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Salmonella in the environment: A review on ecology, antimicrobial resistance, seafood contaminations, and human health implications[☆]

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ABSTRACT

Salmonella is a genus of Gram-negative bacteria that is responsible for numerous food poisoning outbreaks worldwide. With 93.8 million food-borne illnesses and 155,000 fatalities annually, it has emerged as a significant global public health issue. There are currently more than 2,500 distinct *Salmonella* serotypes, and more than half of them are associated with *Salmonella enterica*. An increasing global public health concern for humans and animals is antimicrobial resistance by *Salmonella* species worldwide. *Salmonella* infections can be lethal; conditioned with an increased prevalence of multi-drug resistant (MDR) strains in the future. The emergence of MDR *Salmonella* serotypes is considerably impacting the efficacy of antibiotic treatments. There is a potential association between *Salmonella* growth and proliferation with different environmental factors such as temperature, precipitation, pollution, nutrient availability, and other climate change-induced phenomena. Seafood and shellfish are common vectors for salmonellosis in humans and other animals and are responsible for food poisoning-related deaths every year. Effective food hygiene, water sanitation, and limiting the use of antibiotics in food animals must be upheld to reduce *Salmonella* infections. This article provides an overview of pathogenesis, epidemiology, antibiotic resistance, seafood contamination, and environmental factors affecting *Salmonella* proliferation, in addition to providing an outline of *Salmonella* infection.

Introduction

Salmonella stands out as the predominant microorganism among numerous foodborne pathogens, contributing to a significant number of fatalities worldwide (Eng et al., 2015; de Melo et al., 2021). Food-borne illnesses are one of the many potential sources of diseases that represent a significant risk to human health across the world. A recent survey claims that 420,000 people die yearly, and 1 in 10 individuals get sick after eating food contaminated with pathogens (Soubeiga et al., 2022). Among the most prevalent food-borne microorganisms that cause zoonotic infections in aquatic and terrestrial animals including humans, one of the most common isolates is *Salmonella* (Coburn et al., 2007; Eng et al., 2015; Jajere, 2019; Ehuwa et al., 2021). *Salmonella* infection is a

significant public health concern worldwide along with financial strain due to the expenses of disease prevention, and treatment (Crump et al., 2004; Helms et al., 2005; Mkangara, 2023). The phenomenon of *Salmonella* contamination in food or water causes salmonellosis, resulting from consuming contaminated foods (Gonçalves-Tenório et al., 2018).

Salmonella is a Gram-negative, facultatively anaerobic, non-sporulating, rod-shaped bacterium that belongs to the family *Enterobacteriaceae* (Agbaje et al., 2011; Waldman et al., 2020). They are mesophilic and can grow within 5 to 46 °C with an optimal growth temperature between 35 and 37 °C (Keerthirathne et al., 2016). They cannot multiply at an Aw (water activity) of 0.94, especially when combined with a pH of 5.5 or lower and are less tolerant to pH 4.5 or below (Bibek, 2001; Keerthirathne 2016; Gautam et al., 2020). The cells

Abbreviations: AMR, antimicrobial resistance; ATR, acid tolerance response; CDC, Centers for Disease Control and Prevention; GI, gastrointestinal; IPCC, Intergovernmental Panel on Climate Change; MDR, multi-drug resistant; NARMS, National Antimicrobial Resistance Monitoring System; NTS, non-typhoidal *Salmonella*; RES, reticuloendothelial system; RTE, ready-to-eat; SCV, *Salmonella* containing vacuole; SPIs, *Salmonella* pathogenicity islands; T3SS, type III protein secretion system.

[☆] Classification: Review article

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of this bacteria can multiply in numerous foods and endure being frozen or dried for an extended period without losing their ability to be pathogenic. Additionally, evidence suggests that *Salmonella* can even survive in environments with excessive salt (Petrin et al., 2022).

Salmonella can be divided into typhoidal and nontyphoidal (NTS) serovars. There are two typhoidal serovars: *Salmonella* Typhi and *Salmonella* Paratyphi A. (Johnson et al., 2018) causing typhoid and paratyphoid fever, respectively. In addition, these infectious disorders can cause neurological symptoms, leukopenia, septicemia, and immunological signs. These complications can sometimes lead to deaths in severe cases (Majowicz et al., 2010; Andino and Hanning, 2015; Chong et al., 2017). Typhimurium and Enteritidis are two non-typhoidal *Salmonella* (NTS) serovars that have a wide range of host specificity while some serovars use humans as their exclusive niche like Sendai, Typhi, Paratyphi (A, B, or C). NTS can induce mild to severe gastroenteritis (e.g., vomiting, diarrhea, nausea, etc.) or rare bacteremia (i.e., dissemination of infection in the body) (Andino and Hanning, 2015). Mainly there are three distinct clinical manifestations of salmonellosis: gastroenteritis, septicemia, and enteric fevers (Crump et al., 2015).

Environmental factors alterations due to climate change impact the spread and survivalism of zoonotic pathogens and exert an influence on more than half of all infectious diseases (Morgado et al., 2021; Mora et al., 2022; Dietrich et al., 2023). The development of the genus *Salmonella*, a zoonotic agent, is influenced by the ambient temperature at different stages in the food chain. Among different food sources, ready-to-eat seafood is an important one in *Salmonella* outbreak in the United States (Ehuwa et al., 2021). Recently, Billah and Rahman (2021) demonstrated a correlation between higher temperatures and the proliferation of *Escherichia coli* in the American oyster, an important seafood, in a laboratory study. *Salmonella* also multiplies faster at higher temperatures and this correlation between the *Salmonella* outbreaks and the outdoor temperature has been known for some time (Akil et al., 2014; Zhang et al., 2018). Besides, precipitation, humidity, soil properties, and pH are influential in the spread, reproduction, and survival of *Salmonella* (Dieterich et al., 2018; Robinson et al., 2022). According to a recent report, mean global warming will be increased from 1.5 to 5.8 °C and a rise in the mean global precipitation has been predicted from 5 to 15 % by the end of the century (Duchenne-Moutien and Neetoo, 2021). Therefore, it is indispensable to learn the impact of climate change and pathogen survivalism on food safety, health risks, and vulnerabilities of food systems. This comprehensive review is primarily focused on exploring *Salmonella* as a significant foodborne pathogen, with special emphasis on its incidence in seafood. The review also delved into the critical issues of antibiotic resistance in *Salmonella* strains and explored the impact of global climate change, especially temperature rise on the proliferation of this bacterium. Furthermore, the review offers an extensive and pertinent background encompassing the nomenclature, classification, epidemiology, and pathogenesis of *Salmonella* to provide a comprehensive reference point for researchers, public health professionals, and policy makers.

Methodology

A literature review was carried out utilizing a variety of online resources (e.g., Google Scholar, PubMed, Springer Nature, Science Direct, Taylor & Francis, and John Wiley) to provide the recent existing information regarding our chosen topics on *Salmonella* to prepare a comprehensive and updated review article. The keywords used were mainly *Salmonella*, environmental factors, antimicrobial resistance, fish, and shellfish. In addition, the contents and citations in scholarly journals ratify the excellence of the selected literatures for the article. In our study, we used immunohistological method to show the expression of *Salmonella* in the gills of oysters collected from field sites (e.g., polluted sites) and experimental study (i.e., oysters were exposed to 24, 28, and 32 °C according to the method described by Billah and Rahman (2021) using highly specific anti-mouse *Salmonella* primary antibody according

to the method described by Morrison et al. (2012), Rieger et al. (2015), and Billah and Rahman (2021).

Nomenclature and classification

Salmonella nomenclature has been a source of scientific controversy among bacteriologists until recently because the genus's original classification was not based on DNA relatedness, but on clinical considerations (Brenner et al., 2000; Todar, 2006). Theobald Smith first discovered and isolated *Salmonella* for the first time from the classical swine fever-infected intestines of pigs in 1855, and the bacterial strain was named after Dr. Daniel Elmer Salmon (Schultz, 2008; Eng et al., 2015). The classification of *Salmonella* strains has evolved afterward (Euzéby, 1999).

The phylogeny of bacteria can also be used to classify them by comparing 16S rRNA or other gene sequences and constructing a phylogenetic tree. Based on 16S rRNA sequence analysis, the genus *Salmonella* has been classified into two species, *Salmonella enterica* (2443 serotypes) and *Salmonella bongori* (20 serotypes). The World Health Organization (WHO) Collaborating Centre, Centers for Disease Control and Prevention (Centers for Disease Control and Prevention (CDC) 2023), and other organizations are currently using this system (Popoff et al., 2003). Six additional subspecies of *S. enterica* have been identified based on genetic similarities and biochemical characteristics, including, *S. enterica* subsp. *enterica*, *S. enterica* subsp. *salamae*, *S. enterica* subsp. *arizonae*, *S. enterica* subsp. *diarizonae*, *S. enterica* subsp. *Houtenae* and *S. enterica* subsp. *Indica* (Andino and Hanning, 2015). Notably, more than 2500 serovars, considered potential pathogens for both animals and humans, reflect the antigenic diversity caused by variations in flagellar and lipopolysaccharide architecture (Wan Norhana et al., 2010; Ibrahim and Morin, 2018).

Epidemiology of *Salmonella*

Every year *Salmonella* causes approximately 200 million to over 1 billion infections globally. This includes 93 million cases of gastroenteritis and 155,000 deaths. Shockingly, 85 % of these illnesses are exclusively related to contaminated food (He et al., 2023). Moreover, domestic food poisoning with salmonellosis accounts for 11 % of infectious cases in the United States, 35 % hospitalization, and 28 % death (Scallan et al., 2011; CDC, 2023).

Only five serotypes: *Salmonella* Enteritidis, *S. Typhimurium*, *Salmonella* Infantis, *Salmonella* Newport, and *Salmonella* Heidelberg are responsible for 74 % of the 87,923 verified human cases identified in 2019 (EFSA and ECDC, 2019). The most prevalent species of *Salmonella* is *S. enterica*, which contains roughly 1500 serotypes, and is responsible for 99 % of human and other warm-blooded animal infections (Park et al., 2009; Guibourdenche et al., 2010). Enteric infections caused an estimated 4.5 billion episodes and 1.7 million fatalities (22 deaths per 100,000) worldwide in 2016 (Troeger et al., 2018). On the other hand, *S. Enteritidis* and *S. Typhimurium* are the two most frequent non-typhoid serotypes causing human salmonellosis, among more than 200 serotypes that have been discovered as capable agents of causing disease in humans (Greig and Ravel, 2009; Xu et al., 2021; Xue et al., 2021). The primary cause of bacterial enteritis in humans is non-typhoidal *Salmonella* (NTS), which accounts for 93.8 million cases of gastroenteritis worldwide (Ngogo et al., 2020), the second most prevalent causative agent of salmonellosis (after Norovirus) from food poisoning (Todd, 2014, 2020). NTS is also very common in Sub-Saharan Africa, and they are linked to a 20–25 % case fatality rate in children and adults (Feasey et al., 2012). Besides, a recent multistate outbreak of *Salmonella* Paratyphi B and *Salmonella* weltevreden involving 11 states, 65 patients, and 11 hospitalizations was reported in the United States in 2015 (Hassan et al., 2019). Despite the continued high burden of enteric infections, significant reductions, particularly in mortality, have been achieved recently (Troeger et al., 2018; Foreman et al., 2018) though

overall *Salmonella* outbreaks have not shown any remarkable downturn in the last decades. In addition, anti-microbial resistant (AMR) *Salmonella* spp. has been evolved as a formidable global health concern. The estimated yearly death toll from AMR *Salmonella* is currently 700,000; by 2050, it is anticipated to increase to 10 million, resulting in a \$100 trillion economic loss (Balbin et al., 2020). In the United States alone, AMR affects 2 million people each year, and as a result, 23,000 people die annually as a consequence (Dadgostar, 2019). Recently, Medalla et al. (2021) reported that an estimated yearly occurrence of 1200,000 illnesses is linked to NTS, with at least 100,000 infections being caused by antibiotic-resistant *Salmonella*. The additional healthcare costs associated with the anti-microbial resistant *Salmonella*-derived illnesses is \$20 billion, and the US economy suffers a \$35 billion productivity loss (Weiner et al., 2016).

Salmonella as a food-borne pathogen

One in six citizens in the United States is prone to being infected with food-borne pathogens (Scallan et al., 2011). *Salmonella* is a vital microorganism responsible for food-borne diseases, and non-typhoidal *Salmonella* spp. are more prevalent food-associated pathogens (Martinez-Urtaza et al., 2003). *Salmonella* is mostly present in food items derived from animals, with a particular emphasis on uncooked chicken, raw meat, eggs, and their byproducts, and act as major sources of human salmonellosis (Silva et al., 2011; Carstens et al., 2019), with almost 6 % of all cases linked to pig and/or pork products in the USA (Trinetta et al., 2020). Slaughtering food animals at slaughterhouses is another common source of *Salmonella* contamination from organs and carcasses and slaughter houses contribute to about 12 % of *Salmonella* infections (Gillespie et al., 2005; Akil and Ahmad, 2019). In a research investigation examining the prevalence of *Salmonella* within poultry company-associated slaughterhouses in Europe (EFSA, and ECDP, 2019), it was observed that among the many batches that were sampled, a significant number of fecal samples, specifically 69.4 % (25 out of 36), demonstrated evidence of *Salmonella* shedding. Additionally, *Salmonella* contamination was detected in 46.3 % (100 out of 216) of the carcass samples, encompassing the neck skin and internal cavity (Marin et al., 2022). *Salmonella* can also be transmitted through vegetables and fresh fruits contaminated by animal microflora (Pui et al., 2011; Wu et al., 2015; Jajere, 2019; Carstens et al., 2019). Fresh foods such as spinach, herbs, and leafy greens, are commonly contaminated with coliform bacteria. In a recent study, *Salmonella* was found in 0.3 % of the 360 fresh produce samples, comprising 129 imported and 231 locally grown samples, while 0.8 % of the fresh fruit was imported to the United States (Liu and Kilonzo-Nthenge, 2017). Salmonellosis is a more common phenomenon in developed and developing countries, caused by eating contaminated meat, fruits, and vegetables (Carstens et al., 2019). *Salmonella* is also very pervasive in marine ecosystems and resident animals. The occurrence of *Salmonella* spp. in marine organisms, especially in seafood, mostly arises from terrestrial pollution sources originating from human activities and animals (Billah and Rahman, 2021).

Seafood is a highly nutritional food source but can also come with potential hazards, particularly those related to microbial contamination. A number of outbreaks of *Salmonella* have been linked to seafood in the United States, Europe, and other countries (FDA 2007; EFSA and ECDP, 2019; Popa and Popa, 2021; Porto et al., 2022) especially when consumed raw (Chakroun et al., 2021). *Salmonella* has been found in a wide range of fish and shellfish species such as crabs, clams, lobsters, mussels, scallops, shrimps, oysters, etc. While most types of fish and shellfish are eaten fried, baked, or steamed, some species are ready-to-eat (RTE) and consumed raw (Heinitz et al., 2000; Brands et al., 2005; Durán and Marshall, 2005; Hamilton et al., 2018; Sahu et al., 2019). Fish and shellfish can acquire *Salmonella*, and other pathogens from contaminated waters, or during processing and storage (Panisello et al., 2000; Prabhakar et al., 2020; Atwill and Jearnspong, 2021; Billah and Rahman, 2021).

Incidence of *Salmonella* in seafood

Salmonella is not a native aquatic environment resident, however, multiple *Salmonella* serovars are widely distributed in waters (e.g., sea, estuarine, and river) and seafood such as mollusks, shrimp, clams, and different fish species showing the highest prevalence (de Abreu Correa et al., 2007; Kumar et al., 2015; Novoslavskij et al., 2016; Liu et al., 2018). *Salmonella* is a more common filter-feeding organism because it filters water throughout its life cycle, which causes the pathogen to build up in its tissues (Kumar et al., 2009; Billah and Rahman, 2021). For example wild-caught American oyster (also called Eastern oyster, Atlantic oyster, or Virginia oyster; *Crassostrea virginica*), has been shown to include foodborne pathogens such as *Salmonella*, and *E. coli* (Todd, 2014; Billah and Rahman, 2021). *Salmonella* was found in 7.4 % of the oysters taken from American bays, with *S. newport* being the predominant serovar (Brands et al., 2005). *Salmonella* contamination of seafood can frequently occur from contaminated coastal areas and contaminated surroundings where fish is handled, even though environmental conditions and human activities can largely affect the incidence of *Salmonella* in seafood (Martinez-Urtaza et al., 2003; Ehuwa et al., 2021). For example, a high intensity of *Salmonella* was found in the gills of American oysters collected from polluted sites in the southern Gulf of Mexico (Fig. 1). Because of improper sanitation practices and human and animal waste disposal, *Salmonella* can potentially pollute water sources (Ama-gliani et al., 2012; Pandey et al., 2014; Mkangara, 2023). *Salmonella* can live for extended periods, months, or even years if they enter the soil and aquatic ambience, which facilitate their entrance into new hosts (Winfield and Groisman, 2003; Waldner et al., 2012). *Salmonella* contamination can come from various sources, ranging from diseased animal flesh to polluted water (Majowicz et al., 2010).

Because of its nutritional content, which includes high-quality protein, omega-3 fatty acids, vital vitamins, and minerals, shellfish is regarded by consumers all over the world as a healthy dietary component (Venugopal and Gopakumar, 2017; Billah and Rahman, 2021). Simultaneously, shellfish are potential hosts of viral and bacterial pathogens (Beuret et al., 2003; Rincé et al., 2018), and *Salmonella* species are prevalent in shellfish harvested and consumed raw in many countries in the world including the United States (Hamilton et al., 2018; Billah and Rahman, 2021). Since the 1980s, there has been a sharp increase in the prevalence of *Salmonella* infections, which results in an annual productivity loss of millions of dollars, and many cases have been connected to eating seafood, especially shellfish (Heinitz et al., 2000; Khan et al., 2009; Kumar et al., 2015; Elbashir et al., 2018; Atwill and Jearnspong, 2021). In shellfish fisheries in the United States, the presence of fecal coliform was assessed to determine the risk of exposure to pathogens through shellfish consumption, and a notable amount of *Salmonella* was found in the mollusks (FDA, 2007). A significant amount of *Salmonella* has been found in live oysters gathered from water bodies where shellfish harvesting is allowed in the United States which is a matter of concern (Brands et al., 2005; DePaola et al., 2010). Oysters are important shellfish species that ingest and concentrate particle debris from water during filter feeding including harmful bacteria and viruses (Martinez-Urtaza et al., 2003). The accumulation of pathogenic bacteria and viruses within the oysters makes them hazardous for human consumption.

In United States market surveys, 7.4 to 8.6 % of raw, market-ready oysters tested positive for *Salmonella*, with infection rates as high as 77 % locally (Cox et al., 2015). In another study, *S. enterica* serovars from six different species were discovered in the oysters from U.S. restaurants, indicating multiple instances of *Salmonella* contamination of American oyster supplies. Notably, 12 (43 %) of the 28 infected oysters reported the presence of *S. enterica* serovar Newport strain (Brillhart and Joens, 2011). *S. Typhimurium* has been reported to have a larger concentration in Pacific oysters (*Crassostrea gigas*) than bacteria in a healthy state, even after thirty days of infection (Chakroun et al., 2021). The presence of pathogenic bacteria like *E. coli* and *Salmonella* in the oyster

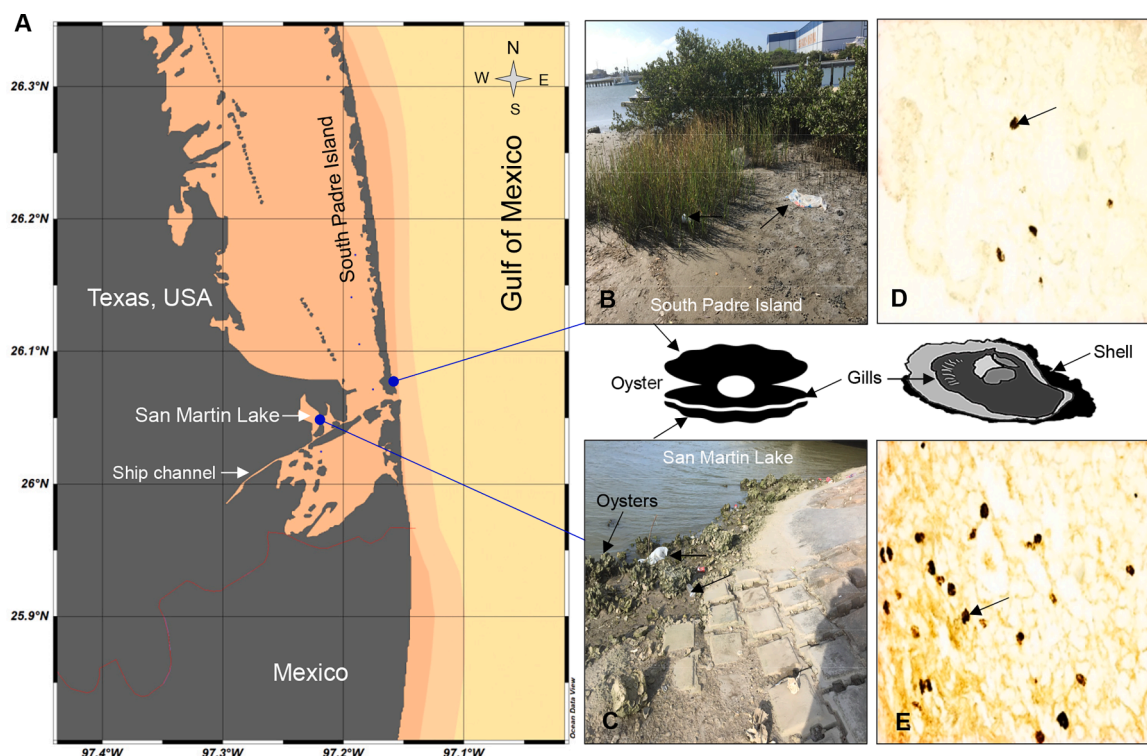


Fig. 1. Oyster collection sites on the southern Texas coast. (A) Gulf of Mexico, a marginal sea basin largely surrounded by the North American continent (modified from Billah and Rahman, 2021), (B) Sampling sites at South Padre Island (location: 26°04'30"N, 97°09'59"W), and (C) San Martine Lake (location: 26°00'10"N, 97°17'56"W) with pictures. (B, C) Arrows indicate source of pollutions (e.g., plastics, containers, bottles, etc.). Blue dots indicate sampling sites. (D, E) Immunohistological detection of representative photographs of gills in oysters collected from South Padre Island (D) and San Martine Lake (E). Expression of *Salmonella* in gills of oysters determined by immunohistochemical analysis using anti-mouse *Salmonella* primary antibody according to the method described by Morrison et al. (2012), Rieger et al. (2015), and Billah (2020). Arrows indicate colonies of *Salmonella*. Magnification = 10X.

habitat is assumed to be a reason for the higher bacterial contamination of oysters (Billah and Rahman, 2021). For instance, *Salmonella* with the highest virulence and antibiotic resistance were found to be present in saltwater microcosms after a year, which may have an impact on the occurrence of *Salmonella* in seafood such as oysters (Chandran and Hatha, 2005). Runoff from agricultural crops may potentially contribute to the summertime increase in *Salmonella* contamination, as most crops are irrigated with recycled water, which may include *Salmonella* and other fecal contamination (Harris et al., 2018).

Environmental conditions like elevated temperatures due to climate change have been found to modulate the pathogen count in seafood species (Billah and Rahman, 2021). The temperature of the water may play a role in the differences in *Salmonella* isolation between summer and winter, with colder waters lowering bacterial presence and warmer waters potentially promoting bacterial survival (Flores Monter et al., 2021). This is supported by recent reports that showed fecal coliform and *Salmonella* spp. contamination levels vary between the summer and winter in fish and shellfish species. *Salmonella*'s movement, fate, growth, and multiplication in the environment can be influenced by several elements, such as temperature, pH, soil moisture, nutrients, microbial competition, water activity of food matrix, and contact surface (Erickson et al., 2014; Alegbeleye et al., 2018; Trinetta et al., 2020; Roy et al., 2021).

Pathogenesis of *Salmonella*

Many pathogenic bacteria infect large domains of host organisms and *Salmonella* spp. is no exception in this regard (Hernández-Reyes and Schikora, 2013). The intensity of salmonellosis in humans depends on the serotype and immune status of the respective host. Compared to healthy individuals, young children, and older people with weak

immune defense systems are highly vulnerable to *Salmonella* (Coburn et al., 2007; Kurtz et al., 2017). *Salmonella* is highly pathogenic and can cause potentially fatal diseases because of its probable capacity to penetrate, multiply, and survive in human host cells. *Salmonella* invades non-phagocytic human host cells by inducing its phagocytic host cells to get easy access (Hansen-Wester et al., 2002).

The *Salmonella* pathogenicity islands are virulence gene clusters responsible for invasion, survival, and extraintestinal transmission. They are considered "quantum leaps" in bacterial evolution (i.e., *Salmonella* pathogenicity islands, SPIs). These gene collections are situated in chromosomal DNA regions that encode for determinants required in the invasion phase and are assumed to be acquired by horizontal gene transfer (Eswarappa et al., 2008; Grassl and Finlay, 2008; Siriken, 2013). *Salmonella* penetrates the intestinal epithelium during host infections and causes gastrointestinal disease when contaminated food or drink is consumed (Fàbrega and Vila, 2013; Dieterich et al., 2018). *Salmonella* pathogenicity island-1 (SPI-1) encodes the type III protein secretion system (T3SS), which produces the effector proteins needed for intestinal invasion and the development of enteritis (Lou et al., 2019; Azimi et al., 2020). The ability of *Salmonella* to modulate actin cytoskeletons of nonphagocytic cells is key to its pathogenicity. It is caused by the co-ordinated actions of several bacterial effector proteins that alternately stimulate and down-regulate host cell responses (Alto and Orth, 2012; Galán and Zhou, 2000). Intracellular pathogens have two options for surviving: either reside in the host cell's cytoplasm or create a self-contained vacuole. In order to become pathogenic or virulent, *Salmonella* typically creates an intracellular vacuole known as *Salmonella* containing vacuole (SCV) (Garai et al., 2012; Castanheira and Garcia-del Portillo, 2017). After entering the host cell, *Salmonella* manipulates inflammatory pathways and autophagy processes. *Salmonella* also evades the adaptive immune system through its interactions with dendritic

cells, and T and B lymphocytes (Bernal-Bayard and Ramos-Morales, 2018). Upon detecting *Salmonella* as a foreign body, the host cell's immune response would secrete the lysosomes and enzymes responsible for bacterial degradation (Sachdeva and Sundaramurthy, 2020). However, the remodeled vacuole prevents the lysosomes from fusing, allowing the bacteria to survive and replicate within the host cells. The bacteria's capacity to thrive inside macrophages permits them to go through the reticuloendothelial system (RES) (Behnsen et al., 2015).

Salmonella as an antibiotic-resistant bacterium

The upsurge of antibiotic-resistant bacteria is a rapidly growing global public health concern as antibiotic-resistant pathogens are insensitive to clinically significant antibiotics (Esperón et al., 2018; Chaudhari et al., 2023). Antimicrobial resistance (AMR) in *Salmonella* has been emerging as a severe health problem worldwide, and a remarkable increase in antibiotic resistance among non-typhoidal *Salmonella* has been elevated in recent times (Chiu et al., 2002; Haeusler and Curtis, 2013; Bell et al., 2014; Higgins et al., 2020; Marchello et al., 2020). Antibiotics including ampicillin, chloramphenicol, trimethoprim-sulfamethoxazole, and other types are typically used as first-line treatments for salmonellosis (Marchello et al., 2020). Early in the 1960s, the first instance of *Salmonella* resistance to a single antibiotic, chloramphenicol, was documented (Montville and Matthews, 2008). Since then, there has been an upsurge in the isolation of *Salmonella* strains that are resistant to one or more antimicrobial treatments in many countries, including the United States, the United Kingdom, and Saudi Arabia (Yoke-Kqueen et al., 2008).

A significant number of drug-resistant *Salmonella* outbreaks in the United States have been found linked to food poisoning. For instance, an intermediate tetracycline and streptomycin-resistant *Salmonella* serovar called *Salmonella* Urbana was discovered in 2017 spreading through papayas (Nair et al., 2018). There was an outbreak in 2015 of the serovar *Salmonella* Poona, isolated from ready-to-eat shrimp, and the isolates were nalidixic acid- or tetracycline-resistant (Nair et al., 2018). In 2018–2019, an outbreak of multidrug-resistant *Salmonella* Heidelberg, *S. Typhimurium*, and *Salmonella* Hadar took place in the United States via contaminated ground turkey, beef, and turkey burgers (Hassan et al., 2018, 2019). In 2014, there was a *Salmonella* Heidelberg outbreak linked to mechanically separated chicken, and 67 % of isolates were antibiotic-resistant across various classes (Punchihewage-Don et al., 2022). In a study conducted by Elhadi (2014) from Saudi Arabia, the *Salmonella* species isolated from seafood exhibited the highest levels of antibiotic resistance to amoxicillin-clavulanic acid (45 %), ampicillin (70 %) and tetracycline (90.71 %). Meanwhile, in a report by Rahimi et al. (2013) in Iran found a predominant resistance rate of 47.4 % of *Salmonella* isolates to nalidixic acid.

The rise of antibiotic-resistant foodborne pathogens has sparked public concern, as these diseases are more virulent, resulting in a higher fatality rate among infected individuals. The extensive use of antibiotics in intensive aquaculture practices increases the emergence of antimicrobial-resistant (AMR) *Salmonella* in the aquatic ecosystem as well. For instance, in a 12-month study across 32 aquaculture farms in Malaysian states, *Salmonella* showed high resistance to antibiotics like ampicillin and streptomycin. In this study, *Salmonella* showed a resistance rate of 20 % to vitally essential human therapeutic antibiotics such

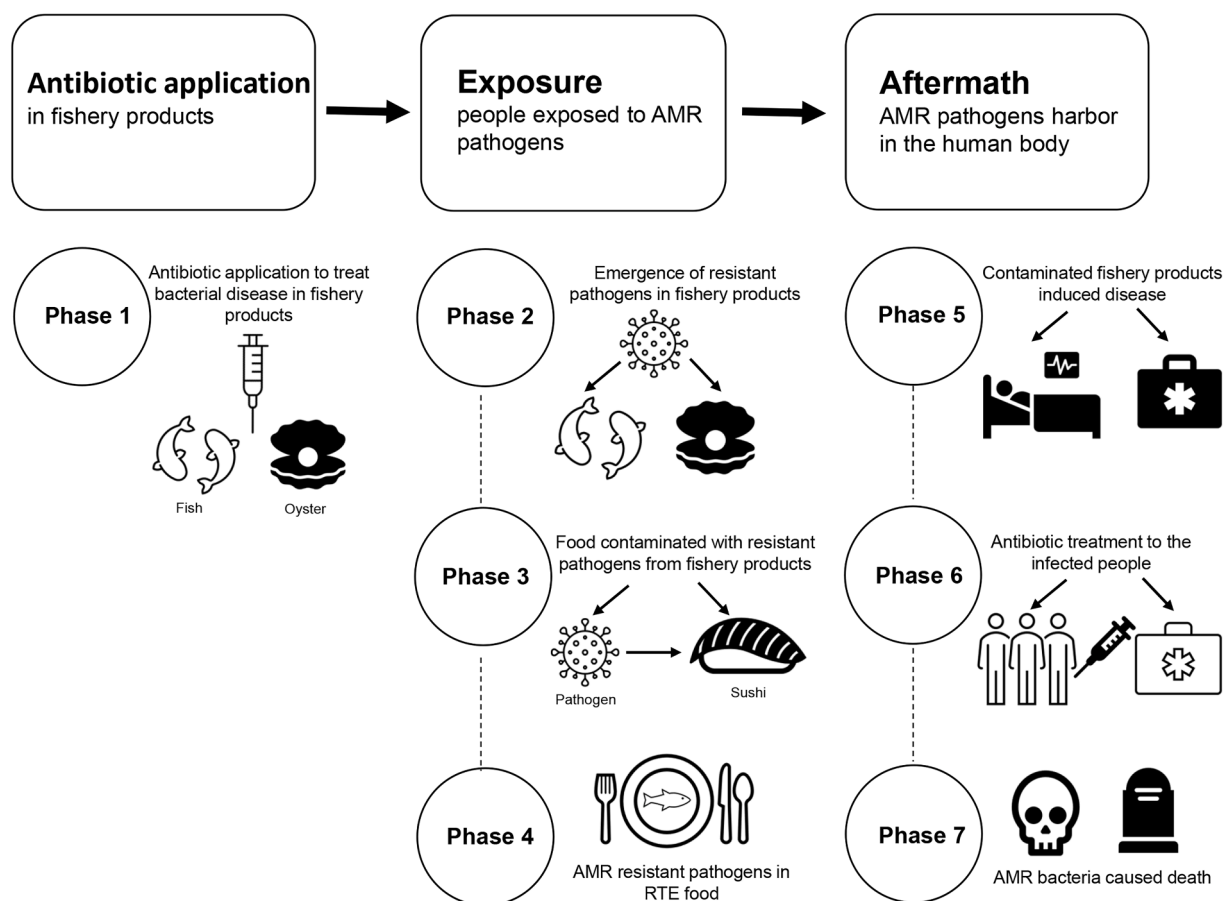


Fig. 2. Phases involved in antibiotic application in fishery products to the final consequence of death from the emergence of antimicrobial resistant (AMR) pathogens. Phase 1: Application of antibiotics in fishery farms to treat pathogens. Phase 2–4: Exposure of AMR to human beings through fish/shellfish or ready-to-eat (RTE) food. Phase 5–7: Aftermath of AMR pathogens accumulation in the human body.

as Colistin. Moreover, multi-drug resistant (MDR) *Salmonella* in tilapia demonstrated a high MDR level of 77.8 %. This underscores the growing public health challenge of antibiotic-resistant *Salmonella* occurring from seafood and aquaculture (Dewi et al., 2022). Fig. 2 represents a schematic pathway of antibiotic application in fishery farms and its final consequence for human beings. Marine and estuarine environments are frequently affected by antibiotic-resistant *Salmonella* contamination that severely impacts human health. Ampicillin, amoxicillin, and chloramphenicol-resistant *Salmonella* strains were previously isolated from marine environment (Chahouri et al., 2022). Seafood is frequently referred to as a means of spreading bacteria resistant to antibiotics (Feldhusen, 2000; Brands et al., 2005), and more than 80 % of the seafood consumed in the United States is imported (Elbashir et al., 2018). In addition, a significant number of dengue fever (7 %), malaria outbreaks (6 %), and diarrhea outbreaks (2.4 %) in industrial countries worldwide are caused by climate change (Campbell-Lendrum et al., 2015). Moreover, climate change-related deaths accounted for 0.3 % of all deaths, while illness burden accounted for 0.4 % (Kendrovski and Gjorgjev, 2012).

Effects of environmental factors on *Salmonella* growth and proliferation

Temperature

Environmental factors such as high temperatures or heat waves significantly impact the emergence of many infectious diseases (Mills et al., 2010; Kumar et al., 2015). According to estimates, the impact of climate change is responsible for 4.6 % of all risks and diseases originating from the environment (Kendrovski and Gjorgjev, 2012). *Salmonella* grows best at temperatures between 35 and 37 °C, though at <15 °C, growth is substantially reduced (Juneja et al., 2007; Zhang et al., 2010). High temperatures can affect the spread of infectious diseases, especially for heat-sensitive bacteria like *Salmonella* (Robinson et al., 2022). Warmer temperatures facilitate faster reproduction of *Salmonella*; hence increase in ambient temperature is positively correlated with gastrointestinal infections caused by bacterial pathogens (Akil et al., 2014). The rate of *Salmonella* cases has been found positively and linearly related to the average temperature of the previous week or month, with the rate peaking in the summer each year (Bentham and Langford, 2001; Russell et al., 2010).

Robust linear relationships between temperature and salmonellosis

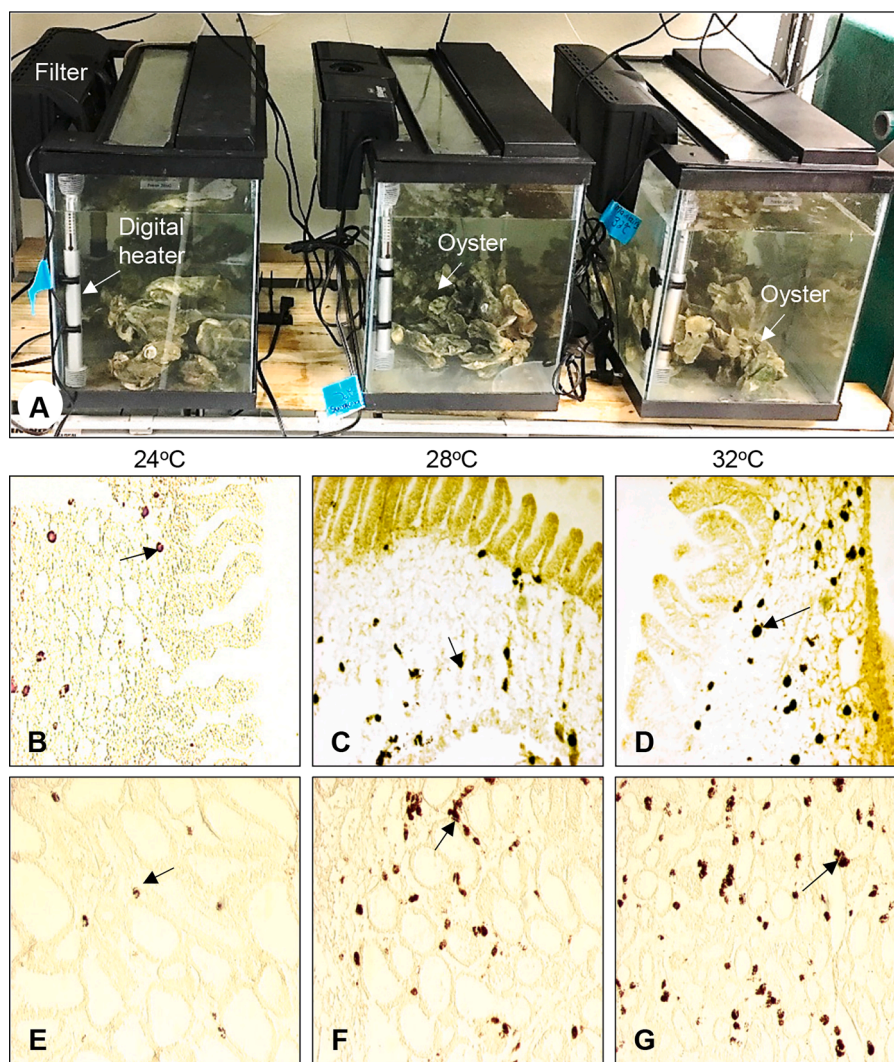


Fig. 3. (A) Experimental setup and heat-exposure experiment for laboratory study in oysters described previously by Billah and Rahman (2021). (B-G) Effects of one-week heat exposure (B: 24 °C, C: 28 °C, and D: 32 °C) on expression of *Salmonella* in gills (B-D) and digestive glands (E-G) of oysters determined by immunohistochemical analysis using anti-mouse *Salmonella* primary antibody according to the method described by Morrison et al. (2012), Rieger et al. (2015), and Billah (2020). Arrows indicate colony of *Salmonella*. Magnification = 10X.

occurrence have been observed in Australia and European countries, with a seasonal relationship for *Campylobacter* (McMichael et al., 2006). The implications of climatic variation on *Salmonella* infections in Mississippi were investigated in a prior study. Results indicated that elevated temperatures are linked to the *Salmonella* outbreak. This study also found a seasonal tendency, with the largest outbreaks occurring in the summer and early fall (Akil et al., 2014). Recent findings from Asia, Australia, Europe, and North America with similar trends showing a positive relationship between temperature and *Salmonella* infections are similar to those found in this study using regression and neural networks (D'Souza et al., 2008; Taylor et al., 2010; Zhang et al., 2010; Akil et al., 2014; Robinson et al., 2022). Because *Salmonella* grows better at higher temperatures, there is a higher concentration of *Salmonella* in seafood during the summer months. In a recent study, we observed that *Salmonella* count was consistently increased in the gills and digestive glands of wild-caught oysters exposed to high temperatures (28 °C and 32 °C) (Fig. 3). Similarly, a member of *Enterobacteriaceae* and facultative anaerobe, *E. coli*, showed a similar trend of proliferation in oyster tissues under high temperatures (Billah and Rahman, 2021). Elevated temperatures have the potential to impact the dissemination of *Salmonella* in a range of ways, including direct and indirect effects on bacterial multiplication along with seasonal eating behaviors (Keerthirathne et al., 2016). For example, seasonal variations in eating habits can be seen in the increased consumption of leafy green vegetables during the warmer months, which is a leading cause of salmonellosis (Liu et al., 2018). After accounting for seasonal and long-term patterns, the frequency of enteric bacterial illnesses usually rises along with the weekly temperature (Fleury et al., 2006). The number of cases could increase by 8.8 % with a 1 °C increase in the mean weekly maximum temperature, while the number of cases could increase by 5.8 % with a 1 °C increase in the mean weekly minimum temperature (Zhang et al., 2010).

Salmonella growth is influenced by the ambient temperature at several points in food processing, including the bacterial burden in raw foods, manufacturing, and transportation practices, and storage conditions. The proliferation of *Salmonella* and *Vibrio cholerae* is heavily influenced by ambient climatic conditions, as they multiply quickly at warmer temperatures: *V. cholerae* in water and *Salmonella* in food and animal guts (Akil et al., 2014). It is believed that, within certain bounds, ambient temperature favorably influences the survival and spread of specific intestinal diseases (Fleury et al., 2006). Furthermore, it was discovered that enteric diseases had a seasonal pattern in temperate latitudes, with the maximum prevalence of illnesses occurring during summer (Dietrich et al., 2023).

Consequently, recent studies empirically predict that salmonellosis rates will likely rise in the future because temperatures are expected to rise above historical norms due to climate change, contributing to an additional 1000 cases per year. By 2050, this will equate to an increase of approximately 1200 lost workdays per year and an estimated \$120,000 will be spent on health care and surveillance (Bambrick et al., 2008; Akil et al., 2014).

Precipitation

Rainfall patterns may affect the survival and movement of environmental *Salmonella*, which in turn may impact the spread of the disease (Lee et al., 2019; Robinson et al., 2022). Numerous studies have found that precipitation and temperature have an impact on patterns of enteric disease occurrence (Carlton et al., 2016; Levy et al., 2016; Stephen and Barnett, 2016). According to other studies, temperature extremity, rainfall, and relative humidity were all positively related to the frequency of *Salmonella* cases. Notably in Canada and the United States, outbreaks of water-borne diseases have been connected to periods of intense rainfall (Curriero et al., 2001; Rose et al., 2001; Cann et al., 2013; Jiang et al., 2015). Studies using daily or weekly precipitation rates found a better correlation with *Salmonella* outbreaks (Akil et al., 2014). In addition, 2–4-week lags between a high temperature or heavy

precipitation event increase in salmonellosis (D'Souza et al., 2008; Zhang et al., 2010). Moreover, extreme rainfall was associated with substantially increased salmonellosis (5 %) compared with no excessive rainfall. In addition, salmonellosis risk was also found notably increased (13 %) in moderate rainfall compared with antecedent dry periods (Jiang et al., 2015; Lee et al., 2019). Along with precipitation, the quality of drinking water has also been linked to gastroenteritis (Zhang et al., 2010; Wolkoff et al., 2021).

Nutrient availability

The growth and virulence of pathogens, the development of the illness, and the disease progression all depend on the pathogen's ability to access host nutrients in infected tissues (Steeb et al., 2013). The nutritional composition of the growth medium significantly affects DNA, proteins, lipid and carbohydrate content, cellular forms and structure, transcriptome, and phenotype of *Salmonella* (Galdiereo et al., 1994; Blair et al., 2013). A previous study shows that cultivation in minimal media inhibits *S. Typhimurium*'s capacity to penetrate epithelial cells in an SPI-1 (*Salmonella* Pathogenicity Island-1) and SPI-2 (*Salmonella* Pathogenicity Island-2) independent way. This study suggests that nutritional deficiency can reduce the pathogenicity of *S. Typhimurium* (Sridhar and Steele-Mortimer, 2016). In an in vivo model, *S. Typhimurium* growth in minimum media did not significantly affect intestinal pathogen loads, inflammation, or pathogen transfer in humans (Yurist-Doutsch et al., 2016). However, *S. Typhimurium* can be affected by nutrient deficiency in different ways. Starvation-induced selective pressure can result in genetic heterogeneity in the pathogen population and chromosomal gene duplication (Sonti and Roth, 1989). Furthermore, malnutrition has been demonstrated to promote acid tolerance in some enterobacteria which can be a leading cause of in vivo virulence (Antunes et al., 2011). Findings from previous studies indicate that prior to infection, short-term fasting has little effect on *S. Typhimurium*'s potential to induce gastrointestinal and systemic illness. In comparison to *S. Typhimurium* cultured in rich media, *S. Typhimurium* cultured in minimal media resulted in a different post-infection GI microbiota composition, including an increase in Bacteroidetes species and a decrease in *Enterobacteriaceae* microbiota members (Singh et al., 2015), and consequently, in relation to this finding, it is believed that rich media-cultured *S. Typhimurium* is a better model for human disease (Yurist-Doutsch et al., 2016).

The processes behind GI microbiota compositional alterations caused by minimal versus rich media-grown pathogens are still unknown. Conventional colitis symptoms, such as the amount of pro-inflammatory cytokines in the gut, may not change depending on the type of infection present, the host's reaction to the infection may vary, and the GI microbiota may be affected differently. Alternately, metabolic alterations in *S. Typhimurium* that occur during cultivation in different media may alter the composition of the microbiota through direct bacterial interactions. The metabolic profiles of various organisms have been shown to change when grown in a minimal versus rich medium (Saito et al., 2010), in turn, a pathogen's interaction with the GI microbiota may be influenced by the pathogen's metabolic state. Increases in the availability of external nutrients speed up intracellular *Salmonella*'s growth, which is dependent on the bacteria's capacity to use particular nutrients (Steeb et al., 2013). For instance, *S. Typhimurium* is shown to be an unusually virulent pathogen that can overcome nutritional limitation and virulence gene inhibition to successfully colonize the host using restricted media cultivation as a model of infection originating from fecal contamination or water-borne disease. Additionally, decreased invasion in human epithelial cells due to this environment causes significant alterations in the bacterium's genetic program and influences its ability to affect the makeup of the host microbiota (Sridhar and Steele-Mortimer, 2016; Yurist-Doutsch et al., 2016).

pH

In bacterial cells, biological and physiological processes can be regulated by both internal and external pH (Lund et al., 2020), and viability loss may result from adverse pH conditions (Choi and Groisman, 2016). Surprisingly, *Salmonella* has strategies for adapting to low pH conditions and maintaining pH homeostasis (Krulwich et al., 2011; Keerthirathne et al., 2019). *Salmonella* can lessen membrane proton conductance and proton extrusion, which also protects the cell from acid stress. The acid tolerance response (ATR) is the mechanism by which *S. Typhimurium* detects an acidic environment and adjusts to endure at low pH (Ryan et al., 2015). The ATR protects *Salmonella* spp. at pH values between 3 and 4, but it becomes active at pH values between 5.5 and 6 in the environment and when pH homeostasis is disrupted. The terms "postshock stage" and "preshock stage" apply to these pH levels. In order to stop and repair acidic damage to macromolecules, 43 acid shock proteins are stimulated during the postshock phase (Foster and Hall, 1991). This feature of *Salmonella* has made the control of the pathogen a complicated task. For instance, pH has an impact on the consistency and stability of mayonnaise, which is mostly formed of eggs, oil, and vinegar (Depree and Savage, 2001). *S. enterica* cells given an initial acid shock at pH 4.5 and 5.8 before inoculating mayonnaise (pH 4.2–4.5) improved the organism's survival and persistence at 4 °C (Leuschner and Boughtflower, 2001).

Although pH has a significant impact on *Salmonella*'s capacity to create biofilm, most strains are unable to do so at pH 4.5 except for *S. dublin*. On the other hand, in tryptic soy broth with 10 % NaCl and pH 7, *S. senftenberg* and the monophasic variety of *S. Typhimurium* demonstrated the highest biofilm development (Petrin et al., 2022). On the other hand, filamentous bacteria appeared to be more tolerant of low pH than planktonic cells after being exposed to pH 2 for 10 min and able to thrive in 10 % bile salts after a 24-hr period of exposure (Stackhouse et al., 2012). The Government of New South Wales (NSW), Australia, suggests in their food safety guidelines that a pH at or below 4.2 has been demonstrated to be helpful in limiting *Salmonella* in raw egg products. Besides the impacts of other factors, the effects of the type of acid, temperature, and water quality on *Salmonella* growth have been described in various literature (Jung and Beuchat, 2000; Mattick et al., 2000; Indu et al., 2006; Zhu et al., 2012; Yang et al., 2014). While environmental stress can trigger reactions in a wide variety of bacterial species (Alvarez-Ordóñez et al., 2015), *Salmonella* spp. can develop cross-tolerance to different stimuli when they are stressed (Hiramatsu et al., 2005).

Conclusion and recommendation

Around the world, *Salmonella* infection is a significant public health concern. This pervasive pathogen can adapt to various habitats, including those with human, animal, and non-animal hosts due to their genetic makeup. According to findings from earlier studies, *Salmonella* infection is not only related to poor hygiene, and it may not be possible to eliminate *Salmonella* contamination in seafood and fisheries products by simply controlling indicator organism levels. Additionally, the development of MDR *Salmonella* strains presents a significant difficulty in treating infections brought on by these strains. On top of that, the anticipated climate change and perturbation of environmental factors will increasingly threaten the safety of the food supply and a gradual rise in the incidence of foodborne infection and intoxication in the coming years. In this context, more stringent preventive and control measures must be adopted. One of the most effective preventive measures is to limit the indiscriminate use of antibiotics in food animals that have been suggested to curb the spread of *Salmonella* infection. Besides, to curb the health risk from foodborne infections, a ubiquitous sanitation measure should be adopted in every sphere of food preparation before consumption. We also recommend utilizing new innovative technologies to trace every step of supply chains including processing and preservation.

On a large scale, a stronger level of cooperation between public health authorities within and between countries is required, in addition to continued funding for human health perspectives.

Data availability

The representative photographs used in this review paper are available from the corresponding author upon reasonable request.

Consent to publish

Both authors have approved the submission of the final version of the manuscript.

Conflict of interest

The authors declare that there is no conflict of interest that could impact or influence the research work reported in this manuscript.

Ethics approval

There was no need to obtain permission from the UTRGV IACUC committee to conduct laboratory experiments on invertebrates including oysters. All wild-caught oysters, however, were collected according to the approved wildlife species capture rules and regulations by the Texas Park & Wildlife Department (scientific permit number: SPR1018–274).

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CRediT authorship contribution statement

Mohammad Maruf Billah: Writing – review & editing, Writing – original draft, Visualization, Validation, Software, Methodology, Investigation, Formal analysis, Data curation. **Md Saydur Rahman:** Writing – review & editing, Visualization, Validation, Supervision, Software, Resources, Project administration, Methodology, Investigation, Funding acquisition, Formal analysis, Data curation, Conceptualization.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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References

- Agbaje, M., Begum, R.H., Oyekunle, M.A., Ojo, O.E., Adenubi, O.T., 2011. Evolution of *Salmonella* nomenclature: a critical note. *Folia. Microbiol. (Praha)* 56 (6), 497–503. <https://doi.org/10.1007/s12223-011-0075-4>.
- Akil, L., Ahmad, H.A., 2019. Quantitative risk assessment model of human salmonellosis resulting from consumption of broiler chicken. *Diseases* 7 (1), 19. <https://doi.org/10.3390/diseases7010019>.
- Akil, L., Anwar Ahmad, H., Reddy, R.S., 2014. Effects of climate change on *Salmonella* infections. *Foodborne Pathog. Dis.* 11 (12), 974–980. <https://doi.org/10.1089/fpd.2014.1802>.

- Alegbeleye, O.O., Singleton, I., Sant'Ana, A.S., 2018. Sources and contamination routes of microbial pathogens to fresh produce during field cultivation: a review. *Food. Microbiol.* 73, 177–208. <https://doi.org/10.1016/j.FM.2018.01.003>.
- Alto, N.M., Orth, K., 2012. Subversion of cell signaling by pathogens. *Cold Spring Harb. Perspect. Biol.* 4 (9), a006114. <https://doi.org/10.1101/2Fcshperspect.a006114>. *Bull. Trimest. Plan. Fam.*
- Alvarez-Ordóñez, A., Broussolle, V., Colin, P., Nguyen-The, C., Prieto, M., 2015. The adaptive response of bacterial food-borne pathogens in the environment, host, and food: implications for food safety. *Int. J. Food. Microbiol.* 213, 99–109. <https://doi.org/10.1016/j.ijfoodmicro.2015.06.004>.
- Amagliani, G., Brandi, G., Schiavano, G.F., 2012. Incidence and role of *Salmonella* in seafood safety. *Food. Res. Int.* 45 (2), 780–788. <https://doi.org/10.1016/j.foodres.2011.06.022>.
- Andino, A., Hanning, I., 2015. *Salmonella enterica*: survival, colonization, and virulence differences among serovars. *Scient. World. J.* 2015, 520179. <https://doi.org/10.1155/2015/520179>.
- Antunes, L.C.M., Han, J., Ferreira, R.B.R., Lolić, P., Borchers, C.H., Finlay, B.B., 2011. Effect of antibiotic treatment on the intestinal metabolome. *Antimicrob. Agents. Chemother.* 55 (4), 1494–1503. <https://doi.org/10.1128/AAC.01664.10>.
- Atwill, E.R., Jeamsripong, S., 2021. Bacterial diversity and potential risk factors associated with *Salmonella* contamination of seafood products sold in retail markets in Bangkok, Thailand. *PeerJ* 9. <https://doi.org/10.7717/PEERJ.12694/SUPP-1>.
- Azimi, T., Zamirastana, M., Sani, M.A., Soltan Dallal, M.M., Nasser, A., 2020. Molecular mechanisms of *Salmonella* effector proteins: a comprehensive review. *Infect. Drug. Resist.* 13, 11–26. <https://doi.org/10.2147/IDR.S230604>.
- Balbin, M.M., Hull, D., Guest, C., Nichols, L., Dunn, R., Thakur, S., 2020. Antimicrobial resistance and virulence factors profile of *Salmonella* spp. and *Escherichia coli* isolated from different environments exposed to anthropogenic activity. *J. Glob. Antimicrob. Resist.* 22, 578–583. <https://doi.org/10.1016/j.JGAR.2020.05.016>.
- Bambrick, H., Dear, K., Woodruff, R., Hanigan, I., McMichael, A., 2008. The impacts of climate change on three health outcomes: temperature-related mortality and hospitalisations, salmonellosis and other bacterial gastroenteritis, and population at risk from dengue. *Gamaut. Climate Change Rev.* [https://web.archive.nla.gov.au/awa/20190509085748/http://www.garnautreview.org.au/CA25734E0016A131/WebObj/03-AThreehealthoutcomes/\\$File/03-A%20Three%20health%20outcomes.pdf](https://web.archive.nla.gov.au/awa/20190509085748/http://www.garnautreview.org.au/CA25734E0016A131/WebObj/03-AThreehealthoutcomes/$File/03-A%20Three%20health%20outcomes.pdf).
- Behnsen, J., Perez-Lopez, A., Nuccio, S.P., Raffatellu, M., 2015. Exploiting host immunity: the *Salmonella* paradigm. *Trends Immunol.* 36 (2), 112–120. <https://doi.org/10.1016/j.IT.2014.12.003>.
- Bell, B.G., Schellevis, F., Stobbering, E., Goossens, H., Pringle, M., 2014. A systematic review and meta-analysis of the effects of antibiotic consumption on antibiotic resistance. *BMC. Infect. Dis.* 14 (1) <https://doi.org/10.1186/1471-2334-14-13>.
- Bentham, G., Langford, I.H., 2001. Environmental temperatures and the incidence of food poisoning in England and Wales. *Int. J. Biometeorol.* 45 (1), 22–26. <https://doi.org/10.1007/s004840000083>.
- Bernal-Bayard, J., Ramos-Morales, F., 2018. Molecular mechanisms used by *Salmonella* to evade the immune system. *Curr. Issues. Mol. Biol.* 25, 133–168. <https://doi.org/10.21775/CIMB.025.133>.
- Beuret, C., Baumgartner, A., Schlupe, J., 2003. Virus-contaminated oysters: a three-month monitoring of oysters imported to Switzerland. *Appl. Environ. Microbiol.* 69 (4), 2292–2297. <https://doi.org/10.1128/AEM.69.4.2292-2297.2003>.
- Bibek, R., 2001. *Fundamental Food Microbiology* (2nd Edn). The CRC Press Ltd, Washington, DC, pp. 56–90.
- Billah, M.M., Rahman, M.S., 2021. Impacts of anthropogenic contaminants and elevated temperature on prevalence and proliferation of *Escherichia coli* in the wild-caught American oyster, *Crassostrea virginica* in the southern Gulf of Mexico coast. *Marine. Biol. Res.* 17 (9–10), 775–793. <https://doi.org/10.1080/17451000.2022.2053161>.
- Billah, M.M., 2020. *Detection and enumeration of bacterial pathogens in the American oyster (Crassostrea virginica)*. MSc. Thesis. School Earth., Environmen., Marine. Sci., Univ. Texas. Rio. Grande. Valley 78.
- Blair, J.M.A., Richmond, G.E., Bailey, A.M., Ivens, A., Piddock, L.J.V., 2013. Choice of bacterial growth medium alters the transcriptome and phenotype of *Salmonella enterica* Serovar Typhimurium. *PLoS. ONE* 8 (5), 63912. <https://doi.org/10.1371/JOURNAL.PONE.0063912>.
- Brands, D.A., Inman, A.E., Gerba, C.P., Maré, C.J., Billington, S.J., Saif, L.A., Levine, J.F., Joens, L.A., 2005. Prevalence of *Salmonella* spp. in oysters in the United States. *Appl. Environ. Microbiol.* 71 (2), 893–897. <https://doi.org/10.1128/AEM.71.2.893-897.2005>.
- Brenner, F.W., Villar, R.G., Angulo, F.J., Tauxe, R., Swaminathan, B., 2000. *Salmonella* nomenclature. *J. Clin. Microbiol.* 38, 2465–2467. <https://doi.org/10.1128/jcm.38.7.2465-2467.2000>.
- Brillhart, C.D., Joens, L.A., 2011. Prevalence and characterization of *Salmonella* serovars isolated from oysters served raw in restaurants. *J. Food. Prot.* 74 (6), 1025–1029. <https://doi.org/10.4315/0362-028X.JFP-10-443>.
- Campbell-Lendrum, D., Manga, L., Bagayoko, M., Sommerfeld, J., 2015. Climate change and vector-borne diseases: what are the implications for public health research and policy? *Philosoph. Transac. Royal. Soc. B. Biol. Sci.* 370 (1665), 1–8. <https://doi.org/10.1098/RSTB.2013.0552>.
- Cann, K.F., Thomas, D.R., Salmon, R.L., Wyn-Jones, A.P., Kay, D., 2013. Extreme water-related weather events and waterborne disease. *Epidemiol. Infect.* 141 (4), 671–686. <https://doi.org/10.1017/S0950268812001653>.
- Carlton, E.J., Woster, A.P., DeWitt, P., Goldstein, R.S., Levy, K., 2016. A systematic review and meta-analysis of ambient temperature and diarrhoeal diseases. *Int. J. Epidemiol.* 45 (1), 117–130. <https://doi.org/10.1093/IJE/DYV296>.
- Carstens, C.K., Salazar, J.K., Darkoh, C., 2019. Multistate outbreaks of foodborne illness in the United States associated with fresh produce from 2010 to 2017. *Front. Microbiol.* 10, 2667. <https://doi.org/10.3389/FMICB.2019.02667>.
- Castanheira, S., García-Del Portillo, F., 2017. *Salmonella* populations inside host cells. *Front. Cell. Infect. Microbiol.* 7, 432. <https://doi.org/10.3389/Ffcmib.2017.00432>. *Bull. Trimest. Plan. Fam.*
- Centers for Disease Control and Prevention (CDC) Foodborne illnesses and germs. [accessed on 28 December 2023]; <https://www.cdc.gov/foodsafety/foodborne-germs.html>.
- Chahouri, A., Radouane, N., Yacoubi, B., Moukrim, A., Banaoui, A., 2022. Microbiological assessment of marine and estuarine ecosystems using fecal indicator bacteria, *Salmonella*, *Vibrio* and antibiotic resistance pattern. *Mar. Pollut. Bull.* 180, 113824. <https://doi.org/10.1016/j.marpolbul.2022.113824>.
- Chakroun, I., Fedhila, K., Mahdhi, A., Mzoughi, R., Saidane, D., Esteban, M.Á., Bakhrouf, A., 2021. Atypical *Salmonella* Typhimurium persistence in the pacific oyster, *Crassostrea gigas*, and its effect on the variation of gene expression involved in the oyster's immune system. *Microb. Pathog.* 160, 105185. <https://doi.org/10.1016/J.MICPATH.2021.105185>.
- Chandhari, A., Hatha, A.A.M., 2005. Relative survival of *Escherichia coli* and *Salmonella typhimurium* in a tropical estuary. *Water. Res.* 39 (7), 1397–1403. <https://doi.org/10.1016/J.WATRES.2005.01.010>.
- Chaudhari, R., Singh, K., Kodgire, P., 2023. Biochemical and molecular mechanisms of antibiotic resistance in *Salmonella* spp. *Res. Microbiol.* 174 (1–2), 103985. <https://doi.org/10.1016/j.resmic.2022.103985>.
- Chiu, C.H., Wu, T.L., Su, L.H., Chu, C., Chia, J.H., Kuo, A.J., Chien, M.S., Lin, T.Y., 2002. The emergence in Taiwan of fluoroquinolone resistance in *Salmonella enterica* serotype Choleraesuis. *New. England. J. Med.* 346 (6), 413–419. <https://doi.org/10.1056/NEJMoa012261>.
- Choi, J., Groisman, E.A., 2016. Acidic pH sensing in the bacterial cytoplasm is required for *Salmonella* virulence. *Mol. Microbiol.* 101 (6), 1024–1038. <https://doi.org/10.1111/mmi.13439>.
- Chong, A., Lee, S., Yang, Y.A., Song, J., 2017. The Role of Typhoid Toxin in *Salmonella typhi* virulence. *Yale. J. Biol. Med.* 90 (2), 283–290.
- Coburn, B., Grassl, G.A., Finlay, B.B., 2007. *Salmonella*, the host and disease: a brief review. *Immunol. Cell. Biol.* 85 (2), 112–118. <https://doi.org/10.1038/sj.icb.7100007>.
- Cox, C.E., Wright, A.C., McClelland, M., Teplitski, M., 2015. Influence of *Salmonella enterica* serovar typhimurium srrB on colonization of Eastern oysters (*Crassostrea virginica*) as revealed by a promoter probe screen. *Appl. Environ. Microbiol.* 82 (1), 328–339. <https://doi.org/10.1128/AEM.02870-15>.
- Crump, J.A., Luby, S.P., Mintz, E.D., 2004. The global burden of typhoid fever. *Bull. World. Health. Organ.* 82 (5), 346–353. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC262843/>.
- Crump, J.A., Sjölund-Karlsson, M., Gordon, M.A., Parry, C.M., 2015. Epidemiology, clinical presentation, laboratory diagnosis, antimicrobial resistance, and antimicrobial management of invasive *Salmonella* infections. *Clin. Microbiol. Rev.* 28 (4), 901–937. <https://doi.org/10.1128/CMR.00002-15>.
- Curriero, F.C., Patz, J.A., Rose, J.B., Lele, S., 2001. The association between extreme precipitation and waterborne disease outbreaks in the United States, 1948–1994. *Am. J. Public Health* 91 (8), 1194–1199. <https://doi.org/10.2105/AJPH.91.8.1194>.
- D'Souza, R.M., Hall, G., Becker, N.G., 2008. Climatic factors associated with hospitalizations for rotavirus diarrhoea in children under 5 years of age. *Epidemiol. Infect.* 136 (1), 56–64. <https://doi.org/10.1017/S0950268807008229>.
- Dadgostar, P., 2019. Antimicrobial resistance: implications and costs. *Infect. Drug. Resist.* 12, 3903. <https://doi.org/10.2147/IDR.S234610>.
- de Abreu Corrêa, A., Albarnaz, J.D., Moresco, V., Poli, C.R., Teixeira, A.L., Simões, C.M.O., Barardi, C.R.M., 2007. Depuration dynamics of oysters (*Crassostrea gigas*) artificially contaminated by *Salmonella enterica* serovar Typhimurium. *Mar. Environ. Res.* 63 (5), 479–489. <https://doi.org/10.1016/j.marenvres.2006.12.002>.
- de Melo, A.N.F., Monte, D.F.M., de Souza Pedrosa, G.T., Balkey, M., Jin, Q., Brown, E., Allard, M., Moreira De Oliveira, T.C.R., Cao, G., Magnani, M., Macarasin, D., 2021. Genomic investigation of antimicrobial resistance determinants and virulence factors in *Salmonella enterica* serovars isolated from contaminated food and human stool samples in Brazil. *Int. J. Food. Microbiol.* 343. <https://doi.org/10.1016/J.IJFOODMICRO.2021.109091>.
- DePaola, A., Jones, J.L., Woods, J., Burkhardt, W., Calci, K.R., Krantz, J.A., Bowers, J.C., Kasturi, K., Byars, R.H., Jacobs, E., Williams-Hill, D., Nabe, K., 2010. Bacterial and viral pathogens in live oysters: 2007 United States market survey. *Appl. Environ. Microbiol.* 76 (9), 2754–2768. <https://doi.org/10.1128/AEM.02590-09>.
- Depree, J.A., Savage, G.P., 2001. Physical and flavour stability of mayonnaise. *Trends Food Sci. Technol.* 12 (5–6), 157–163. [https://doi.org/10.1016/S0924-2244\(01\)00079-6](https://doi.org/10.1016/S0924-2244(01)00079-6).
- Dewi, R.R., Hassan, L., Daud, H.M., Matori, M.F., Nordin, F., Ahmad, N.I., Zakaria, Z., 2022. Prevalence and antimicrobial resistance of *Escherichia coli*, *Salmonella* and *Vibrio* derived from farm-raised red hybrid tilapia (*Oreochromis* spp.) and Asian sea bass (*Lates calcarifer*, Bloch 1970) on the West coast of Peninsular Malaysia. *Antibiotics* (2), 11. <https://doi.org/10.3390/ANTIBIOTICS11020136/S1>.
- Dieterich, W., Schink, M., Zopf, Y., 2018. Microbiota in the gastrointestinal tract. *Med. Sci* 6 (4), 116. <https://doi.org/10.3390/medsci6040116>.
- Dieterich, J., Hammerl, J.A., John, A., Kappenstein, O., Loeffler, C., Nöckler, K., Rosner, B., Spielmeier, A., Szabo, I., Richter, M.H., 2023. Impact of climate change on foodborne infections and intoxications. *J. Health Monitor.* 8 (Suppl 3), 78–92. <https://doi.org/10.25646/11403>.
- Duchenne-Moutien, R.A., Neetoo, H., 2021. Climate change and emerging food safety issues: a review. *J. Food. Prot.* 84 (11), 1884–1897. <https://doi.org/10.4315/JFP-21-141>.

- Durán, G.M., Marshall, D.L., 2005. Ready-to-eat shrimp as an international vehicle of antibiotic-resistant bacteria. *J. Food. Prot.* 68 (11), 2395–2401. <https://doi.org/10.4315/0362-028X-68.11.2395>.
- EFSA (European Food Safety Authority) and ECDC (European Centre for Disease Prevention Control), 2019. The European Union One Health 2018 zoonoses report. *EFSA*. J 17, e05926.
- Ehuwa, O., Jaiswal, A.K., Jaiswal, S., 2021. *Salmonella*, Food safety and food handling practices. *Foods* 10 (5). <https://doi.org/10.3390/FOODS10050907>.
- Elbasher, S., Parveen, S., Schwarz, J., Rippen, T., Jahncke, M., DePaola, A., 2018. Seafood pathogens and information on antimicrobial resistance: a review. *Food. Microbiol.* 70, 85–93. <https://doi.org/10.1016/j.F.M.2017.09.011>.
- Elhadi, N., 2014. Prevalence and antimicrobial resistance of *Salmonella* spp. in raw retail frozen imported freshwater fish to Eastern Province of Saudi Arabia. *Asian. Pac. J. Trop. Biomed* 4 (3), 234–238. [https://doi.org/10.1016/S2221-1691\(14\)60237-9](https://doi.org/10.1016/S2221-1691(14)60237-9).
- Eng, S.K., Pusparajah, P., Ab Mutalib, N.S., Ser, H.L., Chan, K.G., Lee, L.H., 2015. *Salmonella*: a review on pathogenesis, epidemiology and antibiotic resistance. *Front. Life. Sci* 8 (3), 284–293. <https://doi.org/10.1080/21553769.2015.1051243>.
- Erickson, M.C., Habteselassie, M.Y., Liao, J., Webb, C.C., Mantripragada, V., Davey, L.E., Doyle, M.P., 2014. Examination of factors for use as potential predictors of human enteric pathogen survival in soil. *J. Appl. Microbiol.* 116 (2), 335–349. <https://doi.org/10.1111/JAM.12373>.
- Esperón, F., Sacristán, C., Carballo, M., Torre, A., de la, Esperón, F., Sacristán ..., C., Torre, A., de la, 2018. Antimicrobial resistance genes in animal manure, manure-amended and nonanthropogenically impacted soils in Spain. *Advances Biosci. Biotechnol* 9 (9), 469–480. <https://doi.org/10.4236/ABB.2018.99032>.
- Eswarappa, S.M., Janice, J., Nagarajan, A.G., Balasundaram, S.V., Karnam, G., Dixit, N. M., Chakravorty, D., 2008. Differentially evolved genes of *Salmonella* Pathogenicity Islands: insights into the mechanism of host specificity in *Salmonella*. *PLoS. ONE* 3 (12). <https://doi.org/10.1371/JOURNAL.PONE.0003829>.
- Euzéby, J.P., 1999. Revised *Salmonella* nomenclature: designation of *Salmonella enterica* (ex Kauffmann and Edwards 1952) Le Minor and Popoff 1987 sp. nov., nom. rev. as the neotype species of the genus *Salmonella* *lignieres* 1900 (approved lists 1980), rejection of the name *Salmonella choleraesuis* (Smith 1894) Weldon 1927 (approved lists 1980), and conservation of the name *Salmonella typhi* (Schroeter 1886) Warren and Scott 1930 (approved lists 1980). request for an opinion. *Int. J. Syst. Bacteriol.* 49, 927–930. <https://doi.org/10.1099/00207713-49-2-927>.
- Fàbrega, A., Vila, J., 2013. *Salmonella enterica* serovar Typhimurium skills to succeed in the host: virulence and regulation. *Clin. Microbiol. Rev.* 26 (2), 308–341. <https://doi.org/10.1128/CMR.00066-12>.
- FDA, Food, Administration, Drug, 2007. Guide for the control of molluscan shellfish—section IV, chapter 2, 2007, growing areas. 01. Total Coliform stand. <http://www.issc.org/>.
- Feasey, N.A., Dougan, G., Kingsley, R.A., Heyderman, R.S., Gordon, M.A., 2012. Invasive non-typhoidal *Salmonella* disease: an emerging and neglected tropical disease in Africa. *The. Lancet* 379, 2489–2499. [https://doi.org/10.1016/S0140-6736\(11\)61752-2](https://doi.org/10.1016/S0140-6736(11)61752-2).
- Feldhusen, F., 2000. The role of seafood in Bacterial Foodborne diseases. *Microb. Infec* 2, 1651–1660. [https://doi.org/10.1016/S1286-4579\(00\)01321-6](https://doi.org/10.1016/S1286-4579(00)01321-6).
- Fleury, M., Charron, D.F., Holt, J.D., Allen, O.B., Maarouf, A.R., 2006. A time series analysis of the relationship of ambient temperature and common bacterial enteric infections in two Canadian provinces. *Int. J. Biometeorol* 50 (6), 385–391. <https://doi.org/10.1007/s00484-006-0028-9>.
- Flores Monter, Y.M., Chaves, A., Arellano-Reynoso, B., López-Pérez, A.M., Suzán-Azpiri, H., Suzán, G., 2021. Edaphoclimatic seasonal trends and variations of the *Salmonella* spp. infection in Northwestern Mexico. *Infec. Disease. Modell* 6, 805–819. <https://doi.org/10.1016/j.idm.2021.05.002>.
- Foreman, K.J., Marquez, N., Dolgert, A., Fukutaki, K., Fullman, N., McGaughey ..., M., Murray, C.J.L., 2018. Forecasting life expectancy, years of life lost, and all-cause and cause-specific mortality for 250 causes of death: reference and alternative scenarios for 2016–40 for 195 countries and territories. *The. Lancet* 392 (10159), 2052–2090. [https://doi.org/10.1016/S0140-6736\(18\)31694-5/ATTACHMENT/D397904D-428C-4949-B124-D32E9FA7136C/MMC2.PDF](https://doi.org/10.1016/S0140-6736(18)31694-5/ATTACHMENT/D397904D-428C-4949-B124-D32E9FA7136C/MMC2.PDF) <https://doi.org/10.1128/jb.172.2.771-778.1990>.
- Foster, J.W., Hall, H.K., 1991. Inducible pH homeostasis and the acid tolerance response of *Salmonella typhimurium*. *J. Bacteriol.* 173 (16), 5129–5135. <https://doi.org/10.1128/jb.173.16.5129-5135.1991>.
- Galán, J.E., Zhou, D., 2000. Striking a balance: modulation of the actin cytoskeleton by *Salmonella*. *Proc. Natl. Acad. Sci. U.S.A.* 97 (16), 8754. <https://doi.org/10.1073/PNAS.97.16.8754>.
- Galdiereo, E., Donnarumma, G., de Martino, L., Marcantili, A., Cipollaro de l'Ero, G., Merone, A., 1994. Effect of low-nutrient seawater on morphology, chemical composition, and virulence of *Salmonella typhimurium*. *Arch. Microbiol.* 1994. 162:1 162 (1), 41–47. <https://doi.org/10.1007/BF00264371>.
- Garai, P., Gnanadhas, D.P., Chakravorty, D., 2012. *Salmonella enterica* serovars Typhimurium and Typhi as model organisms: revealing paradigm of host-pathogen interactions. *Virulence* 3 (4), 377. <https://doi.org/10.4161/VIRU.21087>.
- Gautam, B., Govindan, B.N., Gänzle, M., Roopesh, M.S., 2020. Influence of water activity on the heat resistance of *Salmonella enterica* in selected low-moisture foods. *Int. J. Food. Microbiol.* 334, 108813 <https://doi.org/10.1016/j.ijfoodmicro.2020.108813>.
- Gillespie, I.A., O'Brien, S.J., Adak, G.K., Ward, L.R., Smith, H.R., 2005. Foodborne general outbreaks of *Salmonella Enteritidis* phage type 4 infection, England and Wales, 1992–2002: where are the risks? *Epidemiol. Infect.* 133 (5), 795–801. <https://doi.org/10.1017/S0950268805004474>.
- Gonçalves-Tenório, A., Nunes Silva, B., Rodrigues, V., Cadavez, V., Gonzales-Barron, U., 2018. Prevalence of pathogens in poultry meat: A meta-analysis of European published surveys. *Foods* 7 (5). <https://doi.org/10.3390/FOODS7050069>.
- Grassi, G.A., Finlay, B.B., 2008. Pathogenesis of enteric *Salmonella* infections. *Curr. Opin. Gastroenterol.* 24 (1), 22–26. <https://doi.org/10.1097/MOG.0b013e3282f21388>.
- Greig, J.D., Ravel, A., 2009. Analysis of foodborne outbreak data reported internationally for source attribution. *Int. J. Food. Microbiol.* 130 (2), 77–87. <https://doi.org/10.1016/j.ijfoodmicro.2008.12.031>.
- Guibourdenche, M., Roggentin, P., Mikoleit, M., Fields, P.I., Bockemühl, J., Grimont, P.A. D., Weill, F.X., 2010. Supplement 2003–2007 (No. 47) to the White-Kauffmann-Le Minor scheme. *Res. Microbiol.* 161 (1), 26–29. <https://doi.org/10.1016/j.resmic.2009.10.002>.
- Haesler, G.M., Curtis, N., 2013. Non-typhoidal *Salmonella* in children: microbiology, epidemiology and treatment. *Adv. Exp. Med. Biol.* 764, 13–26. https://doi.org/10.1007/978-1-4614-4726-9_2.
- Hamilton, K.A., Chen, A., de-Graft Johnson, E., Gitter, A., Kozak, S., Niquice ..., C., Gurian, P.L., 2018. *Salmonella* risks due to consumption of aquaculture-produced shrimp. In: *Microbial. Risk Analysis*, 9, p. 22. <https://doi.org/10.1016/j.MRAN.2018.04.001>.
- Hansen-Wester, I., Stecher, B., Hensel, M., 2002. Type III secretion of *Salmonella enterica* serovar typhimurium translocated effectors and SseFG. *Infect. Immun.* 70 (3), 1403–1409. <https://doi.org/10.1128/IAI.70.3.1403-1409.2002>.
- Harris, C.S., Tertuliano, M., Rajeev, S., Vellidis, G., Levy, K., 2018. Impact of storm runoff on *Salmonella* and *Escherichia coli* prevalence in irrigation ponds of fresh produce farms in southern Georgia. *J. Appl. Microbiol.* 124 (3), 910. <https://doi.org/10.1111/JAM.13689>.
- Hassan, R., Teclé, S., Adcock, B., Kellis, M., Weiss, J., Saupé ..., A., Neil, K.P., 2018. Multistate outbreak of *Salmonella* Paratyphi B variant L(+) tartrate(+) and *Salmonella weltevreden* infections linked to imported frozen raw tuna: USA, March–July 2015. *Epidemiol. Infect.* 146 (11), 1461–1467. <https://doi.org/10.1017/S0950268818001462>.
- Hassan, R., Buuck, S., Noveroske, D., Medus, C., Sorenson, A., Laurent ..., J., Basler, C., 2019. Multistate outbreak of *Salmonella* infections linked to raw turkey products — United States, 2017–2019. *Morbidity. Mortal. Weekly. Report* 68 (46), 1045. <https://doi.org/10.15585/MMWR.MM6846A1>.
- He, Y., Wang, J., Zhang, R., Chen, L., Zhang, H., Qi, X., Chen, J., 2023. Epidemiology of foodborne diseases caused by *Salmonella* in Zhejiang Province, China, between 2010 and 2021. *Front. Public Health* 11, 1127925. <https://doi.org/10.3389/fpubh.2023.1127925>.
- Heinitz, M.L., Ruble, R.D., Wagner, D.E., Tatini, S.R., 2000. Incidence of *Salmonella* in fish and seafood. *J. Food. Prot.* 63 (5), 579–592. <https://doi.org/10.4315/0362-028X-63.5.579>.
- Helms, M., Ethelberg, S., Mølbak, K., Lightfoot, D., Powling, J., Berghold ..., C., Stevenson, J.E., 2005. International *Salmonella typhimurium* DT104 infections, 1992–2001. *Emerging. Infect. Dis.* 11 (6), 859–867. <https://doi.org/10.3201/eid1106.041017>.
- Hernández-Reyes, C., Schikora, A., 2013. *Salmonella*, a cross-kingdom pathogen infecting humans and plants. *FEMS. Microbiol. Lett.* 343 (1), 1–7. <https://doi.org/10.1111/1574-6968.12127>.
- Higgins, D., Mukherjee, N., Pal, C., Sulaiman, I.M., Jiang, Y., Hanna ..., S., Banerjee, P., 2020. Association of virulence and antibiotic resistance in *Salmonella*—statistical and computational insights into a selected set of clinical isolates. *Microorganisms* 8 (10), 1–17. <https://doi.org/10.3390/MICROORGANISMS8101465>.
- Hiramatsu, R., Matsumoto, M., Sakae, K., Miyazaki, Y., 2005. Ability of Shiga toxin-producing *Escherichia coli* and *Salmonella* spp. to survive in a desiccation model system and in dry foods. *Appl. Environ. Microbiol.* 71 (11), 6657–6663. <https://doi.org/10.1128/AEM.71.11.6657-6663.2005>.
- Ibrahim, G.M., Morin, P.M., 2018. *Salmonella* serotyping using whole genome sequencing. *Front. Microbiol.* 9, 2993. <https://doi.org/10.3389/fmicb.2018.02993>.
- Indu, M.N., Hatha, A.A.M., Abirosh, C., Harsha, U., Vivekanandan, G., 2006. Antimicrobial activity of some of the South-Indian spices against serotypes of *Escherichia coli*, *Salmonella*, *Listeria Monocytogenes* and *Aeromonas Hydrophila*. *Brazil. J. Microbiol.* 37 (2), 153–158. <https://doi.org/10.1590/S1517-83822006000200011>.
- 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. <https://doi.org/10.14202/VETWORLD.2019.504-521>.
- Jiang, C., Shaw, K.S., Upperman, C.R., Blythe, D., Mitchell, C., Murtugudde ..., R., Sapkota, A., 2015. Climate change, extreme events and increased risk of salmonellosis in Maryland, USA: evidence for coastal vulnerability. *Environ. Int* 83, 58–62. <https://doi.org/10.1016/J.ENVTINT.2015.06.006>.
- Johnson, R., Mylona, E., Frankel, G., 2018. Typhoidal *Salmonella*: Distinctive virulence factors and pathogenesis. *Cell. Microbiol.* 20 (9), 1–14. <https://doi.org/10.1111/cmi.12939>.
- Juneja, V.K., Valenzuela Melendres, M., Huang, L., Gumudavelli, V., Subbiah, J., Thippareddi, H., 2007. Modeling the effect of temperature on growth of *Salmonella* in chicken. *Food Microbiol.* 24 (4), 328–335. <https://doi.org/10.1016/j.fm.2006.08.004>.
- Jung, Y.S., Beuchat, L.R., 2000. Sensitivity of multidrug-resistant *Salmonella typhimurium* DT104 to organic acids and thermal inactivation in liquid egg products. *Food Microbiol.* 17 (1), 63–71. <https://doi.org/10.1006/FMIC.1999.0287>.
- Keerthirathne, T.P., Ross, K., Fallowfield, H., Whitley, H., 2016. A review of temperature, pH, and other factors that influence the survival of *Salmonella* in Mayonnaise and other raw egg products. *Pathogens* 5 (4). <https://doi.org/10.3390/PATHOGENS5040063>.
- Kendrovski, V., Gjorgiev, D., 2012. Climate change: Implication for food-borne diseases (*Salmonella* and food poisoning among humans in R. Macedonia). *Structure and Function of Food Engineering*. <https://doi.org/10.5772/46183>.

- Khan, A.A., Ponce, E., Nawaz, M.S., Cheng, C.M., Khan, J.A., West, C.S., 2009. Identification and characterization of class 1 integron resistance gene cassettes among *Salmonella* strains isolated from imported seafood. *Appl. Environ. Microbiol.* 75 (4), 1192–1196. <https://doi.org/10.1128/AEM.02054-08>.
- Krulwich, T.A., Sachs, G., Padan, E., 2011. Molecular aspects of bacterial pH sensing and homeostasis. *Nat. Rev. Microbiol.* 9, 330–343. <https://doi.org/10.1038/nrmicro2549>.
- Kumar, R., Surendran, P.K., Thampuran, N., 2009. Distribution and genotypic characterization of *Salmonella* serovars isolated from tropical seafood of Cochin, India. *J. Appl. Microbiol.* 106 (2), 515–524. <https://doi.org/10.1111/j.1365-2672.2008.04020.x>.
- Kumar, R., Datta, T.K., Lalitha, K.V., 2015. *Salmonella* grows vigorously on seafood and expresses its virulence and stress genes at different temperature exposure. *BMC. Microbiol.* (1), 15. <https://doi.org/10.1186/S12866-015-0579-1>.
- Kurtz, J.R., Goggins, J.A., McLachlan, J.B., 2017. *Salmonella* infection: interplay between the bacteria and host immune system. *Immunol. Lett.* 190, 42–50. <https://doi.org/10.1016/j.imlet.2017.07.006>.
- Lee, D., Chang, H.H., Sarnat, S.E., Levy, K., 2019. Precipitation and salmonellosis incidence in Georgia, USA: interactions between extreme rainfall events and antecedent rainfall conditions. *Environ. Health. Perspect.* 127 (9), 1–12. <https://doi.org/10.1289/EHP4621>.
- Leuschner, R.G.K., Boughtflower, M.P., 2001. Standardized laboratory-scale preparation of mayonnaise containing low levels of *Salmonella enterica* serovar Enteritidis. *J. Food. Prot.* 64 (5), 623–629. <https://doi.org/10.4315/0362-028X-64.5.623>.
- Levy, K., Woster, A.P., Goldstein, R.S., Carlton, E.J., 2016. Untangling the impacts of climate change on waterborne diseases: a systematic review of relationships between diarrheal diseases and temperature, rainfall, flooding, and drought. *Environ. Sci. Technol.* 50 (10), 4905–4922. <https://doi.org/10.1021/ACS.EST.5B06186>.
- Liu, S., Kilozon-Nthenge, A., 2017. Prevalence of multidrug-resistant bacteria from U.S.-grown and imported fresh produce retailed in chain supermarkets and ethnic stores of Davidson county, Tennessee. *J. Food. Prot.* 80 (3), 506–514. <https://doi.org/10.4315/0362-028X-JFP-16-178>.
- Liu, H., Whitehouse, C.A., Li, B., 2018. Presence and persistence of *Salmonella* in water: the impact on microbial quality of water and food safety. *Front. Publ. Health* 6, 159. <https://doi.org/10.3389/FPUH.2018.00159>.
- Lou, L., Zhang, P., Piao, R., Wang, Y., 2019. *Salmonella* Pathogenicity Island 1 (SPI-1) and its complex regulatory network. *Front. Cell. Infect. Microbiol.* 9, 270. <https://doi.org/10.3389/FCIMB.2019.00270>.
- Lund, P.A., De Biase, D., Liran, O., Scheler, O., Mira, N.P., Cetecioglu, Z., O'Byrne, C., 2020. Understanding how microorganisms respond to acid pH is central to their control and successful exploitation. *Front. Microbiol.* 11, 556140. <https://doi.org/10.3389/FMICB.2020.556140>.
- Majowicz, S.E., Musto, J., Scallan, E., Angulo, F.J., Kirk, M., O'Brien, S.J., Hoekstra, R.M., 2010. The global burden of nontyphoidal *Salmonella gastroenteritis*. *Clin. Infect. Diseases* 50 (6), 882–889. <https://doi.org/10.1086/650733>.
- Marchello, C.S., Carr, S.D., Crump, J.A., 2020. A systematic review on antimicrobial resistance among *Salmonella typhi* worldwide. *Am. J. Trop. Med. Hyg.* 103 (6), 2518–2527. <https://doi.org/10.4269/AJTMH.20-0258>.
- Marin, C., Cerdà-Cuellar, M., González-Bodi, S., Lorenzo-Rebenaque, L., Vega, S., 2022. Research note: persistent *Salmonella* problems in slaughterhouses related to clones linked to poultry companies. *Poult. Sci.* 101 (8), 101968. <https://doi.org/10.1016/J.PSJ.2022.101968>.
- Martinez-Urtaza, J., Saco, M., Hernandez-Cordova, G., Lozano, A., Garcia-Martin, O., Espinosa, J., 2003. Identification of *Salmonella* serovars isolated from live molluscan shellfish and their significance in the marine environment. *J. Food. Prot.* 66 (2), 226–232. <https://doi.org/10.4315/0362-028X-66.2.226>.
- Mattick, K.L., Jørgensen, F., Legan, J.D., Cole, M.B., Porter, J., Lappin-Scott, H.M., Humphrey, T.J., 2000. Survival and filamentation of *Salmonella enterica* serovar enteritidis PT4 and *Salmonella enterica* serovar typhimurium DT104 at low water activity. *Appl. Environ. Microbiol.* 66 (4), 1274–1279. <https://doi.org/10.1128/AEM.66.4.1274-1279.2000>.
- McMichael, A.J., Woodruff, R.E., Hales, S., 2006. Climate change and human health: present and future risks. *Lancet* 367, 859–869. [https://doi.org/10.1016/S0140-6736\(06\)68079-3](https://doi.org/10.1016/S0140-6736(06)68079-3).
- Medalla, F., Gu, W., Friedman, C.R., Judd, M., Folster, J., Griffin, P.M., Hoekstra, R.M., 2021. Increased incidence of antimicrobial-resistant nontyphoidal *Salmonella* infections, United States, 2004–2016. *Emerging. Infect. Dis.* 27 (6), 1662. <https://doi.org/10.3201/EID2706.204486>.
- Mills, J.N., Gage, K.L., Khan, A.S., 2010. Potential influence of climate change on vector-borne and zoonotic diseases: a review and proposed research plan. *Environ. Health. Perspect.* 118 (11), 1507–1514. <https://doi.org/10.1289/ehp.0901389>.
- Mkangara, M., 2023. Prevention and control of human *Salmonella enterica* infections: an implication in food safety. *Int. J. Food Sci.* 2023, 8899596. <https://doi.org/10.1155/2023/8899596>.
- Montville, T.J., Matthews, K.R., 2008. *Food Microbiology: An Introduction*. ASM Press.
- Mora, C., McKenzie, T., Gaw, L.M., Dean, J.M., von Hammerstein, H., Knudson, T.A., Setter, R.O., Smith, C.Z., Webster, K.M., Patz, J.A., Franklin, E.C., 2022. Over half of known human pathogenic diseases can be aggravated by climate change. *Nat. Clim. Chang* 12 (9), 869–875. <https://doi.org/10.1038/s41558-022-01426-1>.
- Morgado, M.E., Jiang, C., Zambrana, J., Upperman, C.R., Mitchell, C., Boyle, M., Sapkota, A., 2021. Climate change, extreme events, and increased risk of salmonellosis: foodborne diseases active surveillance network (FoodNet), 2004–2014. *Environmen. Health: A. Global. Access. Sci. Source* 20 (1), 1–11. <https://doi.org/10.1186/S12940-021-00787-Y/FIGURES/3>.
- Morrison, C.M., Dial, S.M., Day Jr, W.A., Joens, L.A., 2012. Investigations of *Salmonella enterica* serovar Newport infections of oysters by using immunohistochemistry and knockout mutagenesis. *Appl. Environ. Microbiol.* 78 (8), 2867–2873. <https://doi.org/10.1128/aem.07456-11>.
- Nair, D.V.T., Venkitanarayanan, K., Johny, A.K., 2018. Antibiotic-resistant *Salmonella* in the food supply and the potential role of antibiotic alternatives for control. *Foods* 7 (10). <https://doi.org/10.3390/FOODS7100167>.
- Ngogo, F.A., Joachim, A., Abade, A.M., Rumisha, S.F., Mizinduko, M.M., Majigo, M.V., 2020. Factors associated with *Salmonella* infection in patients with gastrointestinal complaints seeking health care at regional hospital in southern highland of Tanzania. *BMC. Infect. Dis.* 20 (1). <https://doi.org/10.1186/s12879-020-4849-7>.
- Novoslavskij, A., Terentjeva, M., Eizenberga, I., Valcina, O., Bartkevics, V., Berzins, A., 2016. Major foodborne pathogens in fish and fish products: a review. *Ann. Microbiol.* 66 (1), 1–15. <https://doi.org/10.1007/s13213-015-1102-5>.
- Pandey, P.K., Kass, P.H., Soupir, M.L., Biswas, S., Singh, V.P., 2014. Contamination of water resources by pathogenic bacteria. *AMB. Express* 4 (1), 51. <https://doi.org/10.1186/S13568-014-0051-X>.
- Panisello, P.J., Rooney, R., Quantick, P.C., Stanwell-Smith, R., 2000. Application of foodborne disease outbreak data in the development and maintenance of HACCP systems. *Int. J. Food. Microbiol.* 59 (3), 221–234. [https://doi.org/10.1016/S0168-1605\(00\)00376-7](https://doi.org/10.1016/S0168-1605(00)00376-7).
- Park, S.H., Kim, H.J., Cho, W.H., Kim, J.H., Oh, M.H., Kim, S.H., Kim, H.Y., 2009. Identification of *Salmonella enterica* subspecies I, *Salmonella enterica* serovars Typhimurium, Enteritidis and Typhi using multiplex PCR. *FEMS. Microbiol. Lett.* 301 (1), 137–146. <https://doi.org/10.1111/j.1574-6968.2009.01809.x>.
- Petrin, S., Mancin, M., Losasso, C., Deotto, S., Olsen, J.E., Barco, L., 2022. Effect of pH and salinity on the ability of *Salmonella* serotypes to form biofilm. *Front. Microbiol.* 13, 1186. <https://doi.org/10.3389/FMICB.2022.821679/BIBTEX>.
- Popa, G.L., Popa, M.I., 2021. *Salmonella* spp. infection - a continuous threat worldwide. *Germs* 11 (1), 88. <https://doi.org/10.18683/GERMS.2021.1244>.
- Popoff, M.Y., Bockemuhl, J., Gheesling, L.L., 2003. Supplement 2001 (no. 45) to the Kauffmann-White scheme. *Res. Microbiol.* 154 (3), 173–174. [https://doi.org/10.1016/S0923-2508\(03\)00025-1](https://doi.org/10.1016/S0923-2508(03)00025-1).
- Porto, Y.D., Fogaça, F.H.D.S., Andrade, A.O., da Silva, L.K.S., Lima, J.P., da Silva, J.L., Vieira, B.S., Cunha Neto, A., Figueiredo, E.E.S., Tassinari, W.S., 2022. *Salmonella* spp. in aquaculture: an exploratory analysis (integrative review) of microbiological diagnoses between 2000 and 2020. *Animals (Basel)* 13 (1), 27. <https://doi.org/10.3390/ani13010027>.
- Prabhakar, P.K., Vatsa, S., Srivastav, P.P., Pathak, S.S., 2020. A comprehensive review on freshness of fish and assessment: analytical methods and recent innovations. *Food Res. Int* 133, 109157. <https://doi.org/10.1016/j.foodres.2020.109157>.
- Pui, C.F., Wong, W.C., Chai, L.C., Nillian, E., Ghazali, F.M., Cheah, Y.K., Radu, S., 2011. Simultaneous detection of *Salmonella* spp., *Salmonella* Typhi and *Salmonella typhimurium* in sliced fruits using multiplex PCR. *Food Control* 22 (2), 337–342. <https://doi.org/10.1016/j.foodcont.2010.05.021>.
- Punchihewage-Don, A.J., Hawkins, J., Adnan, A.M., Hashem, F., Parveen, S., 2022. The outbreaks and prevalence of antimicrobial resistant *Salmonella* in poultry in the United States: an overview. *Heliyon* 8 (11), e11571. <https://doi.org/10.1016/J.HELIYON.2022.E11571>.
- Rahimi, E., Shakerian, A., Falavarjani, A.G., 2013. Prevalence and antimicrobial resistance of *Salmonella* isolated from fish, shrimp, lobster, and crab in Iran. *Comp. Clin. Path* 22 (1), 59–62. <https://doi.org/10.1007/S00580-011-1368-3/TABLES/2>.
- Rieger, J., Janczyk, P., Hünigen, H., Plendl, J., 2015. Enhancement of immunohistochemical detection of *Salmonella* in tissues of experimentally infected pigs. *Europ. J. Histochem.* 59 (3), 2516. <https://doi.org/10.4081/2Fehj.2015.2516>.
- Rincé, A., Balrière, C., Hervio-Heath, D., Cozien, J., Lozach, S., Parnaudau, S., Gourmelon, M., 2018. Occurrence of bacterial pathogens and human noroviruses in shellfish harvesting areas and their catchments in France. *Front. Microbiol.* 9, 2443. <https://doi.org/10.3389/FMICB.2018.02443/FULL>.
- Robinson, E.J., Gregory, J., Mulvenna, V., Segal, Y., Sullivan, S.G., 2022. Effect of temperature and rainfall on sporadic salmonellosis notifications in Melbourne, Australia 2000–2019: a time-series analysis. *Foodborne Pathog. Dis.* 19 (5), 341–348. <https://doi.org/10.1089/fpd.2021.0093>.
- Rose, J.B., Epstein, P.R., Lipp, E.K., Sherman, B.H., Bernard, S.M., Patz, J.A., 2001. Climate variability and change in the United States: potential impacts on water- and foodborne diseases caused by microbiologic agents. *Environ. Health Perspect.* 109, 211. <https://doi.org/10.1289/EHP.01109S2211>.
- Roy, P.K., Ha, A.J.W., Mizan, M.F.R., Hossain, M.I., Ashrafudoulla, M., Toushik, S.H., Ha, Do, S., 2021. Effects of environmental conditions (temperature, pH, and glucose) on biofilm formation of *Salmonella enterica* serotype Kentucky and virulence gene expression. *Poult. Sci.* 100 (7), 101209. <https://doi.org/10.1016/J.PSJ.2021.101209>.
- Russell, R., Paterson, M., Lima, N., 2010. How will climate change affect mycotoxins in food? *Food. Res. Int* 43, 1902–1914. <https://doi.org/10.1016/j.foodres.2009.07.010>.
- Ryan, D., Pati, N.B., Ojha, U.K., Padhi, C., Ray, S., Jaiswal, S., Singh, G.P., Mannala, G.K., Schultze, T., Chakraborty, T., Suar, M., 2015. Global transcriptome and mutagenic analyses of the acid tolerance response of *Salmonella enterica* serovar Typhimurium. *Appl. Environ. Microbiol.* 81 (23), 8054–8065. <https://doi.org/10.1128/AEM.02172-15>.
- Sachdeva, K., Sundaramurthy, V., 2020. The interplay of host lysosomes and intracellular pathogens. *Front. Cell Infect. Microbiol.* 10, 595502. <https://doi.org/10.3389/fcimb.2020.595502>.
- Sahu, B., Singh, S.D., Behera, B.K., Panda, S.K., Das, A., Parida, P.K., 2019. Rapid detection of *Salmonella* contamination in seafoods using multiplex PCR. *Brazil. J. Microbiol.* 50 (3), 807. <https://doi.org/10.1007/S42770-019-00072-8>.

- Saito, N., Ohashi, Y., Soga, T., Tomita, M., 2010. Unveiling cellular biochemical reactions via metabolomics-driven approaches. *Curr. Opin. Microbiol.* 13, 358–362. <https://doi.org/10.1016/j.mib.2010.04.006>.
- Scallan, E., Hoekstra, R.M., Angulo, F.J., Tauxe, R.V., Widdowson, M.A., Roy ..., S.L., Griffin, P.M., 2011. Foodborne illness acquired in the United States—major pathogens. *Emerging. Infect. Dis.* 17 (1), 7. <https://doi.org/10.3201/EID1701.P11101>.
- Schultz, M., 2008. Theobald Smith. *Emerg. Infect. Dis.* 14 (12), 1940. <https://doi.org/10.3201/EID1412.081188>.
- Silva, J., Leite, D., Fernandes, M., Mena, C., Gibbs, P.A., Teixeira, P., 2011. *Campylobacter* spp. As a foodborne pathogen: a review. *Front. Microbiol.* 2, 200. <https://doi.org/10.3389/fmicb.2011.00200>.
- Singh, P., Teal, T.K., Marsh, T.L., Tiedje, J.M., Mosci, R., Jernigan ..., K., Manning, S.D., 2015. Intestinal microbial communities associated with acute enteric infections and disease recovery. *Microbiome* 3 (1), 45. <https://doi.org/10.1186/s40168-015-0109-2>.
- Siriken, B., 2013. *Salmonella* pathogenicity islands. *Mikrobiyol. Bul* 47 (1), 181–188. <https://doi.org/10.5578/MB.4138>.
- Sonti, R.V., Roth, J.R., 1989. Role of gene duplications in the adaptation of *Salmonella typhimurium* to growth on limiting carbon sources. *Genetics* (1), 123. <https://doi.org/10.1093/genetics/123.1.19>.
- Soubeiga, A.P., Kpoda, D.S., Compaoré, M.K.A., Somda-Belemougri, A., Kaseko, N., Rouamba ..., S.S., Savadogo, A., 2022. Molecular Characterization and the antimicrobial resistance profile of *Salmonella* spp. Isolated from ready-to-eat foods in Ouagadougou, Burkina Faso. *Int. J. Microbiol.* 2022, 1–10. <https://doi.org/10.1155/2022/9640828>.
- Sridhar, S., Steele-Mortimer, O., 2016. Inherent variability of growth media impacts the ability of *Salmonella Typhimurium* to interact with host cells. *PLoS. ONE* 11 (6), 1–14. <https://doi.org/10.1371/journal.pone.0157043>.
- Stackhouse, R.R., Faith, N.G., Kaspar, C.W., Czuprynski, C.J., Wong, A.C.L., 2012. Survival and virulence of *Salmonella enterica* serovar Enteritidis filaments induced by reduced water activity. *Appl. Environ. Microbiol.* 78, 2213–2220. <https://doi.org/10.1128/AEM.06774-11>.
- Steeb, B., Claudi, B., Burton, N.A., Tien, P., Schmidt, A., Farhan ..., H., Bumann, D., 2013. Parallel exploitation of diverse host nutrients enhances *Salmonella* virulence. *PLoS. Pathog.* 9 (4) <https://doi.org/10.1371/journal.ppat.1003301>.
- Stephen, D.M., Barnett, A.G., 2016. Effect of temperature and precipitation on salmonellosis cases in South-East Queensland, Australia: an observational study. *BMJ. Open* 6 (2). <https://doi.org/10.1136/bmjopen-2015-010204>.
- Taylor, E., Kastner, J., Renter, D., 2010. Challenges involved in the *Salmonella* saintpaul outbreak and lessons learned. *J. Public Health. Manag. Practice* 16 (3), 221–231. <https://doi.org/10.1097/PHH.0b013e3181b3a3e4>.
- Todar, K., 2006. *Todar's online textbook of bacteriology*. USA: ©2005 Kenneth Todar University of Wisconsin-Madison department of Bacteriology; 2005. *Salmonella. salmonellosis*.
- Todd, E.C.D., 2014. Foodborne diseases: overview of biological hazards and foodborne diseases. *Encyclopedia. Food Safety* 1, 221. <https://doi.org/10.1016/B978-0-12-378612-8.00071-8>.
- Todd, E., 2020. Food-Borne Disease prevention and risk assessment. *Int. J. Environ. Res. Public Health* 17 (14), 1–13. <https://doi.org/10.3390/IJERPH17145129>.
- Trinetta, V., Magossi, G., Allard, M.W., Tallent, S.M., Brown, E.W., Lomonaco, S., 2020. Characterization of *Salmonella enterica* isolates from selected U.S. swine feed mills by whole-genome sequencing. *Foodborne. Pathog. Dis.* 17 (2), 126–136. <https://doi.org/10.1089/fpd.2019.2701>.
- Troeger, C., Blacker, B.F., Khalil, I.A., Rao, P.C., Cao, S., Zimsen ..., S.R., Reiner, R.C., 2018. Estimates of the global, regional, and national morbidity, mortality, and aetiologies of diarrhoea in 195 countries: a systematic analysis for the global burden of disease study 2016. *Lancet. Infect. Dis* 18 (11), 1211–1228. [https://doi.org/10.1016/S1473-3099\(18\)30362-1](https://doi.org/10.1016/S1473-3099(18)30362-1).
- Venugopal, V., Gopakumar, K., 2017. Shellfish: nutritive value, health benefits, and consumer safety. *Comprehens. Rev. Food Sci. Food Safety* 16 (6), 1219–1242. <https://doi.org/10.1111/1541-4337.12312>.
- Waldman, J., Souza, M.N., Fonseca, A.S.K., Ikuta, N., Lunge, V.R., 2020. Direct detection of *Salmonella* from poultry samples by DNA isothermal amplification. *Br. Poult. Sci.* 61 (6), 653–659. <https://doi.org/10.1080/00071668.2020.1808188>.
- Waldner, L.L., MacKenzie, K.D., Köster, W., White, A.P., 2012. From exit to entry: long-term survival and transmission of *Salmonella*. *Pathogens* 1 (2), 128. <https://doi.org/10.3390/PATHOGENS1020128>.
- Wan Norhana, M.N., Poole, S.E., Deeth, H.C., Dykes, G.A., 2010. The effects of temperature, chlorine and acids on the survival of *Listeria* and *Salmonella* strains associated with uncooked shrimp carapace and cooked shrimp flesh. *Food. Microbiol.* 27 (2), 250–256. <https://doi.org/10.1016/j.fm.2009.10.008>.
- Weiner, L.M., Webb, A.K., Limbago, B., Dudeck, M.A., Patel, J., Kallen ..., A.J., Sievert, D.M., 2016. Antimicrobial-resistant pathogens associated with healthcare-associated infections: summary of data reported to the National Healthcare Safety Network at the Centers for Disease Control and Prevention, 2011–2014. *Infect. Control. Hosp. Epidemiol* 37 (11), 1288. <https://doi.org/10.1017/ICE.2016.174>.
- Winfield, M.D., Groisman, E.A., 2003. Role of nonhost environments in the lifestyles of *Salmonella* and *Escherichia coli*. *Appl. Environ. Microbiol.* 69 (7), 3687–3694. <https://doi.org/10.1128/AEM.69.7.3687-3694.2003>.
- Wolkoff, P., Azuma, K., Carrer, P., 2021. Health, work performance, and risk of infection in office-like environments: the role of indoor temperature, air humidity, and ventilation. *Int. J. Hyg. Environ. Health* 233. <https://doi.org/10.1016/J.IJHEH.2021.113709>.
- Wu, G., Liu, L., Qi, Y., Sun, Y., Yang, N., Xu ..., G., Li, X., 2015. Splenic gene expression profiling in White Leghorn layer inoculated with the *Salmonella enterica* serovar Enteritidis. *Anim. Genet.* 46 (6), 617–626. <https://doi.org/10.1111/AGE.12341>.
- Xu, H., Zhang, W., Zhang, K., Zhang, Y., Wang, Z., Zhang ..., W., Li, Q., 2021. Characterization of *Salmonella* serotypes prevalent in asymptomatic people and patients. *BMC. Infect. Dis.* 21 (1) <https://doi.org/10.1186/s12879-021-06340-Z>.
- Xue, Z.X., Ge, Y., Guo, F.P., Ma, X.J., 2021. *Salmonella* bacteremia and its disseminated infection should not be neglected. *Zhonghua. Nei. Ke. Za. Zhi* 60 (2), 102–105. <https://doi.org/10.3760/CMA.J.CN112138-20200321-00279>.
- Yang, Y., Khoo, W.J., Zheng, Q., Chung, H.J., Yuk, H.G., 2014. Growth temperature alters *Salmonella Enteritidis* heat/acid resistance, membrane lipid composition and stress/virulence related gene expression. *Int. J. Food. Microbiol.* 172, 102–109. <https://doi.org/10.1016/J.IJFOODMICRO.2013.12.006>.
- Yoke-Kqueen, C., Learn-Han, L., Noorzaleha, A.S., Son, R., Sabrina, S., Jiun-Horng, S., Chai-Hoon, K., 2008. Characterization of multiple-antimicrobial-resistant *Salmonella enterica* Subsp. *enterica* isolated from indigenous vegetables and poultry in Malaysia. *Lett. Appl. Microbiol.* 46 (3), 318–324. <https://doi.org/10.1111/j.1472-765X.2007.02311.x>.
- Yurist-Doutsch, S., Arrieta, M.C., Tupin, A., Valdez, Y., Antunes, L.C.M., Yen, R., Finlay, B.B., 2016. Nutrient deprivation affects *Salmonella* invasion and its interaction with the gastrointestinal microbiota. *PLoS. ONE* 11 (7), 1–14. <https://doi.org/10.1371/journal.pone.0159676>.
- Zhang, Y., Bi, P., Hiller, J.E., 2010. Climate variations and *Salmonella* infection in Australian subtropical and tropical regions. *Sci. Total. Environ.* 408 (3), 524–530. <https://doi.org/10.1016/j.scitotenv.2009.10.068>.
- Zhang, L., Fu, Y., Xiong, Z., Ma, Y., Wei, Y., Qu ..., X., Liao, M., 2018. Highly prevalent multidrug-resistant *Salmonella* from chicken and pork meat at retail markets in Guangdong, China. *Front. Microbiol.* 9, 2104. <https://doi.org/10.3389/FMICB.2018.02104>.
- Zhu, J., Li, J., Chen, J., 2012. Survival of *Salmonella* in home-style mayonnaise and acid solutions as affected by acidulant type and preservatives. *J. Food. Prot.* 75 (3), 465–471. <https://doi.org/10.4315/0362-028X.JFP-11-373>.