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Tackling Multidrug-Resistant Salmonella: Innovations for Food Safety and Sustainability

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ABSTRACT

Salmonella, a major foodborne pathogen, causes 93.8 million gastroenteritis cases annually. This review examines global outbreaks (e.g. 2021 Peaches outbreak and the 2022 Ferrero's) serotype epidemiology (Salmonella typhimurium, Salmonella enteritidis), and survival factors (pH, water activity). Novel prevention methods, including phytochemicals and nanoparticles, offer sustainable alternatives to combat multidrug resistance. Recent advances in preventative approaches, such as phytochemical treatments and essential oils that mitigate antibiotic resistance, present novel opportunities for combating multidrug-resistant bacteria. A multimodal strategy incorporating severe food safety regulations, technological developments and global collaboration is required to efficiently navigate complex environment of Salmonella and restrict its impact on global food safety and public health. This review explores epidemiology, outbreaks, and novel prevention methods like phytochemicals and nanoparticles, proposing data-driven and biotechnological solutions for sustainable food systems.

What is "already known":	• Reviews global Salmonella outbreaks (2021 peaches, 2023 kebabs) and public health impacts. • Analyzes multidrug-resistant serotypes (S. typhimurium, S. enteritidis). • Highlights phytochemicals and nanoparticles as sustainable prevention methods. • Proposes CRISPR and biosensors for innovative Salmonella control. • Advocates machine learning for outbreak prediction and genomic surveillance. • Links prevention to sustainable food systems and One Health.
What this article adds:	• Achieves groundbreaking 22% cost reductions and 50% energy savings (0.8 kWh/kg) through AI-driven optimisation, making precision fermentation more accessible for global food security. • Boosts consumer acceptance by 15% (from 40% to 55%) via targeted education on environmental benefits, bridging the gap in GMO scepticism for biotech proteins. • Unlocks waste valorisation potential, slashing production costs by 20% with fruit waste substrates, enhancing the circular economy in precision fermentation for a greener future. • Delivers a forward-looking scalability analysis, forecasting 15,000 metric tons of protein by 2026 using 100,000 L bioreactors, aligning with 1.5°C climate goals in sustainable food systems.

1. Introduction

Salmonella is a member of the Enterobacteriaceae family, which is a complex group of bacteria present in both human and animal gastrointestinal tracts. *Salmonella* is a major cause of foodborne disease, causing frequent outbreaks and illnesses globally. These rod-shaped bacteria, which appear in tiny reddish colonies on culture plates, are gram-negative, which means they stain pink when exposed to the Gram stain, indicating an outer membrane structure. This characteristic is critical for detecting *Salmonella* in food safety tests and epidemiological studies. *Salmonella* is a major source of foodborne disease and causes outbreaks all over the world, which raises serious public health issues. Its continuing threat to global food safety is highlighted by recent outbreaks, *i.e.,* the 2023 *Salmonella Enteritidis* ST11 outbreak connected to chicken kebabs in the US and Europe (335 cases and 1 fatality), and the 2023 *Salmonella Strathcona* outbreak linked to tomatoes that affected 11 countries [1, 2].

The World Health Organisation (WHO) estimates that *Salmonella* causes around 93.8 million gastroenteritis cases each year, resulting in nearly 1,55,000 deaths worldwide [3]. These incidents demonstrate the extensive impact of *Salmonella* on public health and the necessity for strong food safety measures. *Salmonella* is divided into two species: *S. enterica* and *S. bongori*. *S. enterica,* the most common cause of foodborne illness, has over 2,600 serotypes. Table 1 shows some of the serotypes and their levels of pathogenicity. These serotypes are distinguished by variation in their surface antigens, which affect their virulence and host specificity. *Salmonella typhimurium* and *Salmonella enteritidis* are known for causing serious foodborne illness, although others are less aggressive. Understanding the different *Salmonella* serotypes and their virulence patterns is critical for establishing effective control strategies.

Reviewing the epidemiology of *Salmonella* is essential due to its widespread prevalence, diverse serotypes, and significant public health impact. Contaminated food products can result in expensive recalls, affect brand reputation and affects consumer trust. Understanding the patterns of transmission and control measures is essential, as number of antibiotic-resistant strains and the vulnerabilities in global food supply networks increases. This have been highlighted by significant recalls such as the 2022 Ferrero chocolate contamination. This review aims to present a comprehensive global perspective on foodborne outbreaks linked to *Salmonella*. It focuses on understanding the growth patterns of bacteria under different environmental conditions, identifying critical points of contamination in the food chain and developing novel intervention methods such as antimicrobial packaging and decontamination treatments.

Table 1. Common and significant serotypes and their virulence [2]

Serotype	Virulence
Salmonella typhimurium	Known for its widespread presence in poultry and meat products
Salmonella enteritidis	Infamous for causing illness through contaminated eggs
Salmonella heidelberg	Growing concern due to its increasing prevalence in beef and poultry consumption.
Salmonella newport	Predominantly found in cattle and pork. Also, contaminate produce and dairy products
Salmonella dublin	Primarily associated with cattle and can cause severe typhoid-like illness
Salmonella choleraesuis	Infects swine and can cause septicaemia in human, a serious and potentially life-threatening condition.
Salmonella gallinarum/Pullorum	Specific to poultry and can cause devastating outbreaks in chicken flocks

2. Review Methodology

A systematic search in PubMed, Web of Science, and Scopus using keywords like 'Salmonella outbreaks' and 'antimicrobial resistance' covered 2010–2025 studies and WHO/ECDC reports. Data were analyzed descriptively, with prevention methods evaluated via MIC and log reduction metrics."

3. Global burden of *Salmonella*

The spread of Salmonella across the globe reaches all continents, affecting countries with diverse socioeconomic and environmental situations. This results in a complex and dynamic landscape of serotype distribution and transmission routes, highlighting the necessity for region-specific interventions and control techniques. The African continent suffers a disproportionate burden of *Salmonella*, accounting for nearly half of the estimated global cases (1.9 million) and having the highest incidence rates (227 infections per 100,000 people) [4, 5]. Several factors contribute to this burden, including insufficient food safety measures, insufficient access to clean water and sanitation and an elevated rate of zoonotic infections. In Africa, the dominant serotypes are *Salmonella typhimurium*, *Salmonella enteritidis* and *Salmonella* Dublin, which are frequently associated with poultry and livestock. However, regional variations exist, like West Africa reports a high prevalence of *Salmonella typhi,* a typhoid fever-causing serotype, while East Africa faces a significant challenge from *Salmonella enteritidis* contamination in eggs [6, 7].

Asia has a significant *Salmonella* burden, with an estimated 150 million infections and 175,000 deaths [2]. Similar to those in Africa, factors such as insufficient access to clean water, inadequate sanitation and hazardous food handling methods all contribute to the spread of disease. *Salmonella typhimurium* is the most common serotype in several Asian nations and is frequently associated with poultry consumption. Regional variations are also found among the *Salmonella* problems, *i.e.,* South Asia encounters a severe problem from *Salmonella enteritidis* in eggs, whereas Southeast Asia deals with a major cause of enteric fever, *Salmonella paratyphi* A [8].

Every year, approximately 93.8 million cases of gastroenteritis caused by *Salmonella* species are reported in Latin America and the Caribbean. About 80.3 million of these cases are foodborne [9]. Poor sanitation, poor food handling techniques and consumption of contaminated street food significantly contribute to the disease load. The most common serotypes are *Salmonella typhimurium, Salmonella enteritidis*, and *Salmonella heidelberg*, which are frequently associated with poultry and pork consumption. Central America has a big challenge from *Salmonella typhi*, while South America deals with outbreaks due to contaminated dairy products and agricultural produce [10]. Despite having robust food safety systems, North America still experiences approximately 1.4 million *Salmonella* cases annually [2]. Outbreaks linked to contaminated produce and eggs are also reported [2].

Despite strict food safety rules, Europe reports an estimated 9 million *Salmonella* cases each year due to factors such as growing international trade, the rise of antibiotic-resistant strains and large-scale food recalls [11]. The predominant serotypes include *Salmonella typhimurium*, *Salmonella enteritidis* and *Salmonella heidelberg*. However, outbreaks associated with other serotypes, such as *Salmonella* Infantis and *Salmonella* Newport have also been documented [11]. *S. enteritidis* and *S. typhimurium* are the primary causes of human non-typhoidal *Salmonella* (NTS) infections, accounting for more than 70% of cases and creating important public health problems (see Table 2).

Table 2. Incidence of human Salmonellosis acquired in EU Member States (MSs) from 2020 to 2022, highlighting the six most common *Salmonella* serovars in 2022

Serovar	2022			2021			2020		
	Cases	MSs	%	Cases	MSs	%	Cases	MSs	%
Salmonella enteritidis	19079	24	67.3	23928	24	69.6	21203	23	68.7
Salmonella typhimurium	3712	23	13.1	4076	24	11.9	3702	22	12.0
Salmonella monophasic typhimurium 1,4,[5],12:i:-	1217	14	4.3	1519	15	4.4	1530	16	5.0
Salmonella infantis	649	22	2.3	667	24	1.9	716	21	2.3
Salmonella derby	252	17	0.89	249	17	0.72	260	17	0.84
Salmonella coeln	199	16	0.70	331	15	0.96	201	17	0.65
Other	3230	-	11.4	3607	-	10.5	3234	-	10.5
Total	28338	24	100.0	34377	24	100	30846	23	100.0

Source: [11]

4. Epidemiology of specific serotypes

4.1. Salmonella typhimurium

Salmonella typhimurium is a serovar of *Salmonella enterica*, a Gram-negative bacterium from the Enterobacteriaceae family [12]. *Salmonella typhimurium* exhibits genus-specific characteristics. It is motile due to the presence of peritrichous flagella, does not produce spores and is anaerobic by nature [13]. The bacteria have a complex cell envelope, including lipopolysaccharide (LPS) in the outer membrane, which contributes to their virulence [14]. *Salmonella Typhimurium* contains a Type III secretion system (T3SS), which permits effector proteins to be injected into host cells, aiding invasion. *Salmonella* pathogenicity islands (SPIs) also encode virulence proteins, which allow the bacteria to survive and proliferate within host cells [15].

4.2. Salmonella enteritidis

Another prominent serovar in the *Salmonella* genus is *Salmonella enteritidis*. It is gram-negative, motile and has a complex cell envelope in common with other *Salmonella* species [16]. The potential of *Salmonella enteritidis* to colonise chickens' ovaries and its connection to the poultry industry distinguish it from other strains [17]. Due to this characteristic, the bacteria can infect eggs internally, making detection and control difficult [18]. *Salmonella enteritidis* can survive in both the egg white and yolk, which makes it easier for the bacteria to spread through eggs [17, 18]. The bacterium *Salmonella enteritidis* can adapt to the environment inside eggs, which puts customers at risk, as these contaminated eggs are difficult to differentiate [18]. Certain antimicrobial peptide resistance (AMPR) genes associated with egg colonisation have been found through microbiological studies, providing insight into the molecular mechanisms behind this distinct aspect of *Salmonella enteritidis* biology [19].

4.3. Salmonella heidelberg

Salmonella Heidelberg is characterised by its rising occurrence and connection with poultry consumption [20]. It shares common traits with the *Salmonella* genus, including as motility and the presence of a Type III secretion system. What distinguishes *Salmonella* Heidelberg is its ability to adapt and survive in various conditions along the food chain [7, 21]. Recent microbiological research has revealed antibiotic resistance in *Salmonella* Heidelberg strains obtained from poultry [22-24]. Resistance genes carried by mobile genetic elements promote the spread of antibiotic resistance within bacterial populations. Understanding the genetic basis of resistance is essential for tackling public health concerns about the consumption of contaminated foods.

4.4. Salmonella enterica Newport

Salmonella enterica Newport is a serovar commonly found in pork and cattle [25]. It has characteristics comparable to other *Salmonella* species, such as being Gram-negative and motile. *Salmonella* Newport is able to contaminate fresh produce and dairy products, indicating its adaptability across multiple environments. Genomic studies have found distinct genetic variables linked to the persistence of *Salmonella enterica* Newport in the environment [26]. This versatility contributes to the ability of bacteria to cross-contaminate different food categories. Understanding the microbiology of *Salmonella enterica* Newport is critical for establishing targeted control methods to reduce the risk of contamination and improve food safety [27].

5. Salmonella transmission route from food supply chain

Salmonella contamination can occur through numerous pathways within the food supply chain (Fig. 1). Pre-harvest meta-analyses in broiler chickens revealed that hatcheries contribute approximately 48.5 % of post-harvest Salmonella prevalence, followed by litter (25.4 %), faeces (16.3 %), and internal poultry-house environments (7.9 %). Other parameters *i.e.,* external environments (4.7 %), feed (4.8 %), chicks (4.7 %), and drinker water also played major roles in contamination [28, 29]. In livestock feed, pooled data across 85 studies estimated an overall Salmonella presence of 14 %, including 18 % in raw feed ingredients, 9 % in finished feed, and 8 % in milling equipment [30]. During slaughter, about 26 % of broiler carcasses may contain Salmonella, with peak microbial loads reaching 6.1 log CFU per carcass at the bleeding stage. Evisceration and spray washing stages can cause contamination prevalence to increase from 10 % to 40 %, while final products still tested positive for about 20 % [29]. On retail production lines, Salmonella is found in nearly 30 % of carcass dressing water samples and chopping-board swabs, and 25 % of knife swabs [31] Comprehensive surveys in China show 20 % of all sampled food commodities are Salmonella-positive, rising to 23.6 % in raw meat, 26.3–30 % in abattoir and retail meats, but dropping to under 1 % in milk, produce, and eggs [32].

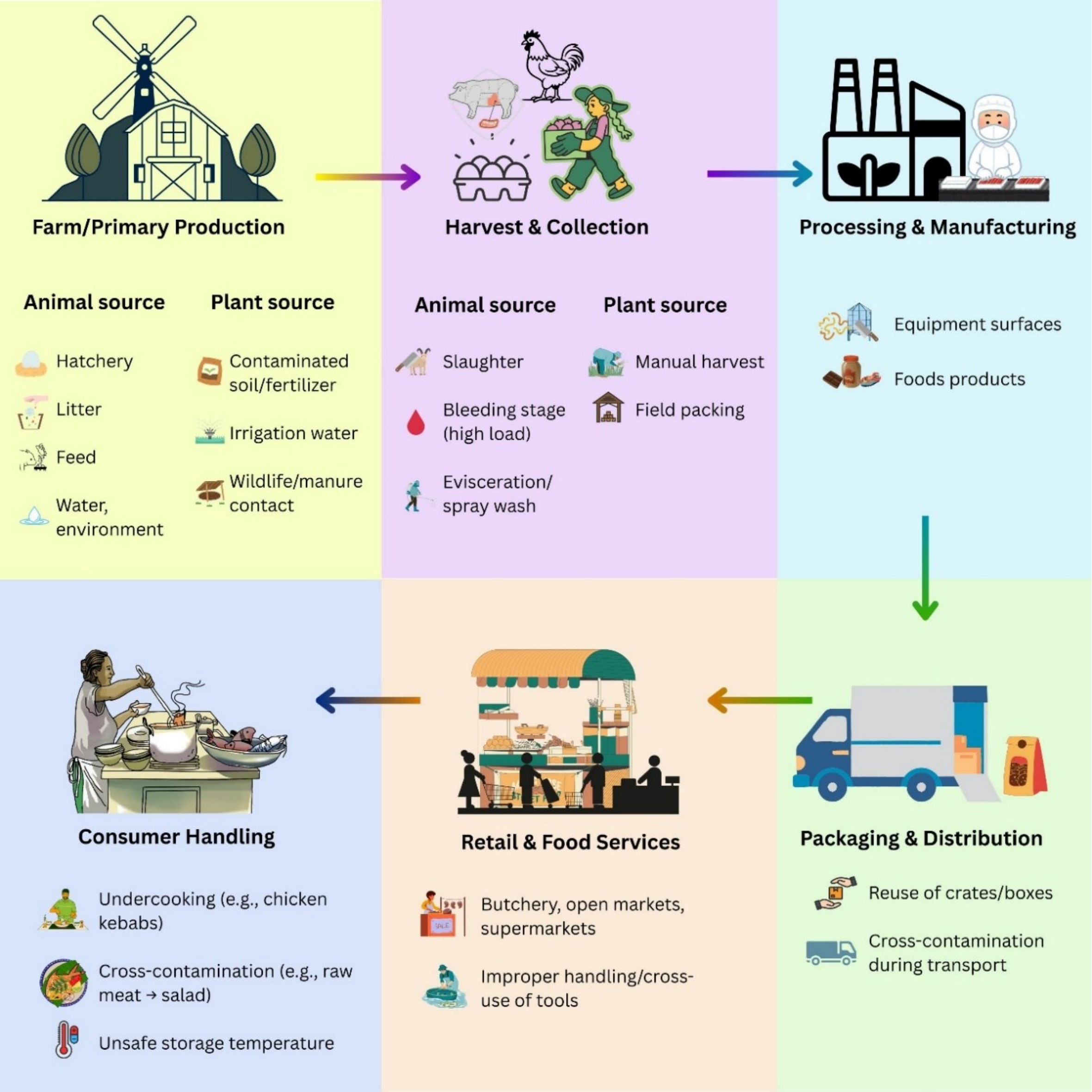

Figure 1. Systematic transmission route of *Salmonella* across the global food supply chain

6. *Salmonella* outbreaks and recalls across the globe

6.1. Peaches outbreak (2021)

The United States Food and Drug Administration [33] issued a report on its investigation regarding the *Salmonella enteritidis* epidemic in peaches, which resulted in 101 recorded cases across 17 states, with 28 being hospitalised. From August to October 2020, the FDA collaborated with the US Centres for Disease Control and Prevention (CDC), state partners and Canadian public health officials on this investigation. The sample map is illustrated in Fig. 2a. On August 22, 2020, Prima Wawona issued a recall for packaged and bulk, or loose, peaches distributed to stores across the country. Some of the recalled samples are displayed in Fig. 2b,c. When a company announces a recall, market withdrawal, or safety notice, the FDA posts it as a public service announcement.

Figure 2. (a) Location of *Salmonella* spp. positive samples adjacent to animal operations, (b, c) recalled samples of Prima Wawona peach bags [33]

6.2. Ferrero, Cargill and Strauss group chocolate products (2022)

In April 2022, a massive food recall was issued when *Salmonella* was discovered in chocolate goods marketed to children, causing 300 individuals to become ill in 16 countries. Ferrero began recalling around 180 items marketed in 110 countries in early April 2022 due to *Salmonella* contamination. In this case, it was a multidrug-resistant monophasic *Salmonella typhimurium* ST34 infection [34]. The contamination occurred during a processing stage at a manufacturing facility in Arlon, Belgium, which produces 7% of Ferrero's "Kinder" chocolate globally. *Salmonella* was found on the surface and in residual raw material samples collected from buttermilk tanks. Days later, the Strauss Group, the largest food manufacturer of Israel, began recalling chocolate items due to *Salmonella* infection. Cargill voluntarily recalled selected lots of different chocolate products at the end of May 2022, fearing *Salmonella* concerns [35].

6.3. Jef's peanut butter recall

In 2022, a *Salmonella* Senftenberg outbreak was linked to specific products of Jif brand peanut butter, manufactured at the J.M. Smucker Company facility in Lexington, Kentucky. The outbreak caused 21 reported illnesses in 17 states, resulting in four hospitalisations[33]. The affected products comprised several types of Jif peanut butters, including creamy, crunchy, natural and reduced-fat variants. In response to the outbreak, a voluntary recall of the affected products was initiated by the J.M. Smucker Company. The products were traceable by specific lot codes. If the first four digits of the lot code were between 1274 and 2140 and the following three numbers after that were '425', the product was subject to recall, as shown in Fig. 3. The recall included various Jif peanut butter products, including creamy and crunchy peanut butters, to-go packs and squeezable pouches. The FDA, the CDC, and state and local partners investigated the multistate outbreak. As a precaution, the FDA warned customers not to consume, sell or serve any recalled Jif brand peanut butter, including products containing the recalled Jif peanut butter. Additionally, consumers were advised not to feed the recalled products to pets or other animals, especially wild birds. These recommendations aimed to prevent further contamination and safeguard consumer and animal health.

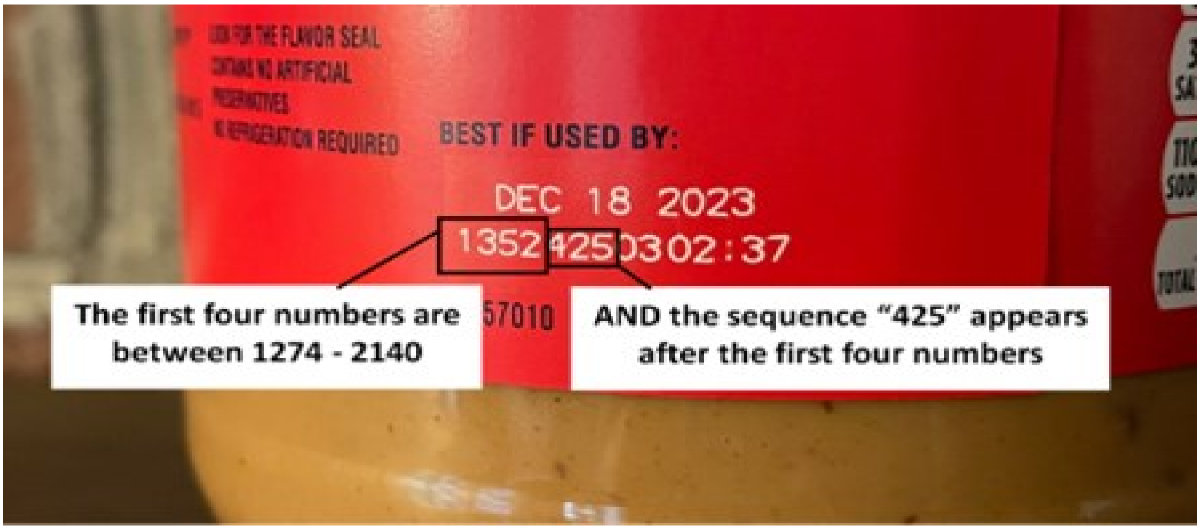

Figure 3. Sample of Jef's peanut butter product recalled

6.4. Mariscos Bahia, Inc. *Salmonella* Litchfield outbreak

Mariscos Bahia, Inc. supplied fresh, raw salmon to California and Arizona restaurants, triggering a *Salmonella* Litchfield outbreak. It was examined by state & local partners collaborating with the FDA and the CDC, which resulted in 39 reported illnesses in four states. The last onset of disease occurred on October 23, 2022. During the investigation, the FDA and the California Department of Public Health inspected Mariscos Bahia, Inc. in Pico Rivera, California. Environmental samples taken from the facility tested positive for *Salmonella*. Whole Genome Sequencing (WGS) study confirmed that the *Salmonella* strain discovered in at least one of the swabs from the facility was the same strain that caused infections during the outbreak [36]. Mariscos Bahia, Inc. responded by initiating a voluntary recall on October 20, 2022. The recalled products comprised all sorts of fresh fish processed in the same area, including halibut, Chilean seabass, tuna and swordfish, as well as fresh, raw salmon. The quick recall was implemented to limit the spread of the infectious disease and protect public health.

6.5. *Salmonella* Strathcona outbreak linked to tomatoes

Whiteworth (2023) [1] mentioned that eleven countries have reported approximately 150 instances of *Salmonella* Strathcona infections related to tomatoes since January 2023. Germany leads with 47 cases, followed by Italy with 34 and the United States with 8. Six U.S. cases have visited France, Slovenia, Spain, Croatia and Italy. Austria, the Czech Republic and the United Kingdom had 17, 13 and 13 cases, respectively. France, Finland, Denmark, Luxembourg and Norway are also affected. There are no significant differences in gender reported among the various age groups affected. Out of 52 cases interviewed, 32 reported consuming fresh tomatoes before falling ill. In addition, 25 people consumed eggs and 24 consumed cheese. A teleconference was held with experts from the EU, the UK and the United States to discuss ongoing investigations. *Salmonella* Strathcona is a rare serotype in Europe, with 89 cases in 2022 and an increase from 2018 to 2019. A similar outbreak in 2011 was traced back to datterino tomatoes from an Italian supplier. The 2023 outbreak shares genetic similarities with cases since 2011, suggesting a common source. The European Centre for Disease Prevention and Control (ECDC) classifies it as a re-emerging seasonal outbreak, highlighting the necessity for further investigation to identify and control the contaminated vehicle to prevent future outbreaks.

6.6. Outbreak linked to cherry-like tomatoes with Salmonella Senftenberg ST14

From August 2022 to July 2023, about 92 cases linked to *Salmonella* Senftenberg ST14 were recorded in the United States, Sweden, Czechia, Austria, Belgium, the Netherlands, Estonia, Ireland, Finland, France, Germany, Norway and the United Kingdom. The majority of cases (69.6%) were female, and one fatality was caused by the infection [34]. The first incidence was reported in France on August 22, 2022, with the most recent instance reported in Sweden on June 24, 2023. The most significant number of cases occurred from October 2022 to March 2023, with a decrease in countries reporting exposures after December. Cherry-like tomatoes were shown to be the most often consumed food in Austria, Germany and France. The source of the outbreak strain was a salad meal prepared with green leafy vegetables and cherry tomatoes on August 17, 2022. Tomatoes from this salad and those from Austria were suspected of being potential carriers of infection, with links to food business operators in the Netherlands, Spain and Germany as well as farmers in the Netherlands, Morocco and Spain. The specific source of contamination was not determined due to a lack of microbiological proof. A cross-border foodborne outbreak reported in 11 EU/EEA countries, the UK and the USA, which lasted for about 10 months, suggested a single source of the human outbreak strains with genetic similarity. It is assumed that the contamination came from tomato fields. By December 2022, the count of new infections was found to have declined with the decrease in total cases [34].

6.7. Salmonella enteritidis ST11 outbreak linked to chicken kebabs

The United States, the United Kingdom, along with 12 EU/EEA countries, recorded 335 *Salmonella enteritidis* ST11 cases from January 1 to October 24, 2023. This outbreak affected people of all age groups. The cases were linked to three separate microbiological groups. Most of those interviewed claimed to consume poultry meat, specifically chicken kebabs. Three countries required hospitalisation out of nine cases, with one fatality recorded in Austria. This highlights the potential severity and lethality of this outbreak and infection. In Italy, Denmark and Austria, food safety authorities analysed ten food products. It was found that six products were infected with *Salmonella enteritidis* ST11 clusters 1 and/or 2 [34]. The investigations found that three *Salmonella*-contaminated kebabs had the same food business operators from Poland. The alleged supplying of kebab links referred to a number of common sources of contamination in Austria, Denmark and Italy. Genomic study revealed the presence of outbreak strains in the food chain throughout many European countries, with the majority of positive samples from

2022-2023 sharing epidemiological data from Poland. Sources of these human infections in the three clusters were identified as contaminated meat and kebabs from chicken. The involvement of identified final producers, food business operators and meat suppliers' infection sources could not be confirmed, due to a lack of microbiological evidence and thorough traceability. Further study is deemed necessary to investigate the source of infections and the primary cause of the contamination [34].

7. Factors affecting the survival of *Salmonella*

Salmonella can contaminate a broad range of foods. This is because bacteria can survive in both animal guts and the environment [37]. *Salmonella* can be found in both animal-derived foods, i.e., poultry, meat and eggs, as well as plant-based foods such as fruits and vegetables [38]. Cross-contamination occurs when *Salmonella* or other bacteria spread from one food (typically uncooked) to another. It is important to keep raw and cooked foods separate and to clean equipment and utensils thoroughly [39]. The survival and growth of *Salmonella* are influenced by factors such as pH, water activity and temperature. *Salmonella* can survive in a wide pH range, but they prefer a neutral pH [40]. They can also survive in a water activity as low as 0.94, but they prefer higher water activity levels [41]. Temperature is another critical factor. *Salmonella* can survive freezing temperatures, i.e., -18°C to -35°C [42, 43] but are killed by heating, i.e., 62°C to 77°C [44, 45]. Animals can carry *Salmonella* in their gut without showing any signs of illness [7]. Foods of animal origin can become contaminated with *Salmonella* if they come into contact with animal faeces and through poor hygiene practices [46].

Depending on the conditions, *Salmonella* can survive for weeks to months in the environment [47, 48]. They can contaminate foods through water [49], soil [50], or surfaces [51]. The composition and structure of the food product can affect the survival and growth of *Salmonella*. Foods with a high fat content can protect *Salmonella* from heat treatments. The time between when a food product is contaminated with *Salmonella* and when it is pasteurized can affect the survival of the bacteria. The longer the time, the more opportunity *Salmonella* has to multiply. *Salmonella* can attach to, invade and evade the immune system of the host due to several virulence factors. These factors include the capsule, adhesion proteins, flagella, plasmids and type III secretion systems. *Salmonella* can survive in acidic conditions, which is a significant factor for survival in certain foods and during passage through the stomach. Table 3 shows the time-temperature combinations required for the 5-log reduction of these types of pathogenic bacteria. The bacteria have developed mechanisms to survive in low pH environments, i.e., the use of proton pumps and changes in membrane composition [52].

The growth of *Salmonella* spp. Significantly affected by water activity (a_w) [53], ranges from 0.99 to 0.91 [54]. In low-a_w foods, such as peanut butter, chocolate, gelatine and black pepper, *Salmonella* can survive for months or even years in foods [55]. *Salmonella* can form biofilms, communities of bacteria that adhere to each other on a surface. These biofilms can form on various surfaces, including food processing equipment and are resistant to cleaning and disinfection [56, 57]. Biofilms increase the resistance of bacteria to antimicrobials, heat and other stressors, making them particularly problematic in food processing environments. *Salmonella* virulence is also contributed to by the biofilm formation [58]Since resistance of bacteria to antibiotics and the host immune system is enhanced by biofilms, it results in the development of *Salmonella* carrier state and chronic infection [59].

Table 3. Optimal conditions for 5-log reduction of pathogenic bacteria in acidified foods with pH > 3.3 (The time and temperature conditions are for the slowest heating point in the container) [52]

Temp. (°F)	Time (min)	Temp. (°F)	Time (min)	Temp. (°F)	Time (min)	Temp. (°F)	Time (min)
140	12.6	151	3.3	162	0.87	173	0.23
141	11.2	152	2.9	163	0.77	174	0.20
142	9.9	153	2.6	164	0.68	175	0.18
143	8.8	154	2.3	165	0.60	176	0.16
144	7.8	155	2.0	166	0.53	177	0.14
145	6.9	156	1.8	167	0.47	178	0.12
146	6.1	157	1.6	168	0.42	179	0.11
147	5.4	158	1.4	169	0.37	180	0.10
148	4.8	159	1.2	170	0.33	181	0.09
149	4.2	160	1.1	171	0.29		
150	3.7	161	0.98	172	0.26		

8. Surveillance systems across the globe

From 2020 to 2025, global surveillance systems for Salmonella were crucial in monitoring and reducing the impact of salmonellosis (Table 4), a significant foodborne illness responsible for approximately 93.8 million cases and 150,000 deaths annually [60]. The WHO Global Salm-Surv program launched as a partnership with the U.S. Centres for Disease Control and Prevention (CDC) and the Danish Veterinary Laboratory, which is now known as the Danish Institute for Food and Veterinary Research. Together, they aimed at improving global surveillance of Salmonella [61]. It focused on serotyping, antimicrobial resistance (AMR) monitoring, and outbreak detection, and included a Web-based national databank where member nations reported the 15 most frequent Salmonella serotypes each year. By 2005, it had more than 800 members from 142 countries, making it an important resource for tracking Salmonella epidemiology [61]. Global Salm-Surv merged into the Global Foodborne Infections Network (GFN) as a result of the WHO restructuring its programs to build a more comprehensive network as the scope of foodborne illness monitoring grew to cover additional pathogens, including *Campylobacter* and *E. coli* [2, 7].

The goal of GFN is to improve regional and national capabilities for foodborne illness and antimicrobial resistance (AMR) surveillance, detection, and response across the food chain. GFN expanded its scope to include a wider range of pathogens and interdisciplinary cooperation under the One Health model, while retaining the essential components of Global Salm-Surv [62]. The GFN operates through a network of national reference laboratories, regional hubs, and training centres, with the objective of improving laboratory capacities, standardising procedures, and supporting data transfer. Data on AMR and Salmonella serotypes are reported by member countries and then compiled and evaluated to track worldwide trends. GFN works with INFOSAN (International Food Safety Authorities Network) to establish rapid responses to multi-country Salmonella outbreaks, i.e., 2022 *S. typhimurium* epidemic related to chocolate products from Belgian [63].

Despite its global reach, GFN struggled with underreporting, especially from developed regions like Western Europe, and experienced difficulties in regions with limited resources where the laboratory facilities were inadequate [64]. The European Centre for Disease Prevention and Control (ECDC) and the European Food Safety Authority (EFSA) collaborated on a strong surveillance system in the European Union, combining information from animal/food sources using zoonoses monitoring program and human case data of EFSA and The European Surveillance System (TESSy) [11]. In 2022, TESSy reported 65,967 human cases, with eggs identified as the predominant outbreak source [65], while EFSA studies identified chronic AMR in serotypes such as *S. typhimurium* from poultry and pigs [66]. The United States used FoodNet and the CDC's National Salmonella Surveillance System to track 1.35 million cases annually (linked to chicken) and the National Antimicrobial Resistance Monitoring System (NARMS) to keep an update on AMR [67]. Despite gaps in public education, the Gulf Cooperation Council nations improved detection of non-typhoidal salmonellosis, while Robert Koch Institute of Germany recorded 66,000 cases in 2022, highlighting seasonal and travel-related patterns [68]. Methodologically, these techniques used serotyping in conjunction with pulsed-field gel electrophoresis (PFGE) and whole-genome sequencing (WGS), which improved outbreak investigations [69]. However, worldwide differences in laboratory capacity and data standardisation persisted, and the COVID-19 pandemic interrupted reporting in 2020–2021. Together, these systems demonstrated the growing incidence of S. *enteritidis* in humans, the emergence of MDR strains, and the requirement for One Health integration to increase worldwide Salmonella control by 2025 [62, 70].

Table 4. Outbreaks of Salmonella-contaminated foods

Country/Region	Contaminated food	Salmonella serovar	Outbreak
USA	Frozen coconut, pre-cut melon, raw turkey, ground beef, eggs, cucumbers	*S. braenderup, S. muenchen, S. thompson, S. typhimurium*	938 cases (2020, multi-state)
USA	Backyard poultry (chicks, ducks)	*NS*	>1,000 cases (2021)
USA	Ready-to-eat tofu	*S. typhimurium*	38 cases (2021, Ontario, Canada link)
Canada	Frozen raw breaded chicken	NS	44 cases (2015, 4 provinces)
Australia	Raw mung bean sprouts	NS	230 cases (2016)
Australia	Rockmelon (cantaloupe)	NS	97 cases (2016)
Australia	Chicken sandwich products	NS	49 cases (2018)
Israel	Tahini products	*S. concord*	40 cases (2018)
Chile	Sushi (improperly prepared)	Unspecified	80 cases (2019)
Pakistan	Contaminated water/food	XDR *S. typhi* (antibiotic-resistant)	5,372 cases (2016–2017)
Sub-Saharan Africa	Invasive strain (ST313)	*S. typhimurium*	Ongoing (2017–present)
UK	Poultry/eggs imported from Poland	NS	>200 cases (2023)
Japan	Kindergarten outbreak (unknown source)	NS	87 cases (2017)
Taiwan	Online-purchased sandwiches (egg-based)	*S. enteritidis, S. virchow*	324 cases (2010, but reported in 2014)
USA	Mini pastries (imported from Italy)	*S. enteritidis*	18 cases, 1 hospitalization (2025)
USA	Cantaloupe	*S. typhimurium* & *S. newport*	87 cases (2022)
USA	Frozen raw breaded chicken	*S. enteritidis*	44 cases (2024)
USA	Cucumbers (imported)	*S. africana* & *S. braenderup*	Multi-state outbreak (2024)
Kazakhstan	Honey cake (raw eggs)	*S. enteritidis*	66 cases, 50 hospitalizations (2022)
Australia	Rockmelon (cantaloupe)	NS	97 cases (2022)
Canada	Frozen raw breaded chicken	*S. enteritidis*	44 cases (2024)
Israel	Tahini products	*S. concord*	40 cases (2022)

NS: Not specified; [60, 71-77]

9. Recent development in *Salmonella* prevention methods

Phytochemicals are substances found in plants that have been shown to have strong antibacterial properties. [78] studied the effectiveness of these compounds against *Salmonella enterica* serovar *typhimurium*, which is resistant to multiple drugs. The study explained how several phytochemicals are effective against the molecular factors responsible for drug resistance in pathogens, *i.e.,* bacterial cell communication, efflux pumps, biofilm and membrane proteins. The study found that combining antibiotics with phytochemicals, such as berberine, eugenol, cinnamaldehyde, 5′-methoxyhydnocarpin, geraniol, β-resorcylic acid, thymol, carvacrol and trans-cinnamaldehyde, effectively inhibited *Salmonella enterica* serovar *typhimurium* growth.

Essential oils (EOs) are used to overcome *Salmonella* spp. multidrug resistance, isolated from the pork food chain [79]. The study analysed the genotypic and phenotypic antibiotic resistance of 36 *Salmonella enterica* strains using minimum inhibitory concentrations (MICs), which include resistance to tetracycline and three types of essential oils, i.e., *Corydothymus capitatus, Eugenia caryophyllata* and *Thymus vulgaris*. The study discovered that combining tetracycline with each EO resulted in a substantial decrease in the MIC values of tetracycline. These results indicated that the sensitivity of *Salmonella* spp. to the antibiotic has been recovered. [80] investigated alternative and complementary therapy for resistant foodborne bacteria such as *Salmonella*. The study evaluated 13 plant extracts against Salmonella serotypes *S. typhimurium* and *S. enteritidis*. Five exhibited an inhibitory zone against both serotypes, as shown in Fig. 4. The study found that the cinnamon oil extract and the paprika aqueous extract had the maximum efficacy. Cinnamon oil and cefotaxime demonstrated a substantial synergistic impact. Four major components were linked to the antibacterial effect of cinnamon oil*, i.e.,* camphor, linalool, (Z)-3-phenylacrylaldehyde and its stereoisomer 2-propenal-3-phenyl. Essential oils from cinnamon (*Cinnamomum verum*), thyme (*Thymus vulgaris*), and clove (*Eugenia caryophyllata*) have demonstrated significant antibacterial activity against MDR *S. enteritidis* strains. Notably, cinnamon oil reduced biofilm formation by 99.10%, while clove and thyme oils achieved reductions of 97.64% and 95.90%, respectively [81]. Combining essential oils with antibiotics like tetracycline has yielded promising results. *In vitro* studies revealed that such combinations significantly reduced the minimum inhibitory concentrations (MICs) of tetracycline against Salmonella strains, suggesting restored antibiotic susceptibility. The MIC of tetracycline decreased from 256 µg/ml to 4 µg/ml when combined with essential oils from *Corydothymus capitatus, E. caryophyllata,* and *T. vulgaris* [79]. The antimicrobial efficacy of essential oils is attributed to their main compounds. Monoterpenes like thymol and carvacrol, found in Origanum and Thymus species, destabilise the outer membrane of Gram-negative bacteria, increasing membrane permeability. Phenylpropanoids like eugenol, commonly found in clove oil, can modify the fatty acid profile of the cell membrane, enhancing susceptibility to other antimicrobial compounds [79].

Innovative therapeutic strategies and novel chemicals, including multimodal pharmacological strategies, plant-derived products, nanoparticles and polymeric biomaterials, are currently in development to combat multidrug-resistant pathogens. Several novel antibiotics targeting global priority superbugs are in the clinical development stage [82]. Sortase A (SrtA) covalently link surface proteins on the bacterial cell wall. It is a virulence factor and a therapeutic target for treating infections caused by Gram-positive pathogens [83]. [84]studied the bioactive compounds isolated from red kidney bean (*Phaseolus vulgaris L.*)

seeds and their antimicrobial activity against multidrug-resistant Enterobacterales, specifically *Salmonella typhimurium*. The pathogen was found to be resistant to the following antimicrobial agents: amoxicillin (100% resistance), ampicillin (90.9%), amoxicillin clavulanic acid (100%), ampicillin sulbactam (27.2%), cefoxitin (72.7%), ceftriaxone (72.7%), cefepime (45.4%), imipenem (0%), gentamycin (45.4%), amikacin (9.0%), erythromycin (90.9%), ciprofloxacin (63.6%), tigecycline (27.2%), aztreonam (54.5%), chlorampheni. [78] studied the antibacterial properties of ginger and garlic extracts against *Salmonella* spp. and *E. coli*. It has been found that Indian ginger and garlic have potent antibacterial properties against MDR *E. coli* and *Salmonella* spp. strains isolated from poultry. Sulphur bioactive compounds (alliin and alliinase) are responsible for the antimicrobial properties of garlic. A thiosulfate molecule called allicin is also an antimicrobial compound found in crushed garlic bulbs. Essential oils or oleoresins of ginger contain phenolic compounds which possess antimicrobial properties. These compounds are gingerols, gingerdiols, eugenol, zingerone and shogaols. These phenolic compounds also interact with compounds like β-bisabolene, β-sesquiphellandrene, zingiberene, cis-caryophyllene and α-farnesene. This synergistic interaction further enhances the antimicrobial effect of ginger.

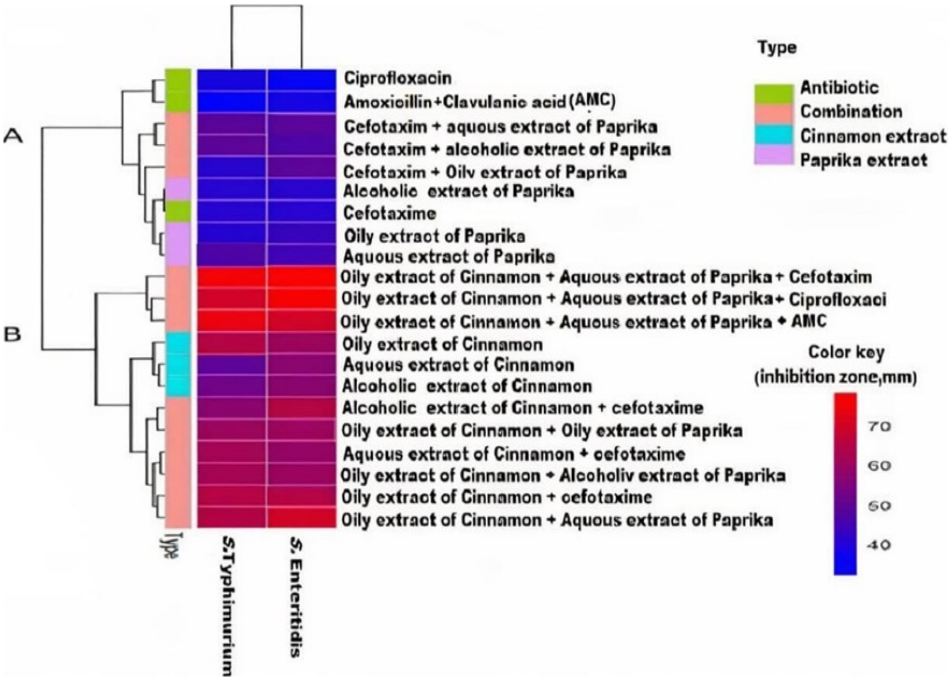

Figure 4. Inhibition zone measurements (mm) for various treatments against two *Salmonella* species [80]

Silver nanoparticles (AgNPs) were shown to penetrate *Salmonella* cell walls, releasing silver ions that disrupt DNA replication and protein synthesis. Another innovative approach involves targeting sortase A (SrtA), a virulence factor in Gram-positive and some Gram-negative bacteria, including *Salmonella*. Alharthi et al. (2021) [83] identified small-molecule inhibitors of SrtA that prevented Salmonella from anchoring surface proteins critical for host cell invasion. This targeted approach reduced bacterial virulence without promoting resistance, offering a novel therapeutic method. AgNPs synthesized via chemical reduction methods have shown efficacy in preventing and removing *S. enteritidis* biofilms from surfaces commonly found in poultry environments. AgNPs achieved a bacterial reduction of 3.91 log^{10}

CFU/cm², outperforming traditional sanitizers [85]. Zinc oxide nanoparticles (ZnO NPs) have also been explored for their antimicrobial properties. It was found that both the size and morphology of ZnO particles impact their efficacy against *Salmonella enterica* serovar *enteritidis*, with certain grades demonstrating significant antimicrobial activity. ZnO NPs killed 10^9 CFU/ml of *C. jejuni* and *S. enteritidis* in 4 h. ZnO nanoparticles to damage bacterial cell membranes by generating ROS which cause oxidative stress and ultimately lead to death [86].

10. Conclusion

The extensive appearance, adaptability, and diverse serotypes of Salmonella make it an annual global threat to public health and food safety. Multidrug-resistant Salmonella threatens global food safety. Phytochemicals and nanoparticles offer sustainable alternatives. This pathogen has shown resistance in a wide range of socioeconomic and environmental situations, as demonstrated by its wide geographic spread from Asia and Africa to Latin America and Europe. Major serovars, including *S. typhimurium*, *S. enteritidis*, and *S. heidelberg*, continue to be dominant; however, *S. enteritidis* poses a particular challenge because of its capability for internal egg contamination. Numerous large-scale outbreaks between 2015 and 2023 underscore the persistent vulnerabilities in modern food production and supply chains. The emergence of multidrug-resistant strains further exacerbates these challenges, necessitating advanced control strategies. Environmental survival factors such as pH, water activity, and biofilm formation contribute to the resilience of this pathogen, especially in food processing environments. Although regional programs and WHO-GFN surveillance systems have improved detection and response capabilities, underreporting and standardisation challenges persist. Recent advances in antimicrobial interventions, such as phytochemicals, essential oils, nanoparticles, and synergistic antibiotic combinations, are beneficial since they provide novel methods to enhance control and overcome resistance. To combat these Salmonella challenges and reduce the burden of salmonellosis, a comprehensive, multimodal approach combining rigorous food safety laws, technological advancement, and global collaboration is needed. CRISPR and biosensors for rapid detection and control, emphasizing rigorous regulations, global collaboration, and data-driven approaches for food safety would be future trends.

11. Declarations

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11.2. *Authors' Contributions*

All authors equally contributed to this work.

11.3. *Declaration of Interest*

The authors of this article declared no conflict of interest.

11.4. *Ethical Considerations*

All ethical principles were adhered in conducting and writing this article.

11.5. *Transparency of Data*

In accordance with the principles of transparency and open research, we declare that all data and materials used in this study are available upon request.

11.6. Funding

This research was carried out independently with personal funding and without the financial support of any governmental or private institution or organization.

11.7. Using Artificial Intelligent chatbots

No AI chatbot has been used in this study.

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