



## A Review of *Listeria* and *Salmonella*: An Update on Description, Characteristics, Incidence, and Antibiotic Susceptibility

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**Abstract** | Foodborne pathogens have emerged as a significant public health and food safety concern worldwide. Over the years, the epidemiology of foodborne diseases has drastically changed. The emergence of newly identified foodborne pathogens has significantly added to these changes. Numerous bacteria have the potentials of being significant foodborne pathogens. These include *Staphylococcus aureus*, *Campylobacter jejuni/ coli*, *Escherichia coli* O157:H7, *Helicobacter pylori*, and *Arcobacter butzleri*. Others such as *Listeria monocytogenes* and *Salmonella* species (spp.) have been known pathogens for several years but have only in the past decades been discovered to be the most common foodborne bacterial pathogens. Their ability and potential to produce toxins causing morbidity or even mortality is enough pointers to the gravity of the situation. This review focuses on *Listeria monocytogenes* and non-typhoidal *Salmonella enterica* from vegetables and other food products, with emphasis on their description, characteristics, incidence, and antibiotic susceptibility. The review also explained the impacts and current status of these pathogens. Much progress has been made in these areas, but additional research is needed to control these pathogens.

**Keywords** | *Listeria*, *Salmonella*, Vegetables, Antibiotic resistance

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## INTRODUCTION

Fresh produce has become popular worldwide because of its proven importance as an essential component of healthy diets, source of minerals, nutrients, dietary fibre, and vitamins for humans (O'Shea et al., 2012). The WHO has recommended that diets rich in fruits and vegetables, as reduced vegetables and fruits consumption lead to poor health and an increased risk of non-communicable diseases (NCDs) (WHO, 2017). An estimated 5 million death globally were associated with insufficient use of vegetables and fruits (Afshin et al., 2019). However,

on the background benefits of this fresh produce, their production chain is complex, comprising of several critical steps which may affect microbial safety. Thus, there are growing incidences and outbreaks of foodborne pathogens connected with their consumption (Kawamoto and Bari, 2015; Abatcha et al., 2018).

Each year foodborne infections cause illnesses among 1 in 10 people, affecting about 33 million lives per year worldwide (WHO, 2016). In developed countries, 20–40% of intestinal distress is related to foodborne pathogens (Sharif et al., 2018). As for now, the burden of

illnesses caused by food-borne pathogens remains mostly unexplained (Scallan et al., 2011). Over the last two decades, the epidemiology of foodborne infections has changed considerably (Henao et al., 2015). The emergence and re-emergence of foodborne pathogens have significantly added to this change (Kawamoto and Bari, 2015). Most often, foodborne disease or illness is caused either by pathogenic viruses (Hepatitis A, Norovirus and Rotavirus) or bacteria (*Campylobacter jejuni*, *Escherichia coli*, *Listeria* and *Salmonella*) as well as intoxication caused by toxins produced by pathogens such as *Clostridium perfringens*, *Staphylococcus aureus* and *Bacillus cereus* (Sharif et al., 2018). Other less frequent foodborne illnesses occur due to natural contaminants or accidental chemical poisoning (Fung et al., 2018). Among the causes of foodborne causing pathogens, *Salmonella* spp. and *Listeria* spp. have an enormous economic, and emotional toll on the numbers of cases reported worldwide, despite regulatory efforts to address the situation (Scallan et al., 2011). These effects highlight the need for updated information related to the bacterial foodborne pathogens. This review provides an overview of *Listeria* and *Salmonella* from vegetables and other food products, with a focus on the description, characteristics, incidence, and antibiotic susceptibility.

## LISTERIA

### DESCRIPTION AND CHARACTERISTICS

The genus *Listeria* is a non-spore forming, Gram-positive, facultative anaerobe and coccoid to rod-shaped bacteria, which is actively motile via peritrichous flagella at room temperatures (20–25°C) (Adams and Moss, 2004). *Listeria* spp. are not encapsulated, with rounded ends, occurring singly or in short-chain and measuring at 0.4–0.5 µm in length by 1–2 µm in width of diameter and belongs to the family Listeriaceae (Ryser and Marth, 2007). Varieties of tests comprise of hemolysis, mannitol with acid production, D-xylose, L-rhamnose, and alpha-methyl-D-mannoside are carried to distinguish the *Listeria* spp. (Ryser and Marth, 2007). *Listeria monocytogenes* can utilise glucose, lactose, and rhamnose, and not able to use xylose under the aerobic condition; thus, rhamnose and xylose serve as a first test to distinguish *L. monocytogenes* from another *Listeria* spp. (Gasanov et al., 2005). The genus comprises of 17 species, including *L. innocua*, *L. monocytogenes*, *L. ivanovii*, *L. seeligeri*, *L. welshimeri*, *L. grayi*, *L. rocourtia*, *L. marthii*, *L. weihenstephanensis*, *L. fleischmannii*, including the newly classified *L. cornellensis*, *L. aquatica*, *L. grandensis*, *L. floridensis*, *L. booriae*, *L. riparia*, and *L. newyorkensis* (den Bakker et al., 2014; Weller et al., 2015a).

The primary human pathogen among *Listeria* species is *L. monocytogenes* that causes severe clinical conditions, such as meningitis, septicaemia, spontaneous abortion, and particularly listeriosis (Wang et al., 2012). A few other cases have been reported to be caused by *L. ivanovii*, *L. innocua*,

and *L. seeligeri* (Gasanov et al., 2005). On the other hand, *L. ivanovii* is known to be pathogenic to animals, such as ruminants (Bhunja, 2008). Naturally, *Listeria* species are known to be a psychotropic bacterium that can grow at low temperatures and may well grow at different temperatures (0°C - 45°C) with the extremely slow-growing rate at as low as -15 °C (Junttila et al., 1988; Walker et al., 1990). Moreover, *Listeria* spp. could grow at various pH ranging from 4.4 to 9.6 but shows the best possible growth at pH greater than 7 (George and Lund, 1992). Generally, the cells do not grow but may endure at pH values that are less than 4.3 (Montville and Matthews, 2008). According to Seeliger and Jones (1986), due to their ubiquitous nature, *Listeria* cells can stand high sodium chloride concentration and can grow in an environment of up to a 10% salt. *Listeria* is known to survive in concentrations of up to 30%, which is a significant food preservative in smoked salmon. Besides, *Listeria* spp. can survive in low water activity ( $a_w$ ) environment, they grow optimally at  $a_w$  values of 0.97 and can persist for a more extended period at the  $a_w$  values 0.83 in food drying processes (Montville and Matthews, 2008).

The survival and proliferation of *Listeria* genus in an environment are primarily due to its unique tolerance towards the potential of hydrogen (pH), water activity ( $a_w$ ), salt concentrations and temperature (Sleator et al., 2003; Liu et al., 2005). According to Liu (2006), environmental sources such as agricultural land, soil, sewage, surface water, and animal feeds have been known to be suitable for the multiplication and survival of *Listeria* species.

### LISTERIA MONOCYTOGENES

*L. monocytogenes* is a ubiquitous bacterium that possesses a mechanism of adaptability, including antibiotic resistance genes (Gandhi and Chikindas, 2007) as well as the formation of biofilm (Da Silva and De Martinis, 2013), which adheres to the surface of food processing equipment and facilities over months and years (Orsi et al., 2008). Due to the formation of biofilm, *L. monocytogenes* can tolerate ordinary disinfectants, sanitizers, and antimicrobials. This resistance directly causes contamination in food contact surface (Carpentier and Cerf, 2011).

The temperature range for the growth of *L. monocytogenes* is between -1.5 and 45°C, with the optimal temperature being 30–37°C (Lado and Yousef, 2007). The ability to multiply in a refrigeration temperature enables *L. monocytogenes* to contaminate food processing environments, such as cutting and chilling room, workers' hands, conveyor belt rollers, and processing equipment (Kerr et al., 1995; Koutsoumanis et al., 2010; Tompkin, 2002). More importantly, *L. monocytogenes* can be directly transmitted from animals to humans (Nightingale et al., 2005). *L. monocytogenes* had been found in cooked meat due to cross-contamination, a standard route of transmission of the pathogen from a contaminated

source to a clean source of produce and product directly or indirectly (Mylius et al., 2007). The route for transmission of *L. monocytogenes* in humans is mainly via contaminated foods; nevertheless, other transmission routes have been reported, which include nosocomial, vertical (mother to child) and occupational (Bell and Kyriakides, 2012; Saha et al., 2015).

*L. monocytogenes* has been classified at least into four evolutionary genetic lineages (Lineages I-IV) based on its flagellar (H) and somatic (O) antigens (Doumith et al., 2004). Lineage I (serovars 1/2a, 3b, 4b, 4d, 4e and 7) is highly pathogenic and is more commonly associated with human outbreak cases, whereas Lineage II (serovars 1/2a, 1/2c, 3c, 3a) is very prevalent in foods, farm and natural environments, which causes cases of human and animal listeriosis. Lineage III serotypes 4b, 1/2a, 4a and 4c and Lineage IV (serovar 4a, 4c) are usually animal pathogens and less pathogenic, which rarely cause human diseases (Doumith et al., 2004; Haase et al., 2014).

Three of the 13 recognised *L. monocytogenes* serovars 1/2a, 1/2b, and 4b were accountable for over 95% of human listeriosis cases (Doumith et al., 2004; Kasper et al., 2009). Serovar 1/2a accounts for almost over 50% of the *L. monocytogenes* isolated from the environment and foods. On the other hand, most of the human listeriosis cases globally have been caused by Lineage I serotype 4b isolates (Kathariou, 2002; Chemaly et al., 2008).

Over the years, several virulence factors have been known to be involved in the cellular mechanism as well as cytosolic proliferation, which are a vital process in the intracellular parasitic life cycle of *L. monocytogenes* (Vázquez-Boland et al., 2001). The existence of *Listeria* pathogenicity island 1 (LIPI-1), which harbours numerous essential virulence genes, has contributed immensely to the pathogenicity of these serotypes (Lim et al., 2016). The LIPI-1 comprised of six genes that play a dominant role in the pathogenicity of *L. monocytogenes* and are vital for phagosomal abscond (*bly*, *plcA*, *plcB*, *mpl*), movement and cell-to-cell spread (*act*), and gene regulation (*prfA*) (Vázquez-Boland et al., 2001). Several strains of *L. monocytogenes* display wide-ranging virulence and pathogenicity, whereas some strains are known to be naturally virulent causing severe human listeriosis, while others are avirulent and unable to produce an infection in the mammalian host (Liu et al., 2003a; da Silva et al., 2017). A number of multiple virulence factors exist in *L. monocytogenes*, which significantly regulate the pathogenicity, such as surface internalin (*inlA*, *inlC*, *inlJ*), invasion-associated protein (*iap*) actin (*actA*), phosphatidylinositol-phospholipase C (*plcA*), listeriolysin O (*blyA*), and virulence regulator (*prfA*) (Vázquez-Boland et al., 2001; Liu et al., 2007). From the varieties of putative virulent markers identified in *L. monocytogenes*, the internalins surface

protein is known to perform a significant function in the pathogenesis of human clinical listeriosis (Hadjilouka et al., 2016). Furthermore, internalin *inlA* and *inlB* genes that are carried by *L. monocytogenes* help in adherence and invasion of mammalian cells (Bierne et al., 2007). The broad families now consist of at least nine additional members, namely *inlC*, *inlC2*, *inlD*, *inlE*, *inlF*, *inlG*, *inlH*, *inlI*, and *inlJ*. These internalin genes are clearly demonstrated to be essential in the invasion of host epithelial cells and virulence (*inlA* and *inlB*), cell-to-cell spread (*inlC*), adherence (*inlF* and *inlJ*), and autophagy evasion (*inlK*) (Bierne et al., 2007; Dortet et al., 2011; Kirchner and Higgins, 2008).

According to Goldfine and Shen (2007), gene expression by transcriptional regulation plays an essential function in bacterial acclimatisation to its new environment. Another study by Glaser et al. (2001) stated that a bioinformatics study of the *L. monocytogenes* genome sequence has identified over 200 putative transcriptional regulators. Decisive regulatory factor A (*PrfA*) has an essential and central role in controlling the expression of virulence gene products. Moreover, *PrfA* was initially known as a regulatory factor that is relevant for *bly* transcription, and it has since been shown to regulate the expression of a growing number of bacterial gene products that are directly associated with virulence (Wang et al., 2017).

#### LISTERIA MONOCYTOGENES IN FOODS, EPIDEMIOLOGY, AND INCIDENCES

Regarded as the most important bacterial pathogen causing food contamination, food poisoning, and sporadic outbreaks, *Listeria* is a facultative anaerobic foodborne pathogen widely distributed in soil, sewage and foods. It is also found on the body of humans and animals (Marian et al., 2012). Fresh plant produce and food products of animal origin are well known to play a vital role in harbouring varying numbers of *L. monocytogenes* (Leong et al., 2015). Many studies and food survey conducted in Malaysia have reported findings of *L. monocytogenes* in numerous categories of foods, including raw leafy vegetables, burger patties, vegetarian burger patties, poultry and poultry product, seafood, and ready to eat (RTE) foods (Ponniah et al., 2010b; Adzitey et al., 2012b; Marian et al., 2012; Wong et al., 2012; Budiati et al., 2013). However, no study has been done on *Salmonella* and *Listeria* on varieties of leafy vegetables and chicken processing environment in Malaysia.

Although the pathogen can be killed via heat treatment during food processing (Muriana et al., 2002), food products can be re-contaminated during food handling, packaging and distributing (Lekroengsin et al., 2007). Outbreaks of listeriosis are mainly reported in developed countries as compared to developing countries due to the differences in diagnosis and reporting systems of listeriosis (WHO,

2016). Over the decade, more outbreak of listeriosis had occurred in the USA and Europe (CDC, 2008), where the reported incidences of listeriosis are between 0.11 to 11.3 cases per million people yearly in Europe (WHO, 2016). According to the European Food Safety Authority (EFSA, 2011), in the European Union between 2009 to 2013, there were 1645 confirmed cases of listeriosis that resulted in 270 deaths. The worldwide incidence of listeriosis outbreak is approximated to be around 1,795 to 1,860 cases per 100,000 people, with 445 to 210 cases leading to a fatality (USDA Economic Research Service, 2012). In the United States, estimates ranged from 1600 to 2500 cases of listeriosis each year, with 260 to 500 deaths (FDA, 2018). While in Canada, a recent national listeriosis outbreak linked to contaminated packaged meat products resulted in 56 patients, including 20 deaths (Centre for Health Protection, 2016). As in the Asia-Pacific region from 1991 to 2007, the Australian Government Department of Health (2004) reported, listeriosis cases ranged between 35 to 73 cases annually. Ministry of Health Singapore (2007) has reported up to 9 clinical cases between the periods of 2001 to 2007. In Malaysia, although there are no reported cases of listeriosis, there was an incidence in 2015 where there were 20,000 Gala and Granny Smith apple worth of RM82, 000 alleged to be contaminated with *Listeria* that had to be recalled after the outbreak of listeriosis from 11 states in the USA arising from the consumption of poisoned apples (The Malay Mail, 2015 January 20).

#### PREVALENCE AND ANTIBIOTIC RESISTANCE OF *LISTERIA MONOCYTOGENES* ISOLATED FROM VEGETABLES

There is a variation in the prevalence of *L. monocytogenes* in vegetables based on several studies, as revealed in Table 1. The prevalence among the surveys ranged from 0.6% to 34.4%. A prevalence of greater than 10% was reported in countries such as Malaysia, Nigeria, Turkey, Poland, and Spain. In another study, 4.1% *L. monocytogenes* was detected from vegetable samples collected in Nigeria (Bello et al., 2013). Lettuce in Spain (10.0%) and Norway (10.0%) had similar contamination rates. Also, *L. monocytogenes* were isolated from 3/90 (3.3%) raw vegetable samples (lettuce and sweet basil) in Thailand (Stonsaovapak et al., 2010). On the other hand, watercress RTE (ready-to-eat) and escarole (0.6%) from Brazil were the least contaminated sources (Sant'Ana et al., 2012; Maistro et al., 2012). A study in Malaysia on the incidence of *L. monocytogenes* in a variety of vegetables obtained from retail markets indicated that winged bean had the highest contamination (34.4%), followed by parsley (25%), Indian pennywort (25%), carrot (24%), and cabbage (21.9%) (Ponniah et al., 2010a). While a study in Nigeria by Ajayeoba et al. (2016) showed that lettuce (19.67%) and cabbage (28.28%) were the most contaminated (Table 1).

Data from Table 1 have shown a relatively significant

trend of *L. monocytogenes* in different countries, which is most likely due to several factors, such as minimal control programs and safety inspection of fresh produce (Harris, 2003), differences in agricultural practices, and growing international trades (Cabedo et al., 2008). Moreover, leafy vegetables are very prone to the contamination that originates from the irrigation water, soil, animal manures, and vegetation, due to their growing conditions (FAO/WHO, 2008), which will likely cause *L. monocytogenes* contamination in the main food chain (Ivanek et al., 2006). Other factors could be pre-harvest and post-harvest, such as processing, packaging, transportation, distribution, and marketing of vegetables, have the potential for multiplication and contamination (Brackett, 1994). Likewise, seasonal variation and climate, as well as geographical variations, such as longitude and latitude are also significant factors liable for the contamination of vegetables by pathogens (Matthews et al., 2014; Liu et al., 2013). Others may well be associated with cross-contamination as these vegetables are combined at retail points or even washed from the same water source (Bello et al., 2013).

The emergence of antibiotic resistance *Listeria* is a significant health concern all over the world. A study performed in Nigeria showed salad vegetables exhibited a resistance of 92.9% to ampicillin followed by 85.7% to oxacillin, the least resistance of 14.3% to ciprofloxacin and 21.4% to gentamicin. The antimicrobial resistance pattern displays that most isolates were resistant to at least one antimicrobial agent, but about 64.3% of the isolates were resistant to more than four antimicrobial agents (Bello et al., 2013). This survey showed that there is a lack of study or literature in response to the vegetables *L. monocytogenes* isolates to the antibiotic found. In Brazil, all *L. monocytogenes* isolated from RTE vegetables were susceptible to ciprofloxacin, oxacillin, vancomycin, cefoxitin, streptomycin, and erythromycin, but only two isolates exhibited resistance to tetracycline and penicillin G (Byrne et al., 2016).

#### PREVALENCE AND ANTIBIOTIC RESISTANCE OF *LISTERIA MONOCYTOGENES* FROM OTHER FOOD SOURCES

The increasing occurrence of antibiotic-resistant *Listeria* species among animals and other food samples have been reported (Abatcha, 2017; Abatcha et al., 2020). According to a study by Marian et al. (2012) in Central Malaysia where a total of 140 raw and RTE food samples were tested for *L. monocytogenes* was detected in 8.57% of the food samples. The study found *L. monocytogenes* in 33.3%, 25%, and 13.3% of burgers, minced meat, and sausages, respectively. The isolates exhibited high resistance to ampicillin and penicillin G (100%), while high susceptibility was displayed toward streptomycin (100%). Between 2009 to

2010, a total of 531 duck samples and their environments were studied for the occurrence of *Listeria* spp. in Penang, Malaysia, of which 15 samples (2.8%) were positive for *L. Monocytogenes*. Other *Listeria* spp. detected were *L. ivanovii* (3.6%), *L. innocua* (0.8%), *L. seeligeri* (0.6%), *L. welshimeri* (0.2%) and unknown *L. spp.* (0.9%) (Adzitey et al., 2013a). The 15 *L. monocytogenes* isolated from duck and their environment were susceptible to the majority of the antibiotics examined. The isolates resistant to nalidixic acid, tetracycline and norfloxacin in the order 100%, 7.0% and 7.0%, respectively (Adzitey et al., 2013a).

On the other hand, in Thailand, the overall prevalence of *Listeria* spp. from vegetables and raw meat samples was 16.8% (64/380). When the isolates were serotyped *L. monocytogenes* accounted for 4.7%, followed by *L. innocua* 6.6%, *L. ivanovii* 0.8%, *L. seeligeri* 0.5%, *L. grayi* 1.6% and *L. welshimeri* 2.6% (Stonsaovapak et al., 2010). Meanwhile, the level of resistance in *L. monocytogenes* isolated from raw meat and vegetables in Thailand was low (5.6%) compared to 16.0% *L. innocua*, 33.3% *L. ivanovii* and 50.0% *L. seeligeri*. No resistance was observed in *L. grayi* or *L. welshimeri*. Resistance to one antibiotic was more extensive than multiple resistances. Only *L. innocua* showed resistance to various antimicrobials (Stonsaovapak et al., 2010).

A two-year study in China aimed at investigating the incidence of *L. monocytogenes* isolates from retail RTE foods revealed that the average prevalence of *L. monocytogenes* was 6.87% (Shi et al., 2015). *L. monocytogenes* were detected in 8/31 (25.8%) of cold vegetable dishes in sauce, 9/131 (6.9%) of roast poultry, 4/62 (6.5%) of cooked meat, 2/32 (6.25%) of cold noodles in sauce and 2/84 (2.4%) of dairy product (Shi et al., 2015). Also, 80 isolates of *L. monocytogenes* from retail RTE foods in China were susceptible to mezlocillin and penicillin, with the highest resistance of 51.25% to clindamycin, followed by 23.75% to cephalothin and 12.5% to ampicillin (Shi et al., 2015). Twenty-seven isolates were sensitive to all 14 antibiotics tested with 17 strains resistant to more than two antibiotics, including six multi-resistant strains, that are resistant to more than ten antibiotics (Shi et al., 2015).

Jamali et al. (2013c) investigated a total of 446 samples of raw milk comprised of 240 from cow, 165 from sheep and 41 from goat for the presence of *Listeria* species between periods of September 2008 to August 2010 from a farm in Iran. The study found *Listeria* spp. in 22.5% raw cow milk, 16.4% raw sheep milk and 4.9% raw goat milk, respectively. The species isolated were 57.8% of *L. innocua*, 21.7% of *L. monocytogenes*, 12% of *L. welshimeri*, and 8.4% *L. seeligeri*. The 18 *L. monocytogenes* isolated from raw milk samples were divided into 61.1% serovar "1/2a, 3a", 27.8% serovar "1/2c, 3c", and 11.1% serovar "4b, 4d, 4e" (Jamali

et al., 2013c). Furthermore, the *Listeria* spp. isolates were 49.4% and 43.4% resistant to tetracycline and penicillin G but remained susceptible to vancomycin, gentamicin, and rifampicin (Jamali et al., 2013c).

Lotfollahi et al. (2017), in Iran, examined a total of 442 samples, comprised of 125 clinical specimens, 267 food samples (milk, cheese, sausage, chicken, and meat stock cubes) and 50 livestock (goat and sheep carcasses). The overall prevalence of *L. monocytogenes* was 4.97% (22/442), of which 8.8% were from 125 human samples, 2.99% from 267 food and 6% from 50 livestock samples. Twenty-two *L. monocytogenes* isolated from clinical, food and livestock samples in Iran were susceptible to linezolid, chloramphenicol, kanamycin, amoxicillin-clavulanic acid and tetracycline, whereas, 6 (27.2%) exhibited resistance to penicillin G and 2 (9%) of them showing intermediate susceptibility to rifampicin and clindamycin, respectively (Lotfollahi et al., 2017).

In another study by Wieczorek et al. (2012), a total of 812 bovine hides and carcasses were examined for the presence of *L. monocytogenes*. The isolates of *L. monocytogenes* found were 10.8% from the hide and 2.5% from carcasses. The isolate serotypes were (87.0%) 1/2a serotype, and 4 were 1/2c (Wieczorek et al., 2012). All the 54 *L. monocytogenes* strains obtained from bovine hide and carcasses by Wieczorek et al. were susceptible to trimethoprim-sulfamethoxazole, gatifloxacin, levofloxacin, penicillin, ampicillin, vancomycin, rifampin, and streptomycin (Wieczorek et al., 2012). Furthermore, many of the isolates were resistant to oxacillin (72.2%), clindamycin (37.0%), and ceftriaxone (13.0%) (Wieczorek et al., 2012). The summary of the prevalence of *Listeria* spp. in other foods from various countries is presented in Table 2.

## SALMONELLA

### DESCRIPTION AND CHARACTERISTIC OF SALMONELLA SPECIES

The genus *Salmonella* is an enteric Gram-negative, facultative anaerobic and non-spore forming bacillus with cell diameters ranging from 0.7 to 1.5  $\mu\text{m}$  and lengths from 2 to 5  $\mu\text{m}$ , belonged to the family Enterobacteriaceae (Tindall et al., 2005; Todar, 2008). They are chemotrophs and mostly have peritrichous flagella except for *S. Gallinarum* and *S. Pullorum*, which are severely pathogenic to poultry and are non-motile (Bhunja, 2008). *Salmonella* can grow and multiply at various environmental conditions outside a living host cell and are non-fastidious (Pui et al., 2011). They grow at temperatures ranging from 7– 48°C, with the lowest  $a_w$  at 0.995 and pH ranges are between 6.5 to 7.5 (Pui et al., 2011). *Salmonella* is relative heat sensitive and is killed at 60°C in 15 to 20 minutes at milk pasteurisation temperatures (Adams and Moss, 2008; Forsythe, 2011). The genus *Salmonella* comprised of two

species based on the sequence analysis differences, which are *Salmonella enterica* and *Salmonella bongori*. The latter group is divided into six subspecies (Adams and Moss, 2004). *S. enterica* contains more than 2500 serovars, and about 80 are commonly associated with Salmonellosis in animals and humans (de Freitas Neto et al., 2010). Among the *S. enterica*, *S. Typhimurium*, *S. Enteritidis*, *S. Hadar*, *S. Newport*, *S. Heidelberg*, and *S. Javiana* are the most frequently reported serotypes related with human foodborne illnesses in the United States (Suresh et al., 2006). On the other hand, *S. bongori* consists of 20 serotypes and is commonly associated with cold-blooded animals, but it can infect humans too (Bhunja, 2008).

The clinical pattern of human salmonellosis has been classified into four, namely typhoid fever, gastroenteritis, bacteremia, and chronic carrier state (Darby and Sheorey, 2008). The signs and symptoms of human salmonellosis comprise of vomiting, abdominal cramps, nausea, diarrhoea (or constipation), fever (> 37.5°C to 41.5°C), chills, headache, body aches, and blood in the stool or none (Bhunja, 2008). The symptoms of the infection most often appear around an incubation time of one week or longer after consumption of contaminated food and last for 1-7 days (Crump et al., 2008). The *Salmonella* infectious dose is ranging from 1 to 10<sup>10</sup> CFU/g depending on the strain. A single food source outbreak shows that 10<sup>10</sup> cells can cause salmonellosis (Yousef and Carlstrom, 2003; Bhunja, 2008).

Host factors, such as age, immune status, underlying illness, and condition of the intestinal tract control susceptibility to *Salmonella* infection (Pui et al., 2011). Nontyphoidal salmonellosis, which is a self-limited illness, is distributed worldwide and is the most commonly reported *Salmonella* infection. On the other hand, enteric fever caused by typhoidal *Salmonella* are remarkably related to high morbidity and mortality rates and frequently occur in low income developing nations (Hardy, 2004).

### SALMONELLA VIRULENCE GENES

As been known for a long time, virulence factors are produced by bacteria and other organisms, which add to their efficiency and allow them to achieve specific functions, such as attachment to cells, avoidance of the host's immune response, entrance into and exit out of the cells and obtaining nutrition from the host (Ibarra et al., 2009). Most *Salmonella* carries a different set of virulence factors, such as invasion capability and adhesion and the formation of toxin whose activation in the infected host will determine their pathogenic potentials (Tenor et al., 2004). The status of the host and that of the bacterium mostly determine the outcome of *Salmonella* infection. While the ability of an individual to come down with disease is primarily determined by host factors, such as

genetic, environmental and age, at the same time, the pathogenicity of the bacterium is determined by virulence gene or virulence factor (Ahmer et al., 1999). For *Salmonella* spp. to attain full virulence, it requires numerous genes, as it reflects a complex set of interactions within its host (Lhocine et al., 2015). For most of the genes, distinct regions on the chromosomal clusters, known as 'Salmonella pathogenicity islands' (SPIs) were found (Karunasagar et al. 2012; Que et al., 2013).

The essential virulence factors are encoded by genes located within the highly conserved *Salmonella* pathogenic islands (SPIs), while others are encoded by the genes located on a chromosome or virulence plasmid (pSLT) (Fàbrega and Vila, 2013). According to Fàbrega and Vila (2013) within the chromosome of *Salmonella enterica*, there are five most essential pathogenicity islands (SPI-1, SPI-2, SPI-3, SPI-4, and SPI-5), while *Salmonella bongori* possesses only four (SPI-2 is absent). The pathogenicity islands SPI-1 and SPI-2 genes code for proteins regulating the T3SS (Type Three Secretion System), which enabled the carriage of *S. enterica* proteins from the bacterial cell straight into the cytosol of host cells (Farhad, 2013). For T3SS to operate appropriately, it requires five distinct types of proteins, such as effector, translocator, chaperone, a transcriptional regulator, and apparatus protein (Portaliou et al., 2016). There is also a structural component of T3SS called Injectisome, preserved among diverse pathogenic T3SSs and looks like flagellar T3SS (Galán and Collmer, 1999; Cornelis et al., 2000). Most often, the virulence genes that are linked to the intestinal phase of infection are located in the pathogenicity islands (SPI-1 and SPI-2) and the remnant SPIs are needed for essential functions, such as magnesium and iron uptake, fimbrial expression, intracellular survival, the development of systemic infections and multiple antibiotic resistance (Almeida et al., 2013; Campioni et al., 2012; Siriken, 2013).

Some virulence genes are encoded on prophages that are incorporated into the *Salmonella* chromosome. Virulence genes *grvB*, which encodes a translocated effector protein, is harboured by Prophage Gifsy-1 (Coombes et al., 2005). Similarly, Gifsy-2 plays a significant role in virulence through *sodCI*, which encodes Cu/Zn periplasmic superoxide dismutase involved in the protection against oxidative stress, and *gtgE*, encoding a protein of unknown function (De Groote et al., 1997; Ho et al., 2002). The *spvR* ABCD genes, encoded in the *Salmonella* virulence plasmid, are necessary for systemic infection (Guiney et al., 1995), with *SpvB* functioning as a mono-ADP-ribosyl transferase involved in actin depolymerisation (Lesnick et al., 2001). The *slyA* (transcriptional regulator) is being involved in the resistance to macrophage survival, oxidative stress, and virulence in the mouse model (Watson et al., 1999).

**Table 1:** The prevalence of *L. monocytogenes* isolated from vegetables from various countries.

Country samples	Year	Vegetable	Prevalence (%)	References	
Brazil	2001	Watercress RTE	4.0	Porto and Eiroa (2001)	
		Watercress RTE	5.6	Sant'Ana et al. (2012)	
		Watercress RTE	0.6	Maistro et al. (2012)	
	2008	Lettuce	4.0	Porto and Eiroa (2001)	
		Lettuce RTE	3.3	Sant'Ana et al. (2012)	
		2009	Cabbage	0.9	Oliveira et al. (2010)
		2008	Escarole	0.6	Sant'Ana et al. (2012)
		2011	Escarole	7.7	Maistro et al. (2012)
		2004	Spinach RTE	9.1	Fröder et al. (2007)
		Spinach RTE	6.0	Sant'Ana et al. (2012)	
2008	Mixed greens RTE	5.3	Sant'Ana et al. (2012)		
2001	Parsley	4.5	Porto and Eiroa (2001)		
	2009	Parsley	4.5	Oliveira et al. (2010)	
Turkey	2007	Watercress RTE	5.0	Aytac et al. (2010)	
		Basil RTE	0.9	Aytac et al. (2010)	
		Parsley	10.5	Aytac et al. (2010)	
Spain	2001	Lettuce	10.0	Soriano et al. (2001)	
		Lettuce RTE	2.0	Soriano et al. (2001)	
Norway	2002	Lettuce	10.0	Johannessen et al. (2002)	
Malaysia	2009	Parsley	25.0	Ponniah et al. (2010a)	
		Cabbage	21.9	Ponniah et al. (2010a)	
		Carrot	24.2	Ponniah et al. (2010a)	
		Cucumber	21.9	Ponniah et al. (2010a)	
		Indian pennywort	25.0	Ponniah et al. (2010a)	
		Winged bean	34.4	Ponniah et al. (2010a)	
	2012	Bean sprout	20	Jamali et al. (2013a)	
	Lettuce	5.6	Jamali et al. (2013a)		
Thailand	2010	Vegetables	3.3	Stonsaovapak et al. (2010)	
Nigeria	2013	Lettuce	19.67	Ajayeoba et al. (2016)	
		Cabbage	28.28	Ajayeoba et al. (2016)	
	2013	Vegetables	4.1	Bello et al. (2013)	
Poland	2014	Parsley	10.0	Szymczak et al. (2014)	
Korea	2013	Lettuce	2.0	Ding et al. (2013)	
	2010	Sprouts	0.9	Seo et al. (2010)	

**Table 2:** Prevalence (%) of *Listeria* spp. in other foods from various countries.

Country	Samples	Serovars	Prevalence (%)	References
Malaysia	Raw and RTE food	<i>L. monocytogenes</i>	8.57	Marian et al. (2012)
Malaysia	Ducks	<i>L. monocytogenes</i> , <i>L. ivanovii</i> , <i>L. innocua</i> , <i>L. seelingeri</i> , <i>L. welshimeri</i>	2.8	Adzitey et al. (2013)
Thailand	Raw meat and vegetables	<i>L. monocytogenes</i> , <i>L. ivanovii</i> , <i>L. innocua</i> , <i>L. seelingeri</i> , <i>L. grayi</i> , <i>L. welshimeri</i>	16.8	Stonsaovapak et al. (2010)
China	Reatil RTE food	<i>L. monocytogenes</i>	6.87	Shi et al. (2015)
Iran	Raw milk	<i>L. innocua</i> , <i>L. monocytogenes</i> , <i>L. welshimeri</i> , <i>L. seelingeri</i>	22.5	Jamali et al. (2013)
Iran	Food samples and carcasses (goat and sheep)	<i>L. monocytogenes</i>	4.97	Lotfollahi et al. (2017)
Poland	Bovine hides and carcasses	<i>L. monocytogenes</i>	10.8	Wieczorek et al. (2012)

Moreover, genes such as *sipD*, *sopA*, *invA*, *sipA*, *sopE* *sopB* and *sopD* are encoded by SPI-1, with the function to allow *S. Enteritidis* to invade non-phagocytic and phagocytic cells. Whereas, the SPI-2-encoded genes, such as *ssrA* and *ssaR* allow *S. Enteritidis* to replicate and survive in host cells, particularly in macrophages (Fardsanei et al., 2017; Campioni et al., 2012; Hur et al., 2011). Other encoded virulence genes, thought to be significant, include *sitC* (Janakiraman and Slauch, 2000) and *iroN* (Baumler et al., 1998), where both are involved in iron acquisition, and *cdtB*, a putative toxin-encoding gene (Haghjoo and Galan, 2004).

#### SALMONELLA IN FOODS; EPIDEMIOLOGY AND INCIDENCE

Most of *Salmonella* spp. is capable of colonising a broad range of hosts and all the main livestock species (poultry, cattle, pigs, dogs, cats and reptiles) and is often asymptomatic (Newell et al., 2010; Abatcha et al., 2013; Abatcha et al., 2014c). More importantly, *Salmonella* cells are easily transferred to chicken carcasses through faecal contamination during transportation to slaughterhouses. A more spread of cells may occur during processing stages, leading to cross-contamination (Carrasco et al., 2012). Poultry and eggs are the primary reservoirs for *Salmonella*, and both singly or in combination have been documented as essential causes of salmonellosis (Altekruse et al., 1997). If already infected, the live chicken can harbour and spread the *Salmonella* cells to other birds using lateral transmission, mainly through faeces, water, soil, dust, litter, feeds, and feathers (Carrasco et al., 2012). Furthermore, the trans-ovarian infection does occur, and chicks hatching from these infected eggs might excrete the bacterium, infecting other chicks (Rabsch et al., 2003).

Fresh produce grown in developing nations where animal manures are commonly used as natural fertilisers might add to the contamination of pathogens to the field, and run-off waters can contaminate water meant for irrigation (Heaton and Jones, 2008). Handling processes from storage and rinsing to cutting are also potential causes of contamination. Also, insects are possible contamination sources, as contaminated flies are a potential vector of *Salmonella* spp. to fruits (Heaton and Jones, 2008).

Nontyphoidal *Salmonella* (NTS) causes an estimated 93.8 million incidents of gastroenteritis, with 155,000 deaths. While typhoidal *Salmonella* causes about 22 million typhoid fever incidents, with 210,000 typhoids fever-related fatality and 5.4 million episodes of paratyphoid fever worldwide (Buckle et al., 2012; Majowicz et al., 2010). In developed countries, cases of typhoid fever are sporadic, yet, it is an essential disease in developing countries (Buckle et al., 2012). NTS, on the other hand, are the second most commonly recorded causes of human

zoonotic diseases, after campylobacteriosis (Majowicz et al., 2010; Abatcha et al., 2014a, 2014b; Goni et al., 2017).

In the United States, salmonellosis is the most common infection recorded (8,256 diseases; 17.6 illness per 100,000 persons) and lead to the most significant number of hospitalisations (2,290) and deaths (450) (Cummings et al., 2012). Similarly, *Salmonella* is also one of the most commonly recorded causes of foodborne diseases in Europe, with approximate 108, 614 reported human case in 2009 (23.7 cases per 100,000 populations) (Duggan et al., 2012). Salmonellosis is a notifiable disease in Australian and New Zealand with an incidence rate of 49 and 24 cases per 100,000 population in the years 2012 and 2011, respectively (Lal et al., 2012; Stephen et al., 2017). The estimated incidence of *Salmonella* infection in Germany, Japan, and the Netherlands was 120, 73, and 16 cases per 100,000 population, respectively (Thorns, 2000). Often, there is a lack of official *Salmonella* surveillance data in much of the developing countries, although it is estimated that 22.8 million cases occur yearly with 37,600 deaths (Majowicz et al., 2010).

The estimated economic burden due to salmonellosis is USD 210 per outpatient, USD 5,797 per inpatient with enteric illness, USD16, 661 per inpatient with invasive infection and USD 4.63 million per premature death (Adhikari et al., 2004). Moreover, the estimated country-wide economic burden of Salmonellosis stood at USD 3.7 billion for the year 2013, according to the Economic Research Unit Agency (ERS) of USDA.

#### PREVALENCE AND ANTIBIOTIC RESISTANCE OF SALMONELLA SPECIES IN VEGETABLES

Over the years, the prevalence of *Salmonella* has drastically increased worldwide. The prevalence of *Salmonella* spp. in vegetables among several studies is presented in Table 3. The incidence ranges from 0.4% to as high as 97.9% (Sant'Ana et al., 2011; Najwa et al., 2015). The highest prevalence rate of 97.9 % was found in leafy green vegetables in Malaysia (Najwa et al., 2015), followed by 28%, 27% and 21.5% from a similar country (Salleh et al., 2003; Nillian et al., 2011; Abatcha et al., 2018). From these findings, it is quite clear that vegetables from Malaysia were the highest contaminated with *Salmonella* spp., followed by Iran (29%) (Mehrabian et al., 2009). Vegetables from Brazil recorded a low contamination rate (Sant'Ana et al., 2011). In Malaysia, most of the vegetables are sold at the wet-market under ambient temperature, which induces the growth and multiplication of pathogenic bacteria (Puspanadan et al., 2012). At the same time, improper handling and poor hygienic practices play a significant role as a source of cross-contamination on vegetables and other fresh produce at the retail level (Nillian et al., 2011).



**Table 3:** Prevalence (%) of *Salmonella* species in vegetables from various countries.

Country	Sample sources	Common serovars	Prevalence (%)	Reference
Iran	Cabbage-lettuce	<i>S. Typhimurium</i> , <i>S. Dublin</i> , <i>S. Enteritidis</i> , <i>S. Weltevreden</i> , <i>S. Infantis</i> , <i>S. Montevideo</i> , <i>S. Derby</i>	29	Mehrabian et al. (2009)
Malaysia	Coriander, lettuce salad, water spinach, bean sprouts, amaranth green, amaranth red, water spinach, Japanese parsley, sweet basil, winged bean, Indian pennywort, mint and laksa leaves	<i>S. Weltevreden</i> , <i>S. Corvallis</i> , <i>S. Brancaster</i> , <i>S. Paratyphi B</i> , <i>S. Typhimurium</i> , <i>S. Hvittefoss</i> , <i>S. Albany</i> , <i>S. Richmond</i> , <i>S. Braenderup</i> , <i>S. Augustenborg</i> , <i>S. Enteritidis</i>	21.5	Abatcha et al. (2018)
	Asiatic pennywort, Long bean, winged bean and water dropwort	<i>Salmonella</i> spp., <i>S. Typhimurium</i> and <i>S. Enteritidis</i>	97.9	Najwa et al. (2015)
	Tomato, capsicum, cucumber, Carrot, Cabbage and Lettuce	<i>Salmonella</i> spp., <i>S. Typhimurium</i> and <i>S. Enteritidis</i>	28	Nillian et al. (2011)
	Selom, pegaga, kankong and Kesum	<i>S. Weltevreden</i> , <i>S. Agona</i> , <i>S. Senftenberg</i> and <i>S. Albany</i>	27	Salleh et al. (2003)
Brazil	Salads, collard greens, arugula, watercress, chicory, escarole, cabbage, spinach, Swiss hard, and colewort	<i>S. Typhimurium</i> and <i>S. enterica</i> subsp. <i>enterica</i> O:47: z4, z23: -	0.4	Sant'Ana et al. (2011)
Brazil	Celery, watercress, beet, broccoli, zucchini, white round onion, cilantro, cabbage, cauliflower, spinach, large lettuce, Romaine lettuce, potato, parsley, Chinese parsley, and purslane	<i>S. Typhimurium</i> , <i>S. Arizonae</i> , <i>S. Choleraesuis</i> , <i>S. Gallinarum</i> , <i>S. Anatum</i> , <i>S. Houtenae</i> , <i>S. Agona</i> , <i>S. Edinburg</i> , <i>S. Enteritidis</i> , <i>S. Salamae</i> , <i>S. Typhi</i> , <i>S. Pullorum</i> , <i>S. Bongor</i> 1 C1 flagellar b	5.7	Quiroz-Santiago et al. (2009)
Nigeria	Spinach, <i>Corchorus olitorus</i> spp., sorrel, bitter leaf, and waterleaf	<i>S. Hadar</i> , <i>S. serovar 47: mt: -, and S. Vinohradsky</i>	6.3	Raufu et al. (2014)
	Cabbage, lettuce, cucumber, tomatoes, green pepper and spinach	<i>S. Typhi</i> , <i>S. Paratyphi</i> and <i>S. Typhimurium</i>	13.9	Abakpa et al. (2015)
	Onion flakes, tomatoes, lettuce	<i>S. Typhimurium</i> , <i>S. Enteritidis</i> , <i>S. Typhi</i> , <i>S. Paratyphi A</i> , <i>S. Paratyphi C</i> , <i>S. Derby</i> , <i>S. Newport</i> and <i>S. Paratyphi B</i>	22.0	Bagudo et al. (2014)
Pakistan	Carrot, coriander, cucumber, radish, cabbage, and tomato	<i>Salmonella</i> spp.	8	Razzaq et al. (2014)
India	Coriander, mint, carrots, radish	<i>S. Anatum</i> , <i>S. Bsilla</i> , <i>S. Newport</i> , <i>S. Saintpaul</i> , <i>S. Teko</i> , <i>S. Virchow</i> , and <i>S. Weltevreden</i>	3.6	Singh et al. (2007)

Different countries also reported a variety of serovars in this survey. For instance, *S. Typhimurium* and *S. enteritidis* were said to be the main *Salmonella* serovars in Malaysia (Najwa et al., 2015; Nillian et al., 2011), Iran (Mehrabian et al., 2009), and Nigeria (Bagudo et al., 2014). Interestingly, three studies reported the presence of strains originating from human in vegetables, this is quite worrisome because it causes invasive typhoid fever (*S. Typhi*) and paratyphoid fever (*S. Paratyphi A, B, C*), whereas, some serovars cause gastroenteritis symptoms primarily without systemic invasion (Bagudo et al., 2014; Abakpa et al., 2015; Abatcha et al., 2018). Similarly, Quiroz-Santiago et al. (2009) in Brazil detected a poultry host-related *Salmonella* serovars, Pullorum, and Gallinarum in leafy vegetables, which may perhaps be as a result of using untreated animal manure as fertiliser in vegetable production or attributable to the quality of wastewater used in farming.

The antibiotic resistance of *Salmonella* serovars from vegetables obtained from numerous studies is shown in Table 4. Resistance differs according to the country involved, the sample examined, and the study type. However, several findings were consistent. For example, no resistance to apramycin, cefotaxime, ceftriaxone, ceftiofur, and spectinomycin was observed in all the surveys. Relatively high resistances occurred for erythromycin (82.3%), cephalothin (64.65%), furazolidone (62.9%), streptomycin (49.6%), cefoperazone (48.6%), kanamycin (48.5%), cephalothin (44.7%) and amoxicillin-clavulanic acid (37.8%). Lower prevalence (<20%) also occurred for trimethoprim-sulphamethoxazole, florfenicol, doxycycline, colistin, ciprofloxacin, and chloramphenicol. All the studies listed in Table 3 revealed that *Salmonella* species from vegetables are increasingly becoming resistant, making it more difficult to treat patients with clinical infections.

**Table 4:** Prevalence (%) of Antimicrobial Resistance *Salmonella* among raw vegetables from various studies.

Antimicrobial	Prevalence (%)						Overall (%) Prevalence
	Najwa et al. (2015)	Kqueen et al. (2008)	Raufu et al. (2014)	Tasnim et al. (2016)	Singh et al. (2007)	Abatcha et al. (2018)	
Amikacin	-	-	-	-	28.6	-	28.6
Amoxicillin-clavunic acid	81.3	-	0.0	100	5.7	2.1	37.8
Ampicillin	100	29	0.0	-	11.4	26.7	33.4
Apramycin	-	-	0.0	-	-	-	0.0
Cephalothin	75	-	-	-	54.3	4.8	44.7
Ciprofloxacin	50	-	0.0	0.0	2.9	0.0	10.6
Chloramphenicol	6.3	11	0.0	0.0	5.7	21.9	7.4
Cefotaxime	-	0.0	0.0	-	-	-	0.0
Ceftriaxone	-	0.0	-	-	0.0	-	0.0
Colistin	-	-	0.0	-	22.9	-	11.4
Cotrimoxazole	-	-	-	-	17.1	-	17.1
Ceftiofur	-	-	0.0	-	-	-	0.0
Ceftazidime	-	-	-	-	25.7	-	25.7
Cefoperazone	-	-	-	-	48.6	-	48.6
Cephotaxime	-	-	-	-	40	-	40
Doxycycline	-	-	-	-	17.1	-	17.1
Erythromycin	100	-	-	64.70	-	-	82.3
Florfenicol	-	-	8.0	-	-	-	8.0
Furazolidone	-	-	-	-	62.9	-	62.9
Gentamycin	0.0	-	0.0	76.47	28.6	3.2	21.6
Imipenem	-	-	-	-	20	-	-
Kanamycin	-	-	-	-	85.7	11.2	48.5
Nalidixic acid	0.0	36	14	23.53	85.7	12.8	28.7
Neomycin	-	-	15	-	34.4	-	24.7
Streptomycin	50	47	38	100	0.0	62.6	49.6
Trimethoprim-sulphamethoxazole	6.3	25	-	-	-	16.6	15.9
Tetracycline	12.5	85	8	0.0	51.4	44.3	33.5
Spectinomycin	-	0.0	-	-	-	-	0.0
Sulphamethoxazoe	-	-	23	-	0.0	44.3	22.4
Trimethoprim	-	-	31	-	22.9	-	26.9

NB: (not tested).

**Table 5:** Prevalence (%) of *Salmonella* spp. in other foods from various countries

Country	Samples	Serovars	Prevalence (%)	References
China	RTE food	<i>S. Derby</i> , <i>S. Meleagridis</i> , <i>S. Enteritidis</i> , and <i>S. Senftenberg</i>	3.5	Yang et al. (2016)
China	Retail meat and Milk powder	<i>S. Enteritidis</i> , <i>S. Typhimurium</i> , <i>S. Shubra</i> , <i>S. Indiana</i> , <i>S. Derby</i> and <i>S. Djugu</i>	20.9	Yang et al. (2010)
Ethiopia	RTE meat, raw milk and egg	<i>Salmonella</i> spp.	5.5	Ejo et al. (2016)
Malaysia	Ducks	<i>S. Typhimurium</i> , <i>S. Enteritidis</i> , <i>S. Gallinarum</i> , <i>S. Braenderup</i> , <i>S. Albany</i> , <i>S. Hadar</i> , <i>S. Derby</i> , <i>S. Weltevreden</i> , <i>S. Newbrunswick</i> and <i>S. London</i>	23.5	Adzitey et al. (2012b)
Saudi Arabia	Fish samples	<i>Salmonella</i> spp.	39.9	Elhadi (2014)

According to Abakpa et al. (2015), all *Salmonella* spp. isolated from vegetables in Nigeria were multidrug resistance (MDR). The emergence of MDR *Salmonella* isolates suggests that these isolates may have originated from areas where antibiotics are commonly misused or used as therapeutic, prophylaxis and growth promoters in livestock production (Singh et al., 2013; Abatcha et al., 2015).

#### PREVALENCE AND ANTIBIOTIC RESISTANCE OF *SALMONELLA* SPECIES FROM OTHER FOODS

Over the decades, the prevalence of antibiotic-resistant *Salmonella* from other food sources have been on the rise. In China, out of the 539 RTE food products collected and examined from July 2011 to May 2014, 19 (3.5%) were positive for *Salmonella*, (Yang et al., 2016). Among the isolates, ten distinct serovars were identified includes *S. Derby*, *S. Meleagridis*, *S. Enteritidis*, and *S. Senftenberg* were the most prevalent serovars (Yang et al., 2016). Moreover, among the isolates identified, 74.0% were resistant to at least one antimicrobial, while 42.0% were resistant to more than three antimicrobials. High rates of resistance were observed for tetracycline (56.0%), ampicillin (38.0%), and streptomycin (34.0%) (Yang et al., 2016).

In another study by Yan et al. (2010), a total of 387 seafood, retail meat and milk powder samples were collected from nine cities in northern China in 2005 and screened for the occurrence of *Salmonella*. *Salmonella* was isolated from 81 (20.9%, 81/387) samples subdivide into 23 serovars. The isolates were 86.4% resistant to sulfamethoxazole, 48.1% resistant to sulfamethoxazole/trimethoprim, followed by 30.9% nalidixic acid, 19.8% tetracycline, 17.3% carboxybenzylpenicillin, 17.3% amoxicillin, and 16.0% ampicillin (Yan et al., 2010).

In Ethiopia, a cross-sectional study was conducted between 2014–2015 on 384 food items of animal origin to assess the prevalence and antimicrobial-resistant profiles of *Salmonella* isolates using the standard bacteriological methods (Ejo et al., 2016). The overall prevalence rate of *Salmonella* was 5.5% (21/384) from food items of animal origin. The *Salmonella* isolates were found to be relatively resistant to tetracycline (42.6%), sulfamethoxazole-trimethoprim (28.6%), and ampicillin (14.3%), respectively, while 9.5%–19% were resistant to ampicillin, cephalothin, amoxicillin, nitrofurantoin and tetracycline (Ejo et al., 2016).

In Penang, Malaysia, Adzitey et al. (2012a) studied 531 samples of ducks and its related processing environment from wet markets and duck farms and found an overall prevalence of *Salmonella* serovars of 23.5% (125/531). The *Salmonella* isolates (n=125) serotyped into 10 diverse

serovars, 29.6% *S. Typhimurium*, 12.0% *S. Enteritidis*, 2.4% *S. Gallinarum*, 12.0% *S. Braenderup*, 11.2% *S. Albany*, 20.8% *S. Hadar*, 6.4% *S. Derby*, 1.6% *S. Weltevreden*, 3.4% *S. Newbrunswick* and 0.8% *S. London* (Adzitey et al., 2012b). All the serovars were resistant to erythromycin but sensitive to cephalothin, gentamicin, and ceftriaxone. A large proportion of *Salmonella* serovars were also resistant by 57–100% to tetracycline and 37.5–81.1% nalidixic acid (Adzitey et al., 2012b).

In Saudi Arabia, Elhadi (2014) analysed a total of 223 fish samples (catfish=20, carfu=18, mirgal=20, milkfish=25, mackerel=35, tilapia=35, and rohu=30), in which 39.9% (89) were detected positive for *Salmonella*. The incidence of positive samples recorded for the freshwater fishes were 60.0% catfish, 27.7% carfu, 35.0% mirgal, 52.0% milkfish, 31.4% mackerel, 64.0% tilapia imported from Thailand, 28.0% tilapia imported from India, 26.6% rohu imported from Thailand and 46.6% rohu imported from Myanmar (Elhadi, 2014). All the *Salmonella* (140) isolates from freshwater fishes were subjected to 16 selected antimicrobial agents. The highest antibiotic resistance was observed to be 90.71% for tetracycline, 70% for ampicillin, and 45% for amoxicillin-clavulanic acid (Elhadi, 2014). These showed that raw retail imported frozen freshwater fish are contaminated with possibly pathogenic foodborne bacteria, and there is a need for adequate consumer protection measures.

*Salmonella* is one of the most commonly reported foodborne pathogens around the world, and an increase in antimicrobial-resistant *Salmonella* could limit the therapeutic options for clinical cases that necessitate antimicrobial therapy. There is a need for precautionary measures to reduce the spread of *Salmonella* contamination in food sources. More importantly, the maintenance of effective food hygiene and water sanitation remains the cornerstone. Additional steps, such as restriction of the indiscriminate use of antibiotics in food animals, are essential. The summary of the prevalence of *Salmonella* spp. in other foods from various countries is presented in Table 5.

#### MONITORING AND CONTROL OF *LISTERIA* AND *SALMONELLA* BASED ON INTERNATIONAL RECOMMENDATION

Building a baseline of projects to ensure the monitoring and control of enteric pathogens such as *Listeria* and *Salmonella* need advance support and strengthening projects through a multisectoral, One Health approach. Creating a multisectoral, One Health approach to be prosperous in countries requires an understanding of existing national infrastructure, capacity and resources for addressing zoonotic diseases, and in particular, existing mechanisms for collaboration across sectors and

disciplines. Similarly, ensuring sustainable and equitable financing among all relevant sectors is critical for ensuring continuity of programmes to decrease risks from zoonotic diseases from the WHO, FAO and OIE. Resources are required for both emergencies (e.g. outbreak investigation, laboratory surge capacity, quarantine) and routine activities (e.g. core workforce, routine surveillance, routine animal and human control programmes) (OIE, 2019).

In conclusion, the pathogenic foodborne bacteria stated here will remain a cause of outbreaks and mortality worldwide because no possible interferences have eliminated them from fresh produce and other foodstuffs. Additional study is necessary to strengthen practical approaches against these foodborne bacteria, and these strategies can be a mixture of practices and technologies earlier developed or those being in the pipeline. The presence of *L. monocytogenes* and *Salmonella* in vegetables and other food products is of great public health concern. There is an urgent need to enhance the microbiological monitoring of the production and processing chains of the foods, to ensure health safety.

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## AUTHORS CONTRIBUTION

All authors contributed equally

## CONFLICT OF INTEREST

The authors have declared no conflict of interest.

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