, it is known that S. Enteritidis and S. Typhimurium are the most isolated serovar (Afshari et al, 2018). Infections caused by Non-Typhoid Salmonella (NTS), particularly S. Enteritidis and S. Typhimurium are the most commonly reported infections associated with Salmonellosis in humans (Yang et al, 2019). S. Enteritidis and S. Typhimurium are pathogenic because of their ability to invade, replicate and survive in human host cells (Sodagari et al, 2020). The pathogenesis of Salmonella and its interaction with the host depends on several virulence factors encoded by many genes distributed on chromosomes and plasmids (Borges et al, 2019).

At the same time, antibiotic resistance in S. Enteritidis and S. Typhimurium has also become one of the most important public health problems worldwide. The emergence of resistance to broad-spectrum cephalosporins and fluoroquinolones is of great public health importance, considering that this class of antibiotics is critical for the management of human salmonellosis cases (Yang et al, 2019). This paper will review the role of poultry and their products that can act as a factor in the spread of multidrug resistant (MDR) Non-Typhoid Salmonella and aspects related to food safety with One Health approach to understand the impact on public health, animals, and the environment.

**DISCUSSION**

**Salmonella**

Bacteria from the genus Salmonella belong to the family *Entrobacteriaceae*, Gram negative, facultative anaerobic, non-producing spores, have petrichous flagella and motile (Cosby et al, 2015), except for S. Gallinarum and S. Pullorum (Jajere, 2019). Salmonella is able to reduce nitrate to nitrite, well grown at 35–40°C (Cosby et al, 2015), can metabolize nutrients chemoorganotrophically and unable to ferment lactose. Salmonella has the broadest predilection for the digestive tract of humans and animals. Salmonella is divided into 2 groups of species, *Salmonella enterica* and *Salmonella bongori*, based on the differences in their 16S rRNA. Based on biochemical properties and genomic linkages, *Salmonella enterica* was classified into six subspecies (S.
enterica subsp. enterica, S. enterica subsp. S. salmonae, S. enterica subsp. arizonae, S. enterica subsp. diarizonae, S. enterica subsp. houtenae and S. enterica subsp. indica (Jajere, 2019).

Through the Kauffman-White scheme, Salmonella is classified based on antigenic differences, namely flagellar (H), capsular (K) and somatic (O) (Heredia and García, 2018). S. enterica subsp. enterica is responsible for more than 99% of cases of human Salmonellosis, of which 1,531 serotypes are S. Typhimurium and S. Enteritidis (Heredia and García, 2018). Non-Typhoid Salmonellaa are zoonotic and are generalist hosts that can infect various warm-blooded animals, including humans (Arya et all, 2017). Salmonella serotypes, such as Enteritidis, Typhimurium, Newport, Heidelberg and Montevideo are known to contribute in Salmonellosis through their contamination of various food products including chicken, pork, eggs, vegetables and milk (Andino and Hanning, 2015). The distribution of Salmonella serotypes in various food products shown in table 1.

| Serotype       | Food Sources                        | References                          |
|----------------|-------------------------------------|-------------------------------------|
| S. Enteritidis | Poultry Meat, Egg, Retail Ground Turkey, Seafood | Carrasco et al., 2012; Yang et al., 2015 |
| S. Dublin      | Minced Beef, Chicken Meat, Goat and Camel Meat | Molla et al., 2003; Tadesse and Gebremedhin, 2015 |
| S. Infantis    | Organic Raw Chicken, Pork            | Rajan et al., 2016; Simpson et al., 2018 |
| S. Montevideo  | Beef                                | Ferrari et al., 2019                |
| S. Typhimurium | Chicken Meat, Sausages, Seafood, Watermelon, Pork, Dairy, Beef | Jarquinet et al., 2015; Bouchrif et al., 2009; D’Aoust, 1994; Simpson et al., 2018 |
| S. Heidelberg  | Retail Ground Chicken               | Rajan et al., 2016; Jarquinet et al., 2015 |
| S. Javiana     | Tomato                              | D’Aoust, 1994                       |
| S. Hadar       | Pork, Frozen Chicken, Duck and Seafood | Ferrari et al., 2019; Bangtrakulnonthet al., 2004 |
| S. Virchow     | Seafood, Egg                        | Simpson et al., 2018                |
| S. Derby       | Pork                                | Ferrari et al., 2019                |
Virulence Factors

Type III Secretion System (T3SS)

The main characteristics of virulence and factors in S. enterica serovars such as invasion or intracellular replication in host cells. These factors include flagella, capsule, plasmid, adhesion system and Type III Secretion System (T3SS) (Hassena et al, 2021). One of the major genetic elements, namely Salmonella Pathogenicity Island -1 (SPI1), determines the virulence ability among Salmonella serotypes (Lostroh and Lee, 2001). Enteropathogenic bacteria, including S. enterica have a type III secretion system (T3SS) which plays an important role in their virulence ability. This system allows the translocation of bacterial virulence proteins into the host cell cytosol (Akopyan et al., 2011)(Park et al., 2018). These proteins are known as effectors, which can modulate or interfere with various host cellular processes (Sun et al., 2016), facilitating bacterial colonization and survival (Feria et al., 2015). The central element of T3SS is the injectisome, a multi-protein machinery (Park et al., 2018) consisting of a needle complex (de Souza Santos and Orth, 2019). T3SS consists of a cylindrical basal body ~26 nm in diameter and ~32 nm in height (Kato et al., 2018), with a two-ring structure encompassing the bacterial inner and outer membranes (de Souza Santos and Orth, 2019). As well as the cytoplasmic structure that is used to sort effector proteins (Kato et al., 2018) and provide energy for the secretory process (Hu et al., 2017). T3SS measures about 3.5 MDa spanning the double membrane and protruding into the extracellular space. About 25 structural proteins and additional proteins are required for their assembly (Puhar et al., 2014).

Salmonella Pathogenicity Island (SPI)

The virulence factor of S. enterica is encoded by a conserved gene on Salmonella Pathogenicity Island (SPI) (Askoura and Hegazy, 2020). The existence of this SPI is obtained horizontally (Eade et al., 2019) which occurs through conjugation, transformation and transduction mechanisms (Pradhan and Negi, 2019) (Zishiri et all, 2016). There are five main SPIs (1-5) (Lamas et all, 2018), of which SPI-1 and SPI-2 contain a large number of virulence genes related to intracellular pathogenesis and co-encode T3SS (Wang et all, 2020). SPI-1 is 40-kb in size, which includes 39 genes encoding T3SS-1, their chaperone and effector proteins. As well as several transcriptional regulators that control the expression of virulence genes inside and outside SPI-1 (Lou et all, 2019). The expression level of the SPI-1 gene is dependent on the HIIA regulator encoded SPI-1, which directly activates...
the expression of the SPI-1 structural gene (Golubeva et al., 2016). SPI-1 T3SS is expressed by Salmonella in the early stages of infection, which can stimulate inflammation (Kim et al., 2018). In contrast, SPI-2 is required by Salmonella for growth in different host cells (Dhanani et al., 2015) (Jennings et al., 2017), including macrophages (Fardsanei et al., 2017). SPI-3 is used by Salmonella in the process of intracellular proliferation and Mg2+ uptake and systemic spread. And SPI-5 which plays an important role in the development of the infection process and intracellular survival (Bertelloni et al., 2017).

**Virulence Plasmid**

Non-Typhoidal Salmonella also carries a virulence plasmid (Dos Santos et al., 2019). Salmonella virulence plasmids are 50–90 kb in size with a low copy number (1-2 plasmids per chromosome) that can be transmitted (Lobato-Márquez, 2016). In *S. Typhimurium*, it has a size of ~90 kb (pSLT) (Passaris et al., 2018) with an 8 kb region and a highly converted gene sequence, termed the Salmonella plasmid virulence (spv) locus (Silva et al., 2017) and functions as serum resistance, adhesion, colonization and promote the growth and reproduction of bacteria in host cells and tissues (Wu et al., 2016). Virulence plasmids also encode genes required for systemic infection (Abraham et al., 2018), such as the pef gene (plasmid encoded fimbriae), which plays a role in adhesion to crypt epithelial cells and induction of proinflammatory responses (Silva et al., 2017); the spv gene which is used to suppress the host's innate immune response (Abraham et al., 2018) and the rck gene which is used to develop resistance capabilities to the host's innate immune complement system (Cheng et al., 2019) (Dos Santos et al., 2019).

**Fimbriae**

Through different virulence factors, Salmonella also develops an adhesin function on the fimbriae which are used to attach to host cells (Rehman et al., 2019). Salmonella uses its fimbriae through interaction with proteins on host cell receptors, to be able to carry out adhesion and colonization in the intestine (Hansmeier et al., 2017). Fimbriae are generally 0.5-10 nm long and 2-8 nm wide (Rehman et al., 2019). Fimbriae in Salmonella are generally grouped into classes according to their assembly mechanism, namely (1) curli fimbriae which are assembled through a nucleation-precipitation (N/P) process through deposition of the main subunit with the extracellular media nucleator (Dufresne et al., 2018); (2) chaperone-usher (CU) fimbriae are assembled using periplasmic chaperones and usher outer periplasmic membranes, to form the main subunit into the final external filament (Rehman et al., 2019) and (3) type IV fimbriae are assembled on the inner and outer membranes.
extended through the periplasm and outer membrane to the extracellular environment. These fimbriae can be assembled or disassembled using ATP (Dufresne et al., 2018). However, fimbriae in S. Enteritidishave different structures, these fimbriae are assembled using the CU system and consist of several subunits (Quan et al., 2019). In addition, it is also classified based on different clades, γ, κ, π, β, α and σ (Rehman et al., 2019). Among these clades, the lpf and fim genes belong to subclade γ1, sef subclade γ3, pef subclade κ and sdc in subclade σ (Quan et al., 2019).

Flagella

Bacterial motility comes from organelles called flagella. More than 40 genes are responsible for flagella assembly and its motor function (Kubori et al., 1992). In each strain of Salmonella, each has flagella of different types of H-antigens, with different primary structures (Asakura et al., 1966). Flagella are morphologically divided into three parts: filaments, hooks and basal structures (Aizawa, 1996). The basal body is an important part of flagella motor function (Kubori et al., 1992) and is morphologically divided into an inner membrane ring (MS), a rod and an outer ring (LP) (Jones and Macnab, 1990) which are embedded in the outer membrane. then extends into the periplasmic space. The MS ring structure is considered as the rotor, the rod as the shaft and the LP ring as the bushings. (Kubori et al., 1992). Filaments and hooks are on the outside of the cell (Aizawa, 1996), while the basal structure is anchored on the outer and inner membranes (Kawamoto et al., 2013). In Salmonella, the genes responsible for flagella formation are about 50 genes grouped into 17 operons, where each operon is divided into three classes according to the order of expression (Alzawa, 1996). The gene is flg, flh, fli or flj. While the genes responsible for flagella function are encoded by flagellar rotation (mot), chemotaxis (che) genes, and transmembrane signal transduction of chemotactic stimuli (tar, trg, tsr, etc.) (Kutsukake et al., 1990). Distribution of Virulence Factors among Salmonella Species is presented in table 2.
| Virulence Factor | Location | Salmonella species | Function | Reference |
|------------------|----------|--------------------|----------|-----------|
| *hilA* | Chromosome (SPI-1) | *S. enterica* | Transcriptional regulation of the genes of SPI-1, Modulation of colonization and invasion | Bottledoorn *et al.*, 2010; Song *et al.*, 2016; Cheng *et al.*, 2019 |
| *invA* | | | Invasive effector protein, production of proteins in T3SS | Cheng *et al.*, 2019; Awad *et al.*, 2020 |
| *sip* | | | Cytoskeleton rearrangement, Membrane ruffling, Invasion | Cheng *et al.*, 2019; Dos Santos *et al.*, 2019 |
| *sop* | | | Colonization and induces remodeling of actin | Ilyas *et al.*, 2017; Cheng *et al.*, 2019; Wang *et al.*, 2020 |
| *sif* | Chromosome (SPI-2) | | Invasion effector, NLRC4 inflammasome, SCV membrane stability, t3SS1-independent inflammation factor, luminal colonization | Beshiru *et al.*, 2019; Wang *et al.*, 2020; Hyeon *et al.*, 2021 |
| *sspH* | Chromosome (SPI-12) | *S. Enteritidis*, *S. Typhimurium* | Intracellular replication | Suez *et al.*, 2013; Shapo *et al.*, 2020 |
| *sef* | Chromosome | *S. Enteritidis*, *S. Gallinarum*, *S. Pullorum*, *S. Typhi*, *S. Dublin*, *S. Typhi* | Mediating attachment in host cells, Uptake or survival in macrophages | Rank *et al.*, 2009; Bottledoorn *et al.*, 2010; Hu *et al.*, 2019 |
| *pef* | Plasmid (pSLT) | *S. Enteritidis*, *S. Typhimurium* | Adhesion to crypt epithelial cells, biofilm growth, induction of a pro-inflammatory response | Silva *et al.*, 2017; Quan *et al.*, 2019; Awad *et al.*, 2020 |
TRANSMISSION

Poultry products are widely consumed globally where the presence of Salmonella bacteria is also found in live poultry, poultry environment, retail meat and meat products. *S. enterica* subsp. *enterica* can be transmitted to humans in different ways. On farms, Salmonella is often excreted in the feces. This allows for fecal-oral transmission. In addition, Salmonella vertical transmission occurs from chicken to egg. Therefore, humans can be contaminated through consumption of contaminated eggs (Monte et al, 2019). Environmental contamination with low antimicrobial levels can lead to an increase and persistence of the population of resistant bacteria. In addition, exposure of bacterial populations to antimicrobials can also result in the exchange of resistant genetic elements, which may include virulence genes (Monte et al, 2019). In addition, nosocomial transmission has also been found between animals of different species, which has implications for the ability of NTS serovars to survive and move from different environmental sources to susceptible hosts (Cheng et all, 2019). Transmission among *Salmonella* species in poultry products shown in table 3.

| Table 3. Transmission and contamination among *Salmonella* species in Poultry Products |
|---------------------------------|---------------------------------|---------------------------------|
| Transmission Routes | Sources of Contamination | References |
| Horizontal | Feed and drinking water, contamination, rodents and insects, environments, poor level of hygiene | Heydrickx *et al*., 2002; Macirowskiet *et al*., 2004; Rasschaert *et al*., 2008 |
| Vertical | Trans-ovarian | Van de Giessen *et al*., 1994 |

©2022. Fanissa. Open access under CC BY-SA license, doi:10.20473/mkh.v33i2.2022.131-162
Received:19-01-2022, Accepted:04-03-2022, Published online:08-05-2022
Available at https://e-journal.unair.ac.id/MKH/index
SALMONELLA CONTAMINATION IN POULTRY PRODUCTS

Various foodborne pathogens have been reported to be associated with consumption of poultry products (meat and eggs) (Lukicheva et all, 2016) (Zhang et all, 2021) caused by Non-Typhoid Salmonella (NTS) contamination (Chousalkar and Gole, 2016). Poultry has been considered as the main cause of Salmonellosis in humans through consumption of contaminated meat and eggs (Siddiky et all, 2021) (Toro et all, 2016). Poultry, especially chickens, are often colonized by Salmonella without symptoms (subclinical infection) (Antunes et al, 2016). Salmonella can enter and survive in the farm environment for long periods of time. According to recent research, it is known that the prevalence of Salmonella in the livestock environment ranges from 10 to 26% (Andino and Hanning, 2015). Infected poultry flocks also play a role as a reservoir for Salmonella which can be transmitted through the food chain (Saravanan et all, 2015) (Varmuzova et all, 2016). Poultry generally carry Non-Typhoid Salmonella (NTS) such as S. Enteritidis and S. Typhimurium (Wang et all, 2020) (Sarker et all, 2021). S. Enteritidis is known to be very well adapted to the cage and egg environment. Salmonella infection in poultry is often caused by S. Enteritidis which transmits vertically and trans-ovarianly. In addition, contamination caused by S. Typhimurium and other serovars occurs externally by penetrating the egg shell (Andino and Hanning, 2015). In addition, the surface of chicken meat can be contaminated with Salmonella from intestinal contents, faecal material or from cross-contamination during the slaughter process (da Cunha-Neto et al, 2018). (Banggera et all, 2019). In the few cases of salmonellosis outbreaks that occurred in Australia, the United States and the United Kingdom, a large number of outbreaks of gastrointestinal infections due to foodborne disease were associated with eggs. The pattern of consumption of raw or undercooked eggs is often associated with cases of salmonellosis. S. Enteritidis is a major

Human Traffic | Employee movement between different farms and contact with different species of animals
---|---
Poultry meat production chain | Scalding, defeathering, evisceration, chilling
Food Product | Contact surfaces, utensils and environmental, Retail chicken meat contamination

Nair et al., 2019; Zeng et al., 2021
Nauta et al., 2000; Nair et al., 2019
Nidaullahet al., 2017; Shang et al., 2019
concern for most of the poultry industry (Chousalkar and Gole, 2016).

Through a number of studies in various countries, the prevalence of Non-Typhoid Salmonella (NTS) contamination in chicken meat in the Hanoi area, Vietnam is 71.8% with the highest percentage of contamination occurring in traditional markets (90%) compared to supermarkets (52.6%). (Nhung et al, 2018). 14.89% of chicken meat in Northern India, much higher than the 7.01% poultry faeces sample (Sharma et al, 2019) and 63.6% in chicken meat in traditional markets in Guangdong region, China (Zhang et al., 2018) and 26.70% in the Malaysian region (Thung et al, 2016). Contamination among Salmonella species in poultry products shown in table 3.

MULTIDRUG RESISTANT SALMONELLA

Antibiotic resistance is a global phenomenon that results in the emergence of pathogens with resistance to clinically important antibiotics, thus requiring new treatment strategies (Nair et al, 2018). During the last few decades, there has been a global increase in the widespread and excessive use of antimicrobial agents. Both in humans and animals (Ammar et al, 2018) (Castro-Vargas et al, 2019), which contributes to the spread of antibiotic resistance (AMR) among Salmonella serotypes (Lenchenko et al, 2020) (Langata et al, 2019). This has resulted in an increase in the frequency of Salmonella serotypes which then develop their resistance ability to become multidrug resistant (MDR) which can cause new problems for human and animal health (Levantesi et al., 2012) (Siddiky et al., 2022). Several studies have shown that multidrug resistance among Salmonella serotypes was most frequently observed in ASSuT (ampicillin, streptomycin, sulfonamide and tetracycline), ACSSuT (ampicillin, chloramphenicol, streptomycin, sulfonamide and tetracycline) (Nair et al, 2018) (Xie et al, 2019) (Xiang et al., 2020). Also, fluoroquinolones, Extended Spectrum Beta-Lactamase (ESBL) (Aldrich et al, 2019), Quinolone (Abatcha et al, 2018) and Ciprofloxacin (González and Araque, 2019) (Harb et al, 2018).

Antimicrobial resistance in Salmonella can be intrinsic, acquired or adaptive (Christakiet et al., 2020). The intrinsic resistance mechanism occurs through decreased permeability of the outer membrane (lipopolysaccharide) and the natural activity of efflux pumps (Reygaert, 2018). Antibacterial resistance is acquired when a susceptible strain becomes resistant as a consequence of the evolution of a new strain, as a result of a mutation in a bacterial population or the acquisition of a specific resistance gene through horizontal gene transfer (HGT) (Verraeset et al., 2013). Adaptive resistance occurs because the modulation results in gene expression in response to environmental changes (stress, growth state, pH, ions concentrations, nutrient conditions and sub-inhibitory levels of antibiotics in the environment).
antibiotics) (Christakiet al., 2020). Multidrug resistance Salmonella isolates adapted to various resistance mechanisms i.e., modification of drug target sites, production of drug-degrading enzymes and overexpression of efflux pumps (Anbazhaganet al., 2019).

The modification of the drug target site, occurs through alteration of the Penicillin-Binding Protein (PBP) in β-lactam, which causes a change in the amount of antimicrobial that can bind to the PBP (Reygaert, 2018). In addition, quinolone resistance occurs as a result of chromosomal mutations in gyrA and parC, subunit of DNA gyrase and topoisomerase IV (Christakiet al., 2020) (Eichenberger and Thaden, 2019). Resistance to drugs that target the ribosomal subunit occurs through ribosomal mutations (aminoglycosides, oxazolidinones) in the erm gene. In addition, mutations in the enzymes dihydropteroate synthase (DHPS, Sulfonamide) and dihydrofolate reductase (DHFR, Trimethoprim) causing structural changes in the binding site with antimicrobial agents (Reygaert, 2018). Multidrug efflux systems are almost invariably encoded by chromosomal genes that are expressed either intrinsically or acquiredly (Poole, 2007) and occur on mobile genetic elements (transposons, integrons, plasmids) (Ruppez et al., 2015) whose acquisition from other resistance organisms (Poole, 2007) which capable of dispensing a wide variety of structurally different compounds (Arzanliuet al., 2017). Modifying enzymes may be plasmid mediated or chromosomal (Sefton, 2002). β-lactamases are the best example of antibiotic resistance mediated by modifying enzymes mechanism (Christakiet al., 2020) and can be acquired via horizontal gene transfer (Eichenberger and Thaden, 2019). Multidrug resistance mechanisms summarized in table 4.

| Table 4. Multidrug Resistance Mechanism |
|-----------------------------------------|
| **Mechanisms of Action** | **Antimicrobial Agents** |
| Efflux Systems | Tetracyclines | β-lactam |
| Mutation | Sulfonamide | Trimethoprim |
| Aminoglycosides | Oxazolidinones |
| Modification of the drug target site | Flouroquinolone | β-lactam |
| | Quinolone |
Mobile Genetic Element – Resistance Plasmid

Multidrug resistant Salmonella is transferred from food of animal origin through the food chain by carrying different Antibiotic Resistance Genes (ARGs) (Liu et al, 2020). Commensal bacteria and pathogens in the gut can exchange cellular genetic elements that mediate resistance (Maka and Popowska, 2016). ARGs carried by Salmonella are located on plasmids, chromosomes, transposons and transferable integrons by cellular genetic elements (MGE) (Ramatla et all, 2019) (Aziz et all, 2018) (Penha Filho et all, 19). DNA fragments encoded in cellular genetic elements can recombine with bacterial chromosomes or with other elements present in bacterial cells (Brown-Jaque et al., 2015). Plasmids are circular DNA extrachromosomal elements capable of replicating independently of the host genome (Mathers et al., 2015). Resistance plasmids are generally conjugative and can be mobilized (Sultan et al., 2018). Through the mechanism of conjugation, plasmids are transferred from the donor to the recipient cell, through contact-dependent transmission and an energy-driven process (Carattoli, 2011). Antimicrobial resistance plasmids were divided into 2 main groups, namely (1) narrow host group, incompatibility F(IncF) and (2) broad host group, IncA/C, IncL/M, and IncN (Mathers et al., 2015). The IncF plasmid in Salmonella is known to carry the genes blaTEM-1 (β-lactam), cmI (chloramphenicol) and integrons with the genes dreA (trimethoprim), aadA1, aadA2 (aminoglycosides) and sul3 (sulfonamides) (Garcia et al., 2014). Meanwhile, the IncA/A plasmid carried 10 AMR genes for more than five antimicrobial classes, such as straAB (aminoglycoside), sul2 (sulfonamide), tetAR (tetracycline), blaCMY-2 (β-lactam) and floR (chloramphenicol) (McMillan et al., 2020). Also, other genes encoding resistance to trimethoprim and cephalosporines (McMillan et al., 2019).

Mobile Genetic Element – Transposons and Insertion Sequences

Transposons (TN) are transposable elements that include small cryptic elements or insertion sequences (IS), transposons and transposition bacteriophages that facilitate the movement of DNA fragments from one location to another on bacterial chromosomes and plasmids (Tripathi and Tripathi, 2017) (Partridge et al., 2018). Insertion sequences (IS) are sandwiched between short, inverted and repeating sequences flanking the coding region of the gene (Brown-Jaque et al., 2015). From 10-40 base pairs at both ends (Sultan et al., 2018). The entire DNA fragment from one IS element to another is transposed as a complete unit (Brown-Jaque et al., 2015). Insertion sequences (IS) are classified according to different nuclease catalytic domains, namely DD (E/D), HUH, phosphoserine and phosphotyrosine site-specific recombinase, which can be found in transportase, invertase or resolvase (Razavi et al., 2020). Meanwhile,
transposons are categorized into two classes, namely (1) composite transposons (carrying various resistance genes that have identical structural and functional characteristics, with small DNA homology) and (2) complex transposons (three distinct but related families; Tn3, Tn21 and Tn2501 (Sultan et al., 2018). Transposons can be transmitted depending on transposition proteins (reverse transcriptase enzymes) i.e., autonomously (pol, gag and open reading frame or ORF genes in them) (Babakhani and Oloomi, 2018) or non-autonomously, which requires the presence of other transposons to move (Babakhani and Oloomi, 2018) Brown-Jaque et al., 2015). Several transposons associated with antimicrobial resistance include Tn5, Tn10 (kanamycin, neomycin, tetracycline) and Tn21 (streptomycin, spectinomycin, sulfonamide) (Tripathi and Tripathi, 2017).

Mobile Genetic Element – Integron

Integrons are mobile DNA elements consisting of site-specific recombination systems (Meng et al., 2017) that are capable of integrating, assembling and expressing resistance-related genes in the gene cassette structure (Tripathi and Tripathi, 2017). As well as transferring from one bacterium to another (Meng et al., 2017). In general, integrons have structures in the form of (1) intI genes encoding site-specific tyrosine recombinase enzyme (Kaushik et al., 2018) which facilitate gene transfer by sequential incorporation of genes at the attI recombination site; (2) the attI recombination site integrated with the gene cassette, located upstream of the intI gene (Escudero et al., 2015); and (3) the promoter (Pc) that regulates the expression of the captured gene (Pereira et al., 2020), resides within the intI gene (between the intI and attI sites) (Escudero et al., 2015) that is oriented to the integration point (Kaushik et al., 2018). Integran-mediated genes are regulated by gene cassettes. Each cassette consists of an open reading frame (ORF) together with an attC recombination site (Pereira et al., 2020). Gene cassettes are relatively small (500–1000bp) (Escudero et al., 2015), can be free-loop, are non-replicative and are found to be inserted inside the integron (Partridge et al., 2018). Integrons are grouped into five classes based on gene integration (IntI) namely classes 1, 2, 3, 4 and 5 (Kaushik et al., 2018). Class 1, 2 and 3 integrons can be found on mobile genetic cellular integrons, while class 4 integrons are found on chromosomal integrons (Sultan et al., 2018). Class 1 integrons were most frequently detected in terms of antimicrobial resistance (Ma et al., 2017) with linkage to the Tn402 transposon (Kaushik et al., 2018). Class I integrons with a high detection frequency were also found among multidrug resistant Salmonella which have conserved regions (5′-CS and 3′-CS) with a gene cassette in them (Gharieb et al., 2015). Integrons are known to play an important role in the spread of...
antimicrobial resistance Salmonella (McMillan et al., 2019) (Begum et al, 2016) (Lamas et al, 2016) through site-specific recombination to transfer resistance genes between defined sites (Partridge et al., 2018). Class I integrons carry aadA resistance determinants (streptomycin-spectomycin), trimethoprim (Sultan et al., 2018). Multidrug resistance mechanism mediated by horizontal gene transfer presented in table 5.

Table 5. Multidrug resistance mediated by mobile genetic elements (MGE)

| Mobile Genetic Elements | Gene | Antimicrobial Agents |
|-------------------------|------|----------------------|
| Plasmid Resistance      | blaTEM-1 | β-lactam |
|                         | blaCMY-2 |           |
|                         | drfA    | Trimethoprim |
|                         | sul2    | Sulfonamide |
|                         | sul3    |             |
|                         | straAB  | Aminoglycoside |
|                         | tetAR   | Tetracycline |
|                         | floR    | Chloramphenicol |
| Transposon (TN)&        | Tn5, Tn10 | Kanamycin |
| Insertion Sequences (IS)|       | Neomycin   |
|                         |         | Tetracycline|
|                         | Tn21    | Streptomycin |
|                         |         | Spectinomycin|
|                         |         | sulfonamide |
| Integron                | attI    | Most of      |
|                         | Intl    | antimicrobial agents |
|                         | aadA    | Streptomycin- |
|                         |         | Spectomycin  |
|                         |         | Trimethoprim |

MULTIDRUG RESISTANT SALMONELLA IMPLICATIONS ON HUMAN HEALTH

Antimicrobial resistance is considered as one of the main threats to human health, as well as a major concern for food safety, which in its transmission involves the food chain (Tollefson and Miller, 2000). Antibiotics are used in animal food production to promote growth, prevent (prophylaxis), treat (therapeutic), and control (metaphylaxis) infectious diseases (Bengtsson and Greko, 2014). The extensive use of antibiotics in animal production systems (Nair et al., 2018) has contributed to increased selection.
pressure on the emergence and spread of multidrug resistance Salmonella isolates (Parisi et al., 2018). Most human infections by MDR Non-typhoidal Salmonella (NTS) are generally of foodborne origin, with animals as reservoirs of resistance and retail meat acting as carriers of human disease (Glenn et al., 2013). The presence of antibiotics in food consumed by humans has its own implications for the development of antibiotic resistance by the human gut microbiome (Lekshmi et al, 2017). The complex route of transmission between farm animals, humans and transfer of AMR genes between bacteria makes the reservoir of AMR genes in livestock poses risks to animal and human health, considering that some of these resistant ones are zoonotic (Argudin et al, 2017). Increased antimicrobial resistance in Salmonella sp. as foodborne bacteria contribute to increasing human health consequences, such as increasing cases of foodborne disease and increasing number of treatment failures (Anderson et al., 2003). Antibiotic resistance in Salmonella is strongly influenced by strains: S. Enteritidis, S. Typhimurium, S. Typhimurium monophasic, S. Infantis and S. Derby, where all five can be found in humans and food products such as poultry meat and eggs (Peruzy et al., 2020).

RISK FACTORS OF MULTIDRUG RESISTANCE SALMONELLA

In recent years, the risk factors associated with multidrug resistance Salmonella isolates have received considerable attention (Hoelzer et al., 2010) and have been conducted around the world. Risk factors associated with salmonella multidrug resistance at farm include biosecurity management practices (Donado-Goody et al., 2012) and antimicrobial usage (Farzan et al., 2010). Season (Vico et al., 2020), cage system (Taddese et al., 2019), bird type flock size, downtime, environment (Odoch et al., 2017), disinfection (Queslati et al., 2022) and waste management (Jibril et al., 2020).

Meat consumption and contact in farm environment are also important risk factors for humans (Hoelzer et al., 2010). Food contact with surfaces, chicken slaughtered process and hygiene practices in wet market (Moe et al., 2017). Low or higher temperature during broiler transportation to the slaughterhouse (Arsenault et al., 2007) have been associated with the risk factors in chicken carcasses.

CONTROL AND PREVENTION

The application of Good Farming Practices (GFPs), Good Agricultural Practices (GAPs) and Good Manufacturing Practices (GMPs) is very important as a preventive measure against contamination caused by
Salmonella spp. from producers to consumers (Camino Feltes et al, 2017). To reduce the risk of AMR, surveillance of resistance in humans and foods of animal origin is important to measure the long-term effectiveness of any control measures. An integrated surveillance system helps measure and compare the prevalence rate of antibiotic resistance in the food chain (Thapa et al, 2019). For the poultry industry, it is very important to control Salmonella related to food safety, such as (i) this zoonotic agent can cause foodborne disease which has a negative impact on public health; (ii) Salmonella is important in terms of antimicrobial resistance; (iii), these bacteria can cause international restrictions on the import and export of chickens and eggs; and (iv) can reduce the health level of poultry (Pulido-Landínez, 2019). At the hatchery level, disinfection of eggs with chemicals, ozone, UV irradiation, electrostatic charging, pulsed light and plasma gas is known to prevent Salmonella contamination. Not only that, passive and active immune response-based strategies, feed modification and feed management can reduce the susceptibility of poultry to infections caused by Salmonella (Dar et al, 2017). To reduce the spread of antibiotic resistance through the food chain and the environment, the use of antibiotics must be carried out effectively, through: (i) limiting antibiotics to only therapeutic uses; (ii) ensure accurate disease diagnosis; (iii) using appropriate antibiotic agents; (iv) use of appropriate dosage and duration of treatment; (v) prohibit the use of antibiotics as growth promoters; and (vi) the use of antibiotics based on a veterinarian’s prescription (Sarter et al, 2015).

CONCLUSIONS

Foodborne disease caused by Salmonella contamination in poultry products (meat and eggs) has consequences for public health problems. The pathogenicity of Salmonella is controlled by various virulence genes found on chromosomes and plasmids, which affect attachment to host cells, invasion and replication in the host body and toxin production. In addition, poultry products have been considered to be a major source of multidrug resistant (MDR) Salmonella contamination which is influenced by genes related to virulence and antimicrobial resistance (AMR) related to the potential virulence of bacteria. The increase in the number of antimicrobial-resistant Salmonella strains has become a significant public health problem. Increased risk factors and rates of multidrug resistance Salmonella contamination has an impact on increasing public health problems and the risk of death from bacteremia which requires the integration of housing biosecurity, hygienic slaughter practices and good food product
processing, to ensure food safety from farm to table.

REFERENCES

Abatcha, M.G., Effarizah, M.E. and Rusul, G. 2018. Prevalence, Antimicrobial Resistance, Resistance Genes and Class 1 Integrons of Salmonella Serovars in Leafy Vegetables, Chicken Carcasses and Related Processing Environments in Malaysian Fresh Food Markets. Food Control. 91: 170-180.

Abraham, A., Stella, S., Ibidunni, B.S., Coulibaly, K.J., Funbi, J.T. and Isaac, A.A. 2019. Serotype Distribution and Virulence Profile of Salmonella enterica Serovars Isolated from Food Animals and Humans in Lagos Nigeria. Microbiol and Biotechnology Letters. 47(2): 310-316.

Afshari, A., Baratpour, A., Khanzade, S. and Jamshidi, A. 2018. Salmonella enteritidis And Salmonella typhimurium Identification in Poultry Carcasses. Iranian Journal of Microbiology. 10(1): 45.

Aizawa, S.I. 1996. Flagellar Assembly in Salmonella Typhimurium. Molecular Microbiology. 19(1): 1-5.

Akopyan, K., Edgren, T., Wang-Edgren, H., Rosqvist, R., Fahlgren, A., Wolf-Watz, H. and Fallman, M. 2011. Translocation of Surface-Localized Effectors in Type III Secretion. Proceedings of the National Academy of Sciences. 108(4): 1639-1644.

Aldrich, C., Hartman, H., Feasey, N., Chattaway, M.A., Dekker, D., Al-Emran, H.M., Larkin, L., McCormick, J., Sarpong, N., Le Hello, S. and Adu-Sarkodie, Y. 2019. Emergence of Phylogenetically Diverse and Fluoroquinolone Resistant Salmonella Enteritidis as a Cause of Invasive Nontyphoidal Salmonella Disease in Ghana. PLoS Neglected Tropical Diseases. 13(6).

Ammar, A. M., Abdeen, E. E., Abo-Shama, U. H., Fekry, E. dan KotbElmahallawy, E. 2019. Molecular Characterization of Virulence and Antibiotic Resistance Genes Among Salmonella Serovars Isolated from Broilers in Egypt. Letters in applied microbiology. 68(2): 188-195.

Anbazhagan, P.V., Thavitiki, P.R., Varra, M., Annamalai, L., Putturu, R., Lakkineni, V. R. and Pesingi, P.K. 2019. Evaluation of Efflux Pump Activity of Multidrug-Resistant Salmonella Typhimurium Isolated from Poultry Wet Markets in India. Infection and Drug Resistance. 12: 1081.

Anderson, A.D., Nelson, J.M., Rossiter, S. and Angulo, F.J. 2003. Public Health Consequences of Use of Antimicrobial Agents in Food Animals in the United States. Microbial Drug Resistance. 9(4): 373-379.
Andino, A. and Hanning, I. *Salmonella enterica*: Survival, Colonization and Virulence Differences Among Serovars. Scientific World Journal. 520179.

Antunes, P., Mourao, J., Campos, J. and Peixe, L. 2016. Salmonellosis: The Role of Poultry Meat. Clinical Microbiology and Infection. 22(2): 110-121.

Arsenault, J., Letellier, A., Quessy, S., & Boulianne, M. 2007. Prevalence and Risk Factors for Salmonella and Campylobacter spp. Carcass Contamination in Broiler Chickens Slaughtered in Quebec, Canada. Journal of Food Protection. 70(8): 1820-1828.

Arya, G., Holtslander, R., Robertson, J., Yoshida, C., Harris, J., Parmley, J., Nichani, A., Johnson, R. and Poppe, C. 2017. Epidemiology, Pathogenesis, Genoserotyping, Antimicrobial Resistance, and Prevention and Control of Non-Typhoidal *Salmonella* Serovars. Curr Clin Micro Rpt. 4: 43-53.

Asakura, S., Eguchi, G. and Iino, T. 1966. *Salmonella* Flagella: In Vitro Reconstruction and Over-All Shapes of Flagellar Filaments. Journal of Molecular Biology. 16(2): 302–IN11.

Askouma, M. and Hegazy, W.A.H. 2020. Ciprofloxacin Interferes with *Salmonella* Typhimurium Intracellular Survival and Host Virulence through Repression of Salmonella Pathogenicity Island-2 (SPI-2) Genes Expression. Pathogens and Disease. 78(1).

Awad, A., Gwida, M., Khalifa, E. and Sadat, A. 2020. Phenotypes, Antibacterial-Resistant Profile and Virulence-Associated Genes of *Salmonella* serovars Isolated from Retail Chicken Meat in Egypt. Veterinary World. 13(3): 440–445.

Aziz, S.A.A., Abdel-Latief, G.K., Shany, S.A. and Rouby, S.R., 2018. Molecular Detection of Integron and Antimicrobial Resistance Genes in Multidrug Resistant *Salmonella* Isolated from Poultry, Calves and Human in Beni-Suef Governorate, Egypt. Beni-Suef University Journal of Basic and Applied Sciences. 7(4): 535-542.

Babakhani, S. and Oloomi, M. (2018). Transposons: The Agents of Antibiotic Resistance in Bacteria. Journal of Basic Microbiology. 58(11): 905-917.

Bangtrakulnonth, A., Pornreongwong, S., Pulskirk, C., Sawanpanyalert, P., Hendriksen, R.S., Lo Fo Wong, D.M. and Aarestrup, F.M. 2004. *Salmonella* Serovars from Humans and Other Sources in Thailand, 1993-2002. Emerging Infectious Diseases. 10(1): 131–136.

Begum, K., Mannan, S.J. and Ahmed, A., 2016. Antibiotic Resistance, Plasmids and Integron Profile of *Salmonella* Species Isolated from Poultry Farm and Patients. Dhaka University
Journal of Pharmaceutical Sciences. 15(2): 209-214.

Bengtsson, B. & Greko, C. 2014. Antibiotic Resistance—Consequences for Animal Health, Welfare and Food Production. Upsala Journal of Medical Sciences. 119(2): 96-102.

Bertelloni, F., Tosi, G., Massi, P., Fiorentini, L., Parigi, M., Cerri, D. and Ebani, V.V. 2017. Some Pathogenic Characters of Paratyphoid Salmonella enterica Strains Isolated from Poultry. Asian Pacific Journal of Tropical Medicine. 10(12): 1161-1166.

Beshiru, A., Igbinosa, I.H. and Igbinosa, E.O. 2019. Prevalence of Antimicrobial Resistance and Virulence Gene Elements of Salmonella Serovars from Ready-To-Eat (RTE) Shrimps. Frontiers in Microbiology. 1613.

Borges, K.A., Furian, T.Q., Souza, S.N., Salle, C.T.P., Moraes, H.L.S. dan Nascimento, V.P. 2019. Antimicrobial Resistance and Molecular Characterization of Salmonella enterica Serotypes Isolated from Poultry Sources in Brazil. Brazilian Journal of Poultry Science. 21(1): 001-008.

Bouchrif, B., Paglietti, B., Murgia, M., Piana, A., Cohen, N., Ennaji, M.M., Rubino, S. and Timinouni, M. 2009. Prevalence and Antibiotic-Resistance of Salmonella Isolated from Food in Morocco. The Journal of Infection in Developing Countries. 3(01): 035-040.

Brown-Jaque, M., Calero-Cáceres, W. and Muniesa, M. 2015. Transfer of Antibiotic-Resistance Genes via Phage-Related Mobile Elements. Plasmid. 79: 1-7.

Camino Feltes, M.M., Arisseto-Bragotto, A.P. and Block, J.M. 2017. Food Quality, Food-Borne Diseases and Food Safety in The Brazilian Food Industry. Food Quality and Safety. 1(1): 13-27.

Carrasco, E., Morales-Rueda, A. and García-Gimeno, R.M. 2012. Cross-Contamination and Recontamination by Salmonella in Foods: A Review. Food Research International. 45(2): 545-556.

Carattoli, A. 2011. Plasmids in Gram Negatives: Molecular Typing of Resistance Plasmids. International Journal of Medical Microbiology. 301(8): 654-658.

Castro-Vargas, R., Fandiño-de-Rubio, L.C., Vega, A. and Rondón-Barragán, I. 2019. Phenotypic and Genotypic Resistance of Salmonella Heidelberg Isolated from One of The Largest Poultry Production Region from Colombia. Int. J. Poult. Sci. 18(12): 610-617.

Cheng, R.A., Eade, C.R. and Wiedmann, M. 2019. Embracing Diversity: Differences in Virulence Mechanisms, Disease Severity, and Host Adaptations Contribute to the Success of Nontyphoidal Salmonella as a
Foodborne Pathogen. Front Microbiol. 10:1368.

Chousalkar, K. and Gole, V.C. 2016. Salmonellosis Acquired from Poultry. Current Opinion in Infectious Diseases. 29(5): 514-519.

Christaki, E., Marcou, M. and Tofarides, A. 2020. Antimicrobial Resistance in Bacteria: Mechanisms, Evolution, and Persistence. Journal of Molecular Evolution. 88(1): 26-40.

Cosby, D.E., Cox, N.A., Harrison, M.A., Wilson, J.L. Buhr, R.J. and Fedorka-Cray, P.J. 2015. Salmonella and Antimicrobial Resistance in Broilers: A Review. Journal of Applied Poultry Research. 24(3): 408-426.

D’Aoust, J.-Y. 1994. Salmonella and The International Food Trade. International Journal of Food Microbiology. 24(1-2): 11-31.

da Cunha-Neto, A., Carvalho, L. A., Carvalho, R. C. T., dos Prazeres Rodrigues, D., Mano, S. B., de Souza Figueiredo, E. E. and Conte-Junior, C. A. 2018. Salmonella Isolated from Chicken Carcasses from a Slaughterhouse in The State of Mato Grosso, Brazil: Antibiotic Resistance Profile, Serotyping, and Characterization by Repetitive Sequence-Based PCR System. Poultry Science. 97(4): 1373-1381.

Dar, M.A., Ahmad, S.M., Bhat, S.A., Ahmed, R., Urwat, U., Mumtaz, P.T., Bhat, S.A., Dar, T.A., Shah, R.A. and Ganai, N. A. 2017. Salmonella typhimurium in Poultry: A Review.

World’s Poultry Science Journal. 73(02): 345–354.

de Souza Santos, M. and Orth, K. 2019. The Role of The Type III Secretion System in The Intracellular Lifestyle of Enteric Pathogens. Microbiology Spectrum. 7(3): 7-3.

Dos Santos, A.M., Ferrari, R.G. and Conte-Junior, C.A. 2019. Virulence Factors in Salmonella Typhimurium: The Sagacity of a Bacterium. Current Microbiology. 76(6): 762-773.

Dhanani, A. S., Block, G., Dewar, K., Forgetta, V., Topp, E., Beiko, R. G. and Diarra, M. S. 2015. Genomic Comparison of Non-Typhoidal Salmonella enterica Serovars Typhimurium, Enteritidis, Heidelberg, Hadar and Kentucky Isolates from Broiler Chickens. PLoS One. 10(6).

Ding, H. and Fu, T.J. 2016. Assessing The Public Health Impact and Effectiveness of Interventions to Prevent Salmonella Contamination of Sprouts. Journal of Food Protection. 79(1): 37-42.

Donado-Godoy, P., Gardner, I., Byrne, B.A., Leon, M., Perez-Gutierrez, E., Ovalle, M. V., Tafuur, M.A. and Miller, W. 2012. Prevalence, Risk Factors, and Antimicrobial Resistance Profiles of Salmonella from Commercial Broiler Farms in Two Important Poultry-Producing Regions of Colombia. Journal of Food Protection. 75(5): 874-883.

Dos Santos, A.M.P., Ferrari, R.G. and Conte-Junior, C.A. 2019. Virulence
Factors in *Salmonella typhimurium*: The Sagacity of a Bacterium. Curr Microbiol. 76(6): 762-773.

Dufresne, K., Saulnier-Bellemare, J. and Daigle, F. 2018. Functional Analysis of The Chaperone-Usher Fimbrial Gene Clusters of *Salmonella enterica* Serovar Typhi. Frontiers in Cellular and Infection Microbiology. 8: 26.

EFSA Panel on Biological Hazards (EFSA BIOHAZ Panel), Koutsoumanis, K., Allende, A., Alvarez-Ordóñez, A., Bolton, D., Bover-Cid, S., Chemaly, M., De Cesare, A., Herman, L., Hilbert, F., Lindqvist, R., Nauta, M., Peixe, L., Ru, G., Simmons, M., Skandamis, P., Suffredini, E., Dewulf, J., Hald, T., Michel, V., Niskanen, T., Ricci, A., Snary, E., Boelaert, F. and Davies, R. 2019. Salmonella Control in Poultry Flocks and Its Public Health Impact. EFSA Journal. 17(2).

Eichenberger, E.M. and Thaden, J.T. 2019. Epidemiology and Mechanisms of Resistance of Extensively Drug Resistant Gram-Negative Bacteria. Antibiotics. 8(2): 37.

Ejo, M., Garedew, L., Alebachew, Z. and Worku, W. 2016. Prevalence and Antimicrobial Resistance of *Salmonella* Isolate from Animal-Origin Food Items in Gondar, Ethiopia. Biomed Research International. Vol. 2016.

Eade, C.R., Bogomolnaya, L., Hung, C.C., Betteken, M.I., Adams, L.G., Andrews-Polymenis, H. and Altier, C. 2019. Salmonella Pathogenicity Island 1 is Expressed in The Chicken Intestine and Promotes Bacterial Proliferation. Infection and Immunity. 87(1): 503-18.

Escudero, J. A., Loot, C., Nivina, A., & Mazel, D. (2015). The Integron: Adaptation on Demand. Microbiology Spectrum. 3(2): 3-2.

Fardsanei, F., Dallal, M.M.S., Douraghi, M., Salehi, T.Z., Mahmoudi, M., Memariani, H. and Nikkhahi, F. 2017. Genetic Diversity and Virulence Genes of *Salmonella enterica* Subspecies *enterica* serotype Enteritidis Isolated from Meats and Eggs. MicrobPathog. 107: 451-456.

Farzan, A., Friendship, R.M., Dewey, C. E., Poppe, C. and Funk, J. 2010. Evaluation of the Risk Factors for Shedding Salmonella with or without Antimicrobial Resistance in Swine Using Multinomial Regression Method. Zoonoses and Public Health, 57, 85–93.

Feria, J.V.M, Lefebre, M.D., Stierhof, Y.D., Galán, J.E. and Wagner, S. 2015. Role of Autocleavage in The Function of a Type III Secretion Specificity Switch Protein in *Salmonella enterica* Serovar Typhimurium. MBio. 6(5).

Ferrari, R.G., Rosario, D.K., Cunha-Neto, A., Mano, S.B., Figueiredo, E.E. and Conte-Junior, C.A. 2019. Worldwide Epidemiology of Salmonella Serovars in Animal-Based Foods: a Meta-
Analysis. Applied and Environmental Microbiology. 85(14): 591-19.

Garcia, P., Hopkins, K. L., Garcia, V., Beutlich, J., Mendoza, M. C., Threlfall, J., Et Al. 2014. Diversity Of Plasmids Encoding Virulence and Resistance Functions In Salmonella enterica Subsp. enterica Serovar Typhimurium Monophasic Variant 4,[5], 12:i:- Strains Circulating In Europe. Plos One. 9: E89635

Gast, R.K. and Porter Jr, R.E. 2020. Salmonella infections. Diseases of Poultry. 717-753.

Gharieb, R. M., Tartor, Y. H., & Khedr, M. H. (2015). Non-Typhoidal Salmonella in Poultry Meat and Diarrhoeic Patients: Prevalence, Antibiogram, Virulotyping, Molecular Detection and Sequencing of Class I Integrons in Multidrug Resistant Strains. Gut Pathogens. 7(1): 1-11.

Glenn, L.M., Lindsey, R.L., Folster, J.P., Pecic, G., Boerlin, P., Gilmour, M. W., Harbottle, H., Zhao, S., McDermott, P.F., Fedorka-Cray, P. J. and Frye, J. G. (2013). Antimicrobial Resistance Genes in Multidrug-Resistant Salmonella enterica Isolated from Animals, Retail Meats, and Humans in the United States and Canada. Microbial Drug Resistance. 19(3): 175-184.

Golubeva, Y.A., Ellermeier, J.R., CottChubiz, J.E. and Slauch, J.M. 2016. Intestinal Long-Chain Fatty Acids Act as a Direct Signal to Modulate Expression of The Salmonella Pathogenicity Island 1 Type III Secretion System. MBio. 7(1).

Gonzalez, F. and Araque, M. 2019. Molecular Typing, Antibiotic Resistance Profiles and Biocide Susceptibility in Salmonella enterica Serotypes Isolated from Raw Chicken Meat Marketed in Venezuela. Germs. 9(2): 81.

Hansmeier, N., Miskiewicz, K., Elpers, L., Liss, V., Hensel, M. and Sterzenbach. 2017. Functional Expression of The Entire Adhesiome of Salmonella enterica Serotype Typhimurium. Sci Rep. 7: 10326

Harb, A., Habib, I., Mezal, E.H., Kareem, H.S., Laird, T., O’Dea, M. and Abraham, S. 2018. Occurrence, Antimicrobial Resistance and Whole-Genome Sequencing Analysis of Salmonella Isolates from Chicken Carcasses Imported into Iraq from Four Different Countries. International Journal of Food Microbiology. 284: 84-90.

Hassena, A. B., Haendiges, J., Zormati, S., Guermazi, S., Gdoura, R., Gonzalez-Escalona, N. dan Siala, M. 2021. Virulence and Resistance Genes Profiles and Clonal Relationships of Non-Typhoidal Food-Borne Salmonella Strains Isolated in Tunisia by Whole Genome Sequencing. International Journal of Food Microbiology. 337: 108941.
Heredia, N. and García, S. 2018. Animals as Sources of Food-Borne Pathogens: A Review. Animal Nutrition. 4(3): 250-255.

Herrera-Leon, S., McQuiston, J.R., Usera, M.A., Fields, P.I., Garaizar, J. and Echeita, M.A. 2004. Multiplex PCR for Distinguishing the Most Common Phase-1 Flagellar Antigens of Salmonella spp. Journal of Clinical Microbiology. 42(6): 2581–2586.

Hoelzer, K., Soyer, Y., Rodriguez-Rivera, L. D., Cummings, K.J., McDonough, P.L., Schoonmaker-Bopp, D.J., Root, T.P., Dumas, N.B., Warnick, L.D., Gro’hn, Y.T., Wledmann, M., Baker, K.N.K., Besser, T.E., Hancock, D.D. and Davis, M.A. 2010. The Prevalence of Multidrug Resistance is Higher among Bovine than Human Salmonella enterica Serotype Newport, Typhimurium, and 4, 5, 12: i− Isolates in the United States but Differs by Serotype and Geographic Region. Applied and Environmental Microbiology. 76(17): 5947-5959.

Hu, B., Lara-Tejero, M., Kong, Q., Galán, J.E. and Liu, J. 2017. In Situ Molecular Architecture of The Salmonella Type III Secretion Machine. Cell. 168(6): 1065-1074.

Hu, L., Stones, R., Brown, E.W., Allard, M.W., Ma, L.M. and Zhang, G. 2019. DNA Sequences and Predicted Protein Structures of Prote6 and sefA Genes for Salmonella Ser. Enteritidis Detection. Food Control. 96: 271-280.

Hyeon, J.Y., Li, S., Mann, D.A., Zhang, S., Kim, K.J., Lee, D.H., Deng, X. and Song, C.S. 2021. Whole-Genome Sequencing Analysis of Salmonella enterica Serotype Enteritidis Isolated from Poultry Sources in South Korea, 2010–2017. Pathogens. 10(1): 45.

Ilyas, B., Tsai, C.N. and Coombes, B.K. 2017. Evolution of Salmonella-Host Cell Interactions through a Dynamic Bacterial Genome. Frontiers in Cellular and Infection Microbiology. 7: 428.

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. Vet World. 12(4): 504-521.

Jarquin, C., Alvarez, D., Morales, O., Morales, A. J., López, B., Donado, P., Valencia, M.F., Arevalo, A., Munoz, F., Walls, I., Doyle, M.P. and Alali, W.Q. 2015. Salmonella on raw Poultry in Retail Markets in Guatemala: Levels, Antibiotic Susceptibility and Serovar Distribution. Journal of Food Protection. 78(9): 1642-1650.

Jennings, E., Thurston, T.L.M. and Holden, D.W. 2017. Salmonella SPI-2 Type III Secretion System Effectors: Molecular Mechanisms and Physiological Consequences. Cell Host Microbe. 22(2):217-231.

Jibril, A.H., Okeke, I.N., Dalsgaard, A., Kudirkiene, E., Akinlabi, O.C., Bello,
M.B., & Olsen, J.E. 2020. Prevalence and Risk Factors of Salmonella in Commercial Poultry Farms in Nigeria. PloS One. 15(9).

Jones, C.J. and Macnab, R.M. 1990. Flagellar Assembly in Salmonella Typhimurium: Analysis with Temperature-Sensitive Mutants. Journal of Bacteriology. 172(3): 1327-1339.

Kato, J., Dey, S., Soto, J.E., Butan, C., Wilkinson, M.C., De Guzman, R.N. and Galan, J.E. 2018. A Protein Secreted by The Salmonella Type III Secretion System Controls Needle Filament Assembly. Elife. 7.

Kaushik, M., Kumar, S., Kapoor, R. K., Virdi, J. S. & Gulati, P. 2018. Integrons in Enterobacteriaceae: Diversity, Distribution and Epidemiology. International Journal of Antimicrobial Agents. 51(2): 167-176.

Kawamoto, A., Morimoto, Y.V., Miyata, T., Minamino, T., Hughes, K.T., Kato, T. and Namba, K. 2013. Common and Distinct Structural Features of Salmonella Injectisome and Flagellar Basal Body. Scientific Reports. 3(1): 1-6.

Kim, S.I., Kim, S., Kim, E., Hwang, S.Y. and Yoon, H. 2018. Secretion of Salmonella Pathogenicity Island 1-Encoded Type III Secretion System Effectors by Outer Membrane Vesicles in Salmonella enterica Serovar Typhimurium. Frontiers in Microbiology. 9: 2810.

Kubori, T., Shimamoto, N., Yamaguchi, S., Namba, K. and Aizawa, S.I. 1992. Morphological Pathway of Flagellar Assembly in Salmonella Typhimurium. Journal of Molecular Biology. 226(2): 433–446.

Kutsukake, K., Ohya, Y. and Iino, T. 1990. Transcriptional Analysis of The Flagellar Regulon of Salmonella Typhimurium. Journal of Bacteriology. 172(2): 741-747.

Lamas, A., Fernandez-No, I.C., Miranda, J.M., Vázquez, B., Cepeda, A. and Franco, C.M. 2016. Prevalence, Molecular Characterization and Antimicrobial Resistance of Salmonella Serovars Isolated from Northwestern Spanish Broiler Flocks (2011–2015). Poultry Science. 95(9): 2097-2105.

Lamas, A., Miranda, J.M., Regal, P., Vázquez, B., Franco, C.M. and Cepeda, A. 2018. A Comprehensive Review of Non-enterica Subspecies of Salmonella enterica. Microbiol Res. 206: 60-73.

Langata, L.M., Maingi, J.M., Musonye, H.A., Kiuru, J. and Nyamache, A.K. 2019. Antimicrobial Resistance Genes in Salmonella and Escherichia coli Isolates from Chicken Droppings in Nairobi, Kenya. BMC Research Notes. 12(1): 1-6.

Lekshmi, M., Ammini, P., Kumar, S. and Varela, M.F. 2017. The Food Production Environment and The Development of Antimicrobial Resistance in Human Pathogens of
Animal Origin. Microorganisms. 5(1): 11.

Lenchenko, E., Blumenkrants, D., Vatnikov, Y., Kulikov, E., Khai, V., Sachivkina, N., Gnezdilova, L., Sturov, N., Sakhno, N., Kuznetsov, V., Strizhakov, A. dan Mansur, T. 2020. Poultry Salmonella Sensitivity to Antibiotics. Systematic Reviews in Pharmacy. 11(2): 170-175.

Levantesi, C., Bonadonna, L., Briancesco, R., Grohmann, E., Toze, S. and Tandoi, V. 2012. Salmonella in Surface and Drinking Water: Occurrence and Water-Mediated Transmission. Food Research International. 45(2): 587–602.

Liu, Y., Zhang, D.F., Zhou, X., Xu, L., Zhang, L. and Shi, X. 2017. Comprehensive Analysis Reveals Two Distinct Evolution Patterns of Salmonella Flagellin Gene Clusters. Frontiers in Microbiology. 8: 2604.

Liu, Y., Dyall-Smith, M., Marenda, M., Hu, H.W., Browning, G. and Billman-Jacobe, H. 2020. Antibiotic Resistance Genes in Antibiotic-Free Chicken Farms. Antibiotics. 9(3): 120.

Lobato-Márquez, D., Molina-García, L., Moreno-Córdoba, I., García-del Portillo, F. and Díaz-Orejas, R. 2016. Stabilization of The Virulence Plasmid pSLT of Salmonella Typhimurium by Three Maintenance Systems and Its Evaluation by Using a New Stability Test. Frontiers in Molecular Biosciences. 3: 66.

Lostroh, C.P. and Lee, C.A. 2001. The Salmonella Pathogenicity Island-1 Type III Secretion System. Microbes and Infection. 3(14-15): 1281-1291.

Lou, L., Zhang, P., Piao, R. and Wang, Y. 2019. Salmonella Pathogenicity Island 1 (SPI-1) and Its Complex Regulatory Network. Front Cell Infect Microbiol. 9:270.

Lukicheva, N., Ebel, E.D., Williams, M.S. and Schlosser, W.D. 2016. Characterizing the Concentration of Pathogen Occurrence Across Meat and Poultry Industries. Microbial Risk Analysis. 4: 29-35.

Ma, L., Li, A.-D., Yin, X.-L. and Zhang, T. 2017. The Prevalence of Integrons as the Carrier of Antibiotic Resistance Genes in Natural and Man-Made Environments. Environmental Science & Technology. 51(10): 5721–5728.

Maka, L. and Popowska, M. 2016. Antimicrobial Resistance of Salmonella spp. Isolated from Food. Roczniki Państwowego Zakładu Higieny. 67(4).

Magdy, O.S., Moussa, I.M., Hussein, H.A., El-Hariri, M.D., Ghereeb, A., Hemeeg, H.A., A-Maary, K.S., Mubarak, A.S., Alwarhi, W.K., Eljakee, J.K.and Kabli, S.A. 2020. Genetic Diversity of Salmonella enterica Recovered from Chickens Farms and Its Potential Transmission to Human. Journal of
Infection and Public Health. 13(4): 571-576.

Mathers, A.J., Peirano, G. and Pitout, J.D. 2015. The Role of Epidemic Resistance Plasmids and International High-Risk Clones in The Spread of Multidrug-Resistant Enterobacteriaceae. Clinical Microbiology Reviews. 28(3): 565-591.

McMillan, E.A., Gupta, S.K., Williams, L.E., Jové, T., Hiott, L.M., Woodley, T.A., Barrett, J.B., Jackson, C.R., Wasilenko, J.L., Simmons, M., Tillman, G.E., McClelland, M. and Frye, J.G. 2019. Antimicrobial Resistance Genes, Cassettes, and Plasmids Present in Salmonella enterica Associated with United States Food Animals. Frontiers in Microbiology 10: 832.

McMillan, E.A., Jackson, C.R. and Frye, J.G. 2020 Transferable Plasmids of Salmonella enterica Associated with Antibiotic Resistance Genes. Front. Microbiol. 11:562181.

Moe, A.Z., Paulsen, P., Pichpol, D., Fries, R., Irigler, H., Baumann, M.P.O. and Oo, K.N. 2017. Prevalence and Antimicrobial Resistance of Salmonella Isolates from Chicken Carcasses in Retail Markets in Yangon, Myanmar. Journal of Food Protection. 80(6): 947–951.

Molla, B., Alemayehu, D. and Salah, W. 2003. Sources and Distribution of Salmonella Serotypes Isolated from Food Animals, Slaughterhouse Personnel and Retail Meat Products in Ethiopia: 1997-2002. Ethiopian Journal of Health Development. 17(1): 63-70.

Monte, D.F., Lincopan, N., Fedorka-Cray, P.J. and Landgraf, M. 2019. Current Insights on High Priority Antibiotic-Resistant Salmonella enterica in Food and Foodstuffs: A Review. Current Opinion in Food Science. 26: 35-46.

Nair, D.V.T., Venkitanarayanan, K. and Johny, A.K. 2018. Antibiotic-Resistant Salmonella in The Food Supply and The Potential Role of Antibiotica Alternatives for Control. Foods. 7(10): 167.

Nhung, N.T., Van, N.T.B., Cuong, N.V., Duong, T.T.Q., Nhat, T.T., Hang, T.T.T., Nhi, N.T.H., Kiet, B.T., Hien, V.B., Ngoc, P.T., Campbell, J., Thwaites, G. and Carrique-Mas, J. 2018. Antimicrobial Residues and Resistance Against Critically Important Antimicrobials in Non-Typhoidal Salmonella from Meat Sold at Wet Markets and Supermarkets in Vietnam. Int J Food Microbiol. 266:301-309.

Nidaullah, H., Abirami, N., Shamila-Syuhada, A.K., Chuah, L.O., Nurul, H., Tan, T.P., Abidin, F.W.Z. and Rusul, G. (2017). Prevalence of Salmonella in Poultry Processing Environments in Wet Markets in Penang and Perlis, Malaysia. Veterinary World. 10(3): 286.
O’Bryan, C.A., Ricke, S.C. and Marcy, J.A. 2022. Public Health Impact of Salmonella spp. on Raw Poultry: Current Concepts and Future Prospects in The United States. Food Control. 132: 108539.

Odoch, T., Wasteson, Y., L’Abée-Lund, T., Muwonge, A., Kankya, C., Nyakarahuka, L., Tegule, S. and Skjerve, E. 2017. Prevalence, Antimicrobial Susceptibility and Risk Factors Associated with Non-Typhoidal Salmonella on Ugandan Layer Hen Farms. BMC Veterinary Research. 13(1): 365.

Parisi, A., Crump, J.A., Glass, K., Howden, B.P., Furuya-Kanamori, L., Vilkins, S., Gray, D.J. & Kirk, M.D. 2018. Health Outcomes from Multidrug-Resistant Salmonella Infections in High-Income Countries: A Systematic Review and Meta-Analysis. Foodborne Pathogens and Disease. 15(7): 428–436.

Park, D., Lara-Tejero, M., Waxham, M.N., Li, W., Hu, B., Galán, J.E. and Liu, J. 2018. Visualization of The Type III Secretion Mediated Salmonella-Host Cell Interface using Cryo-Electron Tomography. Elife. 7.

Partridge, S.R., Kwong, S.M., Firth, N. and Jensen, S.O. 2018. Mobile Genetic Elements Associated with Antimicrobial Resistance. Clinical Microbiology Reviews. 31(4): e00088-17.

Passaris, I., Cambré, A., Govers, S.K. and Aertsen, A. 2018. Bimodal Expression of The Salmonella typhimurium spv Operon, Genetics, 210(2): 621–635.

Penha Filho, R.A.C., Ferreira, J.C., Kanashiro, A.M.I., Junior, A.B. and da Costa Darini, A.L. 2019. Emergent Multidrug-Resistant Nontyphoidal Salmonella Serovars Isolated from Poultry in Brazil Coharboring blaCTX-M-2 and qnrB or blaCMY-2 in Large Plasmids. Diagnostic Microbiology and Infectious Disease. 95(1): 93-98.

Peruzzi, M.F., Capuano, F., Proroga, Y.T.R., Cristiano, D., Carullo, M.R. and Murru, N. 2020. Antimicrobial Susceptibility Testing for Salmonella Serovars Isolated from Food Samples: Five-Year Monitoring (2015–2019). Antibiotics. 9(7): 365.

Perreira, M. B., Österlund, T., Eriksson, K.M., Backhaus, T., Axelsson-Fisk, M. and Kristiansson, E. 2020. A Comprehensive Survey of Integron-Associated Genes Present in Metagenomes. BMC Genomics. 21(1): 1-14.

Piddock, L.J.V. 2006. Multidrug-Resistance Efflux Pumps? Not Just for resistance. Nature Reviews Microbiology. 4(8):, 629–636.

Pires, S.M. and Hald, T. 2010. Assessing The Differences in Public Health Impact of Salmonella Subtypes using a Bayesian Microbial Subtyping Approach for Source Attribution. Foodborne Pathogens and Disease. 7(2): 143-151.
Poole, K. 2007. Efflux Pumps as Antimicrobial Resistance Mechanisms. Annals of Medicine. 39(3): 162-176.

Pradhan D. and Negi, D.V. 2019 Stress-Induced Adaptations in Salmonella: A Ground for Shaping Its Pathogenesis. Microbiol Res. 229:126311.

Puhar, A. and Sansonetti, P.J. 2014. Type III Secretion System. Current Biology. 24(17): R784-R791.

Pulido-Landínez, M. 2019. Food safety-Salmonella Update in Broilers. Animal Feed Science and Technology. 250: 53-58.

Quan, G., Xia, P., Zhao, J., Zhu, C., Meng, X., Yang, Y., Wang, Y., Tian, Y., Ding, X. and Zhu, G. 2019. Fimbriae and Related Receptors for Salmonella enteritidis. Microbial Pathogenesis. 357-362.

Rajan, K., Shi, Z. and Ricke, S.C. 2016. Current Aspects of Salmonella Contamination in The US Poultry Production Chain and The Potential Application of Risk Strategies in Understanding Emerging Hazards. Critical Reviews in Microbiology. 43(3): 370-392.

Rank, D.L., Saeed, M.A. and Muriana, P.M. 2009. Cloning of Salmonella enterica Serovar Enteritidis Fimbrial Protein SefA as a Surface Protein in Escherichia coli Confers the Ability to Attach to Eukaryotic Cell Lines. Applied and Environmental Microbiology. 75(20): 6622-6625.

Rasschaert, G., Houf, K., Godard, C., Wildemauwe, C., Pastuszczak-Farak, M. and De Zutter, L. 2008. Contamination of Carcasses with Salmonella during Poultry Slaughter. Journal of Food Protection. 71(1): 146-152.

Razavi, M., Kristiansson, E., Flach, C. F. and Larsson, D. J. 2020. The Association Between Insertion Sequences and Antibiotic Resistance Genes. Msphere. 5(5): e00418-20.

Rehman, T., Yin, L., Latif, M.B., Chen, J., Wang, K., Geng, Y., Huang, X., Abaidullah, M., Guo, H. and Ouyang, P. 2019. Adhesive Mechanism of Different Salmonella Fimbrial Adhesins. Microbial Pathogenesis. 137: 103748.

Reygaert, W.C. 2018. An Overview of The Antimicrobial Resistance Mechanisms of Bacteria. AIMS Microbiology. 4(3): 482.

Ruppé, É., Woerther, P.L., and Barbier, F. 2015. Mechanisms of Antimicrobial Resistance in Gram-negative Bacilli. Annals of Intensive Care. 5(1)L 1-15.

Saravanan, S., Purushothaman, V., Murthy, T.R., Sukumar, K., Srinivasan, P., Gowthaman, V., Balusamy, M., Atterbury, R. and Kuchipudi, S.V. 2015. Molecular Epidemiology of Nontyphoidal

©2022. Fanissa. Open access under CC BY-SA license, doi:10.20473/mkh.v33i2.2022.131-162
Received:19-01-2022, Accepted:04-03-2022, Published online:08-05-2022
Available at https://e-journal.unair.ac.id/MKH/index
Salmonella in Poultry and Poultry Products in India: Implications for Human Health. Indian J Microbiol. 55(3):319-26.
Sarker, B.R., Ghosh, S., Chowdhury, S., Dutta, A., Deb, L.C., Sarker, B.K., Sultana, T. and Hossain, K.M.M. 2021. Prevalence and Antimicrobial Susceptibility Profiles of Non-Typhoidal Salmonella Isolated from Chickens in Rajshahi, Bangladesh. Vet Med Sci. 7(3):820-830.
Sarter, S., Ho, P.H. and To, K.A. 2015. Current Context of Food Safety in Vietnam: A Glance at Food of Animal Origin. Quality Assurance and Safety of Crops & Foods. 57-62.
Sefton, A.M. 2002. Mechanisms of Antimicrobial Resistance. Drugs. 62(4): 557-566.
Shang, K., Wei, B., Jang, H. K. and Kang, M. 2019. Phenotypic Characteristics and Genotypic Correlation of Antimicrobial Resistant (AMR) Salmonella Isolates from a Poultry Slaughterhouse and its Downstream Retail Markets. Food Control. 100: 35-45.
Sharma, J., Kumar, D., Hussai, S., Pathak, A., Shukla, M., Kumar, V.P., Anisha, P.N., Rautela, R., Upadhyay, A.K. and Singh, S.P. 2019. Prevalence, Antimicrobial Resistance and Virulence Genes Characterization of Nontyphoidal Salmonella Isolated from Retail Chicken Meat Shops in Northern India. Food Control. 104-111.
Siddiky, N.A., Sarker, M.S., Khan, M.S.R., Begum, R., Kabir, M.E., Karim, M.R., Rahman, M.T., Mahmud, A. and Samad, M.A. 2021 Virulence and Antimicrobial Resistance Profiles of Salmonella enterica Serovars Isolated from Chicken at Wet Markets in Dhaka, Bangladesh. Microorganisms. 9(5): 952.
Silva, C., Puente, J.L. and Calva, E. 2017. Salmonella Virulence Plasmid: Pathogenesis and Ecology. Pathogens and Disease. 75(6).
Simpson, K.M., Hill-Cawthorne, G.A., Ward, M.P. and Mor, S.M. 2018. Diversity of Salmonella Serotypes from Humans, Food, Domestic Animals and Wildlife in New South Wales, Australia. BMC Infectious Diseases. 18(1): 1-11.
Sodagari, H.R., Wang, P., Robertson, I., Habib, I. and Sahibzada, S. 2020. Non_Typhoidal Salmonella at The Human-Food-of-Animal-Origin Interface in Australia. J. MDPI Animals. 10(1192): 1-33.
Song, Q., Shen, X., Yang, Y., Zhang, D. and Gao, H. 2016. Genetically Similar Isolates of Salmonella enterica Serotype Enteritidis Persistent in China for a Long-Term Period. Journal of Food Science. 81(7): M1778-M1781.
Suez, J., Porwollik, S., Dagan, A., Marzel, A., Schorr, Y.I., Desai, P.T., Agmon, V., McClelland, M., Rahav, G. and Gal-Mor, O. 2013. Virulence
Gene Profiling and Pathogenicity Characterization of Non-Typhoidal Salmonella Accounted for Invasive Disease in Humans. PloS One. 8(3).

Sultan, I., Rahman, S., Jan, A.T., Siddiqui, M.T., Mondal, A.H. and Haq, Q.M.R. 2018. Antibiotics, Resistome and Resistance Mechanisms: A Bacterial Perspective. Frontiers in Microbiology. 9: 2066.

Sun, H., Kamanova, J., Lara-Tejero, M. and Galán, J.E. 2016. A Family of Salmonella Type III Secretion Effector Proteins Selectively Targets The NF-Kb Signaling Pathway to Preserve Host Homeostasis. PLoS Pathogens. 12(3).

Tadesse, G. and Gebremedhin, E.Z. 2015. Prevalence of Salmonella in Raw Animal Products in Ethiopia: a Meta-Analysis. BMC Research Notes. 8(1): 1-8.

Taddese, D., Tolosa, T., Deresa, B., Olani, A., & Shumi, E. 2019. Antibiograms and Risk Factors of Salmonella Isolates from Laying Hens and Eggs in Jimma Town, South Western Ethiopia. BMC Research Notes. 12(1): 1-7.

Tasmin, R., Gulig, P.A. and Parveen, S. 2019. Detection of Virulence Plasmid-Encoded Genes in Salmonella Typhimurium and Salmonella Kentucky Isolates Recovered from Commercially Processed Chicken Carcasses. Journal of Food Protection. 82(8): 1364-1368.

Thapa, S.P., Shrestha, S. and Anal, A.K. 2019. Addressing the Antibiotic Resistance and Improving the Food Safety in Food Supply Chain (Farm-to-Fork) in Southeast Asia. Food Control. 106809.

Thung, T.Y., Mahyudin, N.A., Basri, D.F., Wan Mohamed Radzi, C.W., Nakaguchi, Y., Nishibuchi, M. and Radu, S. 2016. Prevalence and Antibiotic Resistance of Salmonella enteritidis and Salmonella typhimurium in Raw Chicken Meat at Retail Markets in Malaysia. Poult Sci. 95(8):1888-93.

Tollefson, L. and Miller, M.A. 2000. Antibiotic use in food animals: controlling the human health impact. Journal of AOAC International. 83(2) 245-254.

Toro, M., Retamal, P., Ayers, S., Barreto, M., Allard, M., Brown, E.W. and Gonzalez-Escalona, N. 2016. Whole-Genome Sequencing Analysis of Salmonella enterica Serovar Enteritidis Isolates in Chile Provides Insights into Possible Transmission Between Gulls, Poultry and Humans. Applied and Environmental Microbiology. 82(20):6223-6232.

Tripathi, V. and Tripathi, P. 2017. Antibiotic Resistance Genes: An Emerging Environmental Pollutant. In Environmental Science and Engineering. 183-201. Springer, Cham.

Van de Giessen, A.W., Ament, A.J.H.A. and Notermans, S.H.W.
1994. Intervention Strategies for Salmonella Enteritidis in Poultry Flocks: a Basic Approach. International Journal of Food Microbiology. 21(1-2): 145-154.

Varmuzova, K., Kubasova, T., Davidova-Gerzova, L., Sisak, F., Havlickova, H., Sebkova, A., Faldynova, M. and Rychlik, I. 2016. Composition of Gut Microbiota Influences Resistance of Newly Hatched Chickens to Salmonella Enteritidis Infection. Frontiers in Microbiology. 7: 957.

Verraes, C., Van Boxstael, S., Van Meervenne, E., Van Coillie, E., Butaye, P., Catry, B., de Schaetzen, M.A., Huffel, X.V., Imberchts, H., Dicrick, K., Daube, G., Saegerman, C., De Block, J., Dewulf, J.and Herman, L. 2013. Antimicrobial Resistance in The Food Chain: A Review. International Journal of Environmental Research and Public Health. 10(7): 2643-2669.

Vico, J.P., Lorenzutti, A.M., Zogbi, A.P., Aleu, G., Sánchez, I.C., Caffer, M.I., Rosmini, M.R. and Mainar-Jaime, R.C. 2020. Prevalence, Associated Risk Factors, and Antimicrobial Resistance Profiles of Non-Typhoidal Salmonella in large Scale Swine Production in Córdoba, Argentina. Research in Veterinary Science. 130: 161-169.

Wang, J., Li, J., Liu, F., Cheng, Y. and Su, J. 2020. Characterization of Salmonella enterica Isolates from Diseased Poultry in Northern China Between 2014 and 2018. Pathogens. 9(2): 95.

Wang, M., Qazi, I.H., Wang, L., Zhou, G. and Han, H. 2020. Salmonella Virulence and Immune Escape. Microorganisms. 8(3): 407.

Wu, S.Y., Wang, L.D., Li, J.L., Xu, G.M., He, M.L., Li, Y.Y. and Huang, R. 2016. Salmonellaspv Locus Suppresses Host Innate Immune Responses to Bacterial Infection. Fish Shellfish Immunol. 58: 387-396.

Xiang, Y., Li, F., Dong, N., Tian, S., Zhang, H., Du, X., Zhou, X., Xu, X., Yang, H., Xie, J., Yang, C., Liu, H., Qiu, S., Song, H. and Sun, Y. 2020. Investigation of a Salmonellosis Outbreak Caused by Multidrug Resistant Salmonella Typhimurium in China. Frontiers in Microbiology. 11: 801.

Xie, T., Wu, G., He, X., Lai, Z., Zhang, H. and Zhao, J. 2019. Antimicrobial Resistance and Genetic Diversity of Salmonella enterica from Eggs. Food Science & Nutrition. 7(9): 2847-2853.

Yang, X., Wu, Q., Zhang, J., Huang, J., Chen, L., Liu, S., Yu, S. and Cai, S. 2015. Prevalence, Enumeration and Characterization of Salmonella Isolated from Aquatic Food Products from Retail Markets in China. Food Control. 57: 308-313.

Yang, X. and Wu, Q. 2019. Prevalence, Bacterial Load and Antimicrobial Resistance of Salmonella Serovars Isolated from Retail Meat and Meat...
Products in China. Frontiers in Microbiology. 10: 2121.
Zeng, H., De Reu, K., Gabriël, S., Mattheus, W., De Zutter, L. and Rasschaert, G. 2021. Salmonella Prevalence and Persistence in Industrialized Poultry Slaughterhouses. Poultry Science, 100(4), 100991.
Zhang, J., Luo, W., Liu, G., Wang, Y., Geng, S. and Pan, Z. 2021. High Genetic Similarity of Salmonella Enteritidis as a Predominant Serovar by An Independent Survey in 3 Large-Scale Chicken Farms in China. Poultry Science. 100(4): 100941.

Zhang, L., Fu, Y., Xiong, Z., Ma, Y., Wei, Y., Qu, X., Zhang, H., Zhang, J. and Liao, M. 2018. Highly Prevalent Multidrug-Resistant Salmonella from Chicken and Pork Meat at Retail Markets in Guangdong, China. Front Microbiol. 9:2104.

Zishiri, O.T., Mkhize, N. and Mukaratirwa, S. 2016. Prevalence of Virulence and Antimicrobial Resistance Genes in Salmonella spp. Isolated from Commercial Chickens and Human Clinical Isolates from South Africa and Brazil. Onderstepoort Journal of Veterinary Research. 83(1): 1-11.