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Current Status of *Salmonella* in Humans and Animals

Tariku Geinoro*, Sead Aliyi and Omer Idris

Hawassa University Faculty of Veterinary Medicine, Ethiopia

**Corresponding author*

Abstract

Salmonella, whose serovars have a broad host range, can infect a wide variety of animals, humans and contaminate environment. Thus, significant pathogen in the one health aspect of the globe. From the two major species of the bacteria, *Salmonella enterica* and *Salmonella bongori*, the former one interplays among animal, human and environment becoming food-borne infection of public health and economic significance. Humans acquire infection mostly through feco-oral route and rarely through direct contact. Diarrhea, enteric fever, and abdominal pain are the common clinical manifestations followed by death with extreme cases. Costs related to disease surveillance; and prevention, control and treatment are the possible economic impacts. Worldwide increment of single and multi-drug resistant strains of the microorganism is the most alarming issue of the date. According to current updates in the reviews and research works, the issue is particularly severe in developing nations such as Ethiopia because there are barriers to maintaining the best possible hygienic food handling procedures and irrational drug usage habits. Both conventional (bacteriological culturing, biochemical tests) and advanced (immunological and molecular based) diagnostic approaches are being used to identify the pathogen and to ascertain the anti-microbial susceptibility profile. Biosecurity is the main approach of *Salmonella* prevention. Treatment is possible with antibiotics. Vaccines are also being utilized for some strains of bacteria. Therefore, this paper is intended for reviewing overall current status of *Salmonella* in humans and animals, concurrently serving as insights for researchers, policy makers and academicians as well. More will be expected from developing world like Ethiopia regarding implementation of detailed investigation aligned with possible corrective actions.

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Introduction

Salmonella is one of the key global causes of diarrheal diseases. It is a genus of a remarkably diversified group of bacteria inhabiting the digestive tract of humans and animals (Meneguzi *et al.,* 2021). Numerous domestic and wild animals, including pigs, cattle, poultry, rodents, wild birds, pets, and exotic species, can harbour *Salmonella* and thus serve as reservoirs. In reality, by excreting *Salmonella*, which can infect humans and other animals throughout the environment, exotic animals like reptiles and amphibians, as well as pets like dogs and cats, may contribute significantly to the pathogen's spread throughout the environment (Galán-Relaño *et al.,* 2023).

There are two classes of *Salmonella*: non-thyphoidal (NTS) and thyphoidal (TS). Worldwide reports of non-typhoidal *Salmonella* infections are widespread, and the prevalence of *Salmonella* is high. On the other hand, different regions have different rates of *Salmonella* (Cuypers *et al.,* 2018). For example, NTS is the second most common causative bacterium for food-borne illness in the USA (Rama *et al.,* 2022), while typhoidal salmonellosis is a major problem in South and Southeast Asia. Once more, bacteremia with substantial morbidity has been linked to invasive non-typhoidal *Salmonella* in sub-Saharan Africa including Ethiopia (Cuypers *et al.,* 2018).

Drug resistance and devastating emergence of multi-drug resistance issues of the bacteria are current pivot areas in the world. The serious health concern posed by the proliferation of antibiotic-resistant bacteria affects both humans and animals.

Despite recent efforts to reduce the use of antibiotics, antimicrobial resistance (AMR) is still considered a zoonosis and poses a serious threat to public health (Gargano *et al.,* 2021). The overall prevalence and anti-microbial resistance rate of the organism has been increasing from time to time (Talukder *et al.,* 2023).

Numerous investigation techniques and diagnostic approaches have been applied on animal, human and environment subjects to identify the status and impacts of *Salmonella* (Bell *et al.,* 2016). For many State and Federal authorities, conventional microbiological culture methods have been the “gold standard”. Sadly, the turnaround time is too long to monitor food products efficiently, particularly those with extremely short shelf lives.

Over the past 30 years, developments in molecular biology and conventional microbiology have significantly increased the rate at which this agent is detected. Currently, a variety of detection techniques, each with its own unique detection system, are available for the identification of Salmonella.

These techniques include immunological-based approaches, molecular-based approaches, mass spectrometry, spectroscopy, optical phenotyping, and biosensor approaches (Bell *et al.,* 2016; Awang *et al.,* 2021).

The economic and public health significance; one health aspect by far of the organism have been also assessed globally and nationally (Asfaw *et al.,* 2022; Li *et al.,* 2022; Ramatla *et al.,* 2022; Galán-Relaño *et al.,* 2023). The disease has grown to be a major global public health concern. It also has a detrimental economic impact because of the high expense of surveillance, investigation, treatment, and illness prevention (Shekhar, 2018).

Frequent and periodical status reviews for such globally concerned pathogen are paramount in order to update the information and to indicate the future insights. Therefore, this paper is aimed with briefing the overall current situation of *Salmonella* with focus on animal-human pathogens and related issues.

Salmonella Classification and Nomenclature

Salmonella was initially discovered and isolated by Dr. Daniel Elmer Salmon and his co-worker Theobald Smith in 1855 from pigs infected with Hog cholera caused by *Salmonella* Choleraesuis so that given the name *Salmonella* (Bhat *et al.,* 2022; Kazmi, 2022).

The *Salmonella* species are classified into serovars (serotypes) based on the lipopolysaccharide (O), flagellar protein (H), and sometimes the capsular (Vi) antigens. Accordingly, there are more than 2700 known serovars. Within a serovar, there are strains that differ in virulence (Ryan *et al.,* 2017; Pearce *et al.,* 2021).

The nomenclature system of *Salmonella* is a complex process. This genus is composed of two main species, *Salmonella enterica* and *Salmonella bongori*. The type species *Salmonella enterica* is further divided into six subspecies on the basis of biochemical properties and genomic relatedness (Pearce *et al.,* 2021). The subspecies are denoted by Roman numerals: I. *S. enterica subsp. enterica*; II. *S. enterica subsp. salamae*; III. *S. enterica subsp. arizonae*; IIIa. *S. enterica subsp. diarizonae*; IV. *S. enterica subsp. houtenae*; V. *S. enterica subsp. indica*. Recently, based on genomic data, it has been proposed to extend the number of subspecies within *S. enterica* to include subspecies *londinensis* (VII)*, brasiliensis* (VIII)*, hibernicus* (IX)*, essexiensis* (X) and *reptilium* (XI), while elevating *S. enterica subspecies arizonae* to the species level, *S. arizonae*. The *S. enterica subsp. enterica* (I) is most common subspecies of *Salmonella* and is found to be predominant infections in humans & warm blooded animals. The remaining five subspecies and *S. bongori* are mainly attributed to infections in cold blooded animals and rare in humans (Dieckmann *et al.,* 2008; Pearce *et al.,* 2021; Sedrakyan *et al.,* 2022).

To avoid confusion between serotypes and species, the serotype name is not italicized and starts with a capital letter. The genus name is given followed by the word "serotype" or abbreviation "ser." and then the serotype name, e.g. *Salmonella* serotype or ser. Typhi. Afterward the name may be shortened with the genus name followed directly by the serotype name, e.g. *Salmonella Typhi* or *S. Typhi* (Brown *et al.,* 2021).

Epidemiology

Sources of infection and Mode of transmission

Salmonellosis has been recognized in all countries but appears to be most prevalent in areas of intensive animal husbandry, especially poultry and swine production. It has complex epidemiology largely because there are several distinct serotypes (serovars) with different reservoirs and diverse geographic incidences.

Changes in food consumption, production, and distribution have led to an increasing frequency of multi-state outbreaks associated with fresh produced and processed foods. They are carried asymptomatically in the intestines or gall bladder of many animals, and are continuously or intermittently shed in the feces. These bacteria are also shed in the feces of animals and humans that are ill. Fomites and mechanical vectors (e.g. insects such as flies) can also spread *Salmonella* (Khan *et al.,* 2022; Ramtahal *et al.,* 2022).

Salmonella species are mainly transmitted by the fecal-oral route. Animals can become infected by ingestion of contaminated feed (including pastures), drinking water or close contact with an infected animal (including humans). Birds and rodents can spread *Salmonella* to livestock. Carnivores are also infected through meat, eggs and other animal products that are not thoroughly cooked (e.g. raw meat diets). People are often infected when they eat contaminated foods of animal origin like meat (poultry, pork, and beef), egg and dairy products (Ryan *et al.,* 2017; Brown *et al.,* 2021; Adem, 2022).

Aerosol transmission, vertical transmission from dam to fetus and horizontal transmission through coitus are proposed modes of transmission in some animals like bovine and equine (Hanson *et al.,* 2016; Holschbach and Peek, 2018).

These bacteria can survive for long periods in the environment and can be isolated from many sources. They can thrive between 8^0C and 45^0C (optimally at 37^0C) and at a pH of 4 to 9. A temperature higher than 70^0C quickly kills them. Pasteurization at 71.1^0C for 15 seconds is sufficient to destroy *Salmonella* in milk (Li *et al.,* 2022). *Salmonella ser.* Choleraesuis can survive for at least 3 months in wet swine feces and 13 months in dry swine feces. *Salmonella ser. Typhimurium* has been isolated from cattle feces at 48 days; the bacterium may survive even longer in water (152 days) and soil (231 days) (Abunna *et al.,* 2017; Brown *et al.,* 2021).

Risk factors

Salmonellosis in animals is mainly associated with contaminated feed, water and environment, which may be attributed to indiscriminate feeding habits. Some animals like dogs and cats are considered to be asymptomatic carriers of the pathogen (Holschbach and Peek, 2018). Working with animals is regarded as occupational hazard for the possibility humans get infected. Consumption of contaminated raw or under-cooked animal products (meat, milk, and egg), vegetables and indirect mechanical contact to equipments are also the potential risk areas for humans acquiring infection (Fegan *et al.,* 2022).

Public Health and Economic Importance

Most of the isolates that cause disease in humans and other mammals belong to *S. enterica subsp. enterica. Salmonella* serovars, sometimes referred to as non-typhoidal *Salmonella*, are potentially zoonotic. The most common serovars infecting humans worldwide are *Salmonella ser. Typhimurium* and *Salmonella ser.* Enteritidis. Some host-adapted serovars such as *S.* Choleraesuis and *S.* Dublin have also been shown to cause serious diseases in humans (Li *et al.,* 2022). Highly exposed human groups such as farmers, slaughterhouse workers, cookers and animal product handlers have a higher ratio of resistant *Salmonella* in their feces than the general population (Noto, 2022). Apart from its potential harm to human health, *Salmonella* is a major animal production infection globally.

The rise of antibiotic-resistant strains, primarily as a result of animal medicine, poses an additional risk to human and animal health. Additionally, it has detrimental economic effects because of surveillance, inquiry, and illness prevention and treatment (Yada, 2023). The use of antibiotics in food animals has a favourable economic impact because they cost farms money to reduce diseases and to prevent and control potential zoonotic diseases. A farm's ability to make money is directly impacted by antibiotic resistance, which is a result of overuse and misuse of antibiotics in veterinary practice. Treatment failure also has a direct detrimental influence on animal welfare, production, and health. In the context of public health, the economic significance of antibiotic resistance is linked to prolonged hospital stays, the use of more costly antibiotics, longer employee sick days, the expense of research and development, and high rates of resistance in both developed and developing nations (Noto, 2022; Yada, 2023).

According to recent projections, if significant efforts are not made to address the effects of antibiotic resistance, the world's economy would lose $100 trillion and around 10 million people would die by 2050 (Fuonou *et al.,* 2017; Noto, 2022).

Pathogenesis and Clinical Aspects

The favorable outcome of a pathogen is based on its capability to enter a host, evade host defense barrier and initiate infection. *Salmonella* has developed deviating schedule to disrupt normal host cellular functions that enable the entry and proliferation inside the host cell (Bhat *et al.,* 2022). Different virulence factors that *Salmonella* generates are crucial to its pathogenicity. These include the ability to invade the cell, a perfect lipopolysaccharide coat, to replicate intra-cellularly and capability to secrete toxins (van Asten *et al.,* 2005; Beshiru *et al.,* 2018; Moxley, 2022; Salim and Motaweq, 2022).

Following entry into the host cell, the bacterium is encased in a membrane compartment called a vacuole, which is composed of the host cell membrane. Under normal circumstances, the presence of a bacterial foreign body would activate the host cell's immune response, resulting in the fusion of the lysosomes and the secretion of digesting enzymes to degrade the intracellular bacteria. However, *Salmonella* uses the type III secretion system to inject other effector proteins into the vacuole, causing the alteration of the compartment structure. The remodeled vacuole blocks the fusion of the lysosomes, and this permits the intracellular survival and replication of the bacteria within the host cells. The capability of the bacteria to survive within macrophages allows them to be carried in the reticulo-endothelial system (RES) (Li *et al.,* 2022).

Based on the clinical patterns in human salmonellosis, *Salmonella* strains can be grouped into typhoid *Salmonella* and non-typhoid *Salmonella* (NTS). Non-typhoidal serotypes can be transferred from animal to human and from human-to-human. They usually invade only the gastrointestinal tract and cause salmonellosis, the symptoms of which can be resolved without antimicrobials. In human infections, the four different clinical manifestations are enteric fever (mostly typhoidal serovars), gastroenteritis (NTS), bacteremia and other extra intestinal complications, and chronic carrier state. Diarrhea, cramping, abdominal pain and fever are major symptoms with infective dose being 10^4 colony forming unit (CFU) (Asfaw *et al.,* 2022; Li *et al.,* 2022).

Isolation and Identification of *Salmonella*

Culture

Depending on the form of the disease, *Salmonella* may be detected in feces; placenta, fetal tissues and vaginal discharge; blood; or various internal organs at necropsy. Embryonated eggs can be cultured from birds. Foods of animal origin like milk, meat from poultry, swine and bovine are also possible sources of the agent.

Intensive methods (pre-enrichment) to detect *Salmonella* can resuscitate stressed organisms and increase the probability that small numbers of organisms can be detected. *Salmonella* grow on many selective and non-selective media (Brown *et al.,* 2021). *Salmonella* species can be identified with biochemical tests. Distinctive features are observed in various culture media and tests (Table 1).

Serology

Immunological-based (serology) can identify the somatic (O), flagellar (H) and capsular (Vi) antigens (Ryan *et al.,* 2017). A huge improvement to these methods has been made with the introduction of more specific target antibodies and genes. Immunological methods detect unique *Salmonella* molecules using two antibodies; a surface-bound primary antibody to capture the target molecule and a reporter antibody to detect the antibody target complex. The techniques can replace isolation agars, lowering the time to presumptive positive result to one to two days. The immunological assays available for *Salmonella* detection are latex agglutination, lateral flow devices (LFD), enzyme linked immunosorbant assay (ELISA), immunochromatography strip test (ICG) (Xia *et al.,* 2016), immunomagnetic separation (Leon-Velarde *et al.,* 2009) and Enzyme-linked fluorescent assay (ELFA).

Table.1 Characteristic features of *Salmonella* on some culture media and biochemical tests

No	Culture media or Biochemical test	Characteristic feature	Description
1	Gram's stain	Gram-ve bacilli/ Red or pink coloured/	Take Safranin/counter stain/ not Crystal violet
2	Rappaport-Vassiliadis with soya (RVS)	Turbid	Malachite green inhibits many G+ves and enriches *Salmonella*; MgCl inhibits Proteus sp and *E. coli*
3	Muller-Kauffman Tetrathionate novobiocin Broth (MKTTn)	Turbid	Ox bile inhibits growth of G+ves; Sodium thiosulphate pentahydrate sulphur source which is selective agent; Brelliant green inhibits growth of G+ves & some G-ves; and Novobiocin is selective agent ant inhibits Proteus sp
4	MacConkey agar	Colonies are colourless	Lactase –ve; non-lactose fermenter
5	Brelliant green agar	Colonies are red	Brelliant green inhibits growth G+ves & most G-ve bacilli
4	Xylose lysine deoxycholate agar (XLD)	pink colonies with black centers	L-lysine differentiate *Salmonella*; Xylose differentiate Shigella; Sodium deoxycholate inhibits G+ves & Sodium thiosulphate indicates H_2S production
5	Hektoen enteric agar (HE)	Colonies are blue-green with black centers	Bile salt mixture inhibits G+ves; Sodium thiosulphate indicates H_2S production; & Acid fuchsin & Bromothymol blue differentiate non-pathogenic organisms, *Salmonella*& Shigella
6	Urease test	phenol red, be yellow or orange/no change	No urease production, negative reaction
7	Simmons Citrate (Citrate utilization)	Bromothymol blue from green to blue	Sodium carbonate, a byproduct of Krebs cycle raises pH
8	Methyl red test	diffuse red color (+ve)	There is mixed acid fermentation
9	Vagus-Proskauer test	VP-negative, no pink-to-red color throughout bro	No production of non-acidic end product
10	Triple Sugar Iron Agar (TSIA)	Alkaline (red) slants and acid (yellow) butts with blackening of the agar	Red or unchanged slant: lactose and sucrose negative (no fermentation of lactose or sucrose); Yellow butt: glucose positive (glucose fermentation);
11	Indole test	Yellow-brown (-ve)	Absence of Tryptophanase enzyme

Source: (Akter *et al*., 2018; Andrews *et al*., 2018; Moxley, 2022)

Table.2 List of antimicrobials reported about last decade for inefficiency against *Salmonella*

R/N	Antimicrobial	Reference
1	Gentamycin	Addis *et al*., 2011; Pritha *et al*., 2020; Sohail *et al*., 2021
2	Ampicillin	Abunna *et al*., 2018; Banti, 2018; Mthembu *et al*., 2019; Yang *et al*., 2019; Bawa *et al*., 2020; Hussain *et al*., 2020; Geresu and Desta., 2021; Gutema *et al*., 2021; Gebeyehu *et al*., 2022
3	Streptomycin	Addis *et al*. , 2011; Wabeto *et al*., 2017; Mthembu *et al*., 2019; Yang *et al*., 2019; Pritha *et al*., 2020; Geresu *et al*., 2021; Alemu *et al*., 2022; Gebeyehu *et al*., 2022
4	Kanamycin	Banti, 2018; Mthembu *et al*., 2019; Geresu and Desta, 2021
5	Nitrofurantoine	Wabeto *et al*., 2017; Bawa *et al*., 2020; Geresu and Desta, 2021
6	Doxycycline	Ghoddusi *et al*., 2015; Sohail *et al*. , 2021
7	Cefpodoxime	Sohail *et al*. , 2021
8	Ciprofloxacin	Hussain *et al*., 2020; Pritha *et al*., 2020; Sohail *et al*. , 2021
9	Enrofloxacin, Colistin sulphate and Erythromycin	Pritha *et al*., 2020
10	Neomycin	Hussain *et al*., 2020; Alemu *et al*., 2022
11	Cefotaxime	Sohail *et al*., 2021; Gebeyehu *et al*., 2022
12	Trimethoprim-sulfamethoxazole	Mthembu *et al*., 2019; Yang *et al*., 2019; Bawa *et al*., 2020
13	Chloramphenicol	Ghoddusi *et al*., 2015; Wabeto *et al*., 2017; Abunna *et al*., 2018; Gutema *et al*., 2021
14	Cefoxitin	Banti, 2018
15	Nalidixic acid	Abunna *et al*., 2018; Banti, 2018; Yang *et al*., 2019
16	Tetracycline	Wabeto *et al*., 2017; Mthembu *et al*., 2019; Yang *et al*., 2019; Bawa *et al*., 2020; Hussain *et al*., 2020; Pritha *et al*., 2020; Geresu and Desta, 2021; Gutema *et al*., 2021
17	Amoxicillin-Clavulonate	Abunna *et al*., 2018; Banti, 2018; Mthembu *et al*., 2019; Bawa *et al*., 2020; Hussain *et al*., 2020; Worku *et al*., 2022
18	Ceftriazone	Mthembu *et al*., 2019
19	Florfenicol	Ghoddusi *et al*., 2015
20	Cephalothin	Bawa *et al*., 2020
21	Sulfamethoxazole	Gutema *et al*., 2021; Talal *et al*., 2022
22	Clindamycin	Talal *et al*., 2022

Molecular methods

Molecular-based assays are the fastest analytical detection methods developed due to the advancement in molecular sciences. These involve the hybridization of short oligonucleotide fragment known as a DNA/RNA probe or primer to detect specific targeted DNA/RNA sequences.

Specific primer/probe can be isolated from microorganisms or engineered according to their specific target. Conventional PCR, real-time PCR, multiplex PCR, and reverse transcriptase PCR have all been used to detect *Salmonella* (RT-PCR) (Lin *et al.,* 2020). *InvA* gene (Ferretti *et al.,* 2001) and 496-bp segment of histidine transport operon gene (Cohen *et al.,* 1993) have been mostly used primer targets to detect the highly conserved regions of *Salmonella* genus in the gel electrophoresis technique.

Prevention and Treatment

In all animals, the risk of clinical salmonellosis can be decreased by good hygiene and minimizing stressful events. Colostrum is important in preventing disease in young animals. Measures to prevent salmonellosis in pets, such as dogs and cats, include those that minimize consumption of raw foods. Biosecurity is the cornerstone of *Salmonella* prevention on the farm. The risk of introducing the bacterium into a herd/flock can be decreased by buying animals or eggs from *Salmonella*–free sources; isolating newly acquired animals; and practicing all-in/all-out herd or flock management, where appropriate. Fecal contamination of feed and water supplies should be prevented (Brown *et al.,* 2021). Contaminated buildings and equipment should be cleaned and disinfected, and contaminated material should be disposed off. Livestock vaccines are available for some serovars such as *Salmonella* ser. Dublin, *Salmonella* ser. Typhimurium, *Salmonella* ser. Abortusequi and *Salmonella* ser. Choleraesuis in some countries. There are also two licensed vaccines currently available against *S. Typhi*: the injectable Vi capsular polysaccharide (Vi CPS) vaccine (Typherix or Typhim Vi) and the oral live attenuated vaccine Ty21a (Vivotif) (Kopecko *et al.,* 2009; Gayet *et al.,* 2017). To decrease the risk of salmonellosis, both food safety practices and the prevention of transmission from animals are important (Brown *et al.,* 2021; Li *et al.,* 2022).

Severe salmonellosis can be treated with a number of antimicrobials including ampicillin, amoxicillin, gentamicin, trimethoprim/sulfamethoxazole, fluoroquinolones and third generation cephalosporins (e.g. cefotaxime, ceftriaxone). Choice of drugs should be based on susceptibility testing when possible. Unfortunately, resistance to many of the drugs used to treat both human and animal salmonellosis has been increased in recent years (Patel *et al.,* 2020; Usmael *et al.,* 2022).

Antimicrobial Resistance Pattern of *Salmonella*

Antimicrobial resistance is the ability of bacteria to resist the bacteriostatic and/or bactericidal effects of one or more antimicrobial agents at clinically achievable concentrations, leading to treatment failure (Noto, 2022). Most identified foodborne bacterial pathogens, including *Salmonella* species, in Ethiopia exhibited high levels of antimicrobial resistance today (Asfaw *et al.,* 2022). Inactivation of the antimicrobial agent, decreased permeability, an active efflux pump system, alteration of the target site, and overproduction of the target site in numerous serotypes to overwhelm the antimicrobials utilized are the main mechanisms of antimicrobial resistance in the *Salmonella* species (van Duijkeren *et al.,* 2018; Auda *et al.,* 2020; Noto, 2022).

Antimicrobial resistant *Salmonella* species counteract the action of different antimicrobials through such a resistance mechanisms. For example, the inactivation of aminoglycosides is mediated by the enzymes adenyl transferases, acetyltransferases, and phosphotransferases. Cleaving β-lactam rings by β-lactamases is the most common resistance mechanism conferred against β-lactams, preventing it from binding to and inactivating bacterial cell wall (Adamczuk *et al.,* 2015; Wójcicki *et al.,* 2022). Similarly, *Salmonella* resist the effects of phenicols, chloramphenicols, through inactivation with chloramphenicol acetyltransferases (CATs) enzyme. Active efflux is also known to be the most common resistance mechanism observed in *Salmonella* against tetracyclines (Maka and Papowska, 2016). Most of currently available antimicrobials against *Salmonella* have been reported to develop resistance at least with 50% (Table 2). Previously effective drugs may loose their potency with standard concentration because of overdose, underdose and misuse in human and veterinary medicines (Girma, 2015; Noto, 2022).

Current Status of *Salmonella* in Ethiopia

The problem is serious in Ethiopia as developing country due to limitations in ensuring optimal hygienic food handling practices and irrational drug use practices (Girma, 2015). A study in Jimma, South West Ethiopia, (Geresu and Desta, 2021) Gondar, Ethiopia (Ejo *et al.,* 2016) and Wolita Sodo, South Ethiopia (Wabeto *et al.,* 2017) showed high contamination rates of *Salmonella* species isolated from raw beef. In another study conducted in Addis Ababa, Ethiopia, in a selected number of butcher shops also found inadequate meat quality and microbiological safety (Zerabruk *et al.,* 2019). Additionally, another study found that cooked meat and fish posed a public health risk in Ethiopia (Bedada *et al.,* 2020). A higher percentage of multidrug-resistant isolates were also detected in ready to eat raw meat (beef, mutton and chevon) at Arba Minch town hotels and restaurants, which may result in serious risk of transmission to handlers, consumers and the environment (Tonjo *et al.,* 2022).

As a review report, among the pathogenic bacteria *Salmonella* species are one of the most common isolates from milk and dairy products in Ethiopia (Keba *et al.,* 2020). Research in the East Wollega Zone of Sibu Sire districts (Adugna and Eshetu, 2021) and Lume and Siraro districts of Oromia state (Amenu *et al.,* 2014) showed poor hygienic practices and microbiological quality of milk obtained from farmers and markets. Collectively, a number of review articles (Pieracci *et al.,* 2016; Asante *et al.,* 2019; Abebe *et al.,* 2020 and Cavalerie *et al.,* 2021) and primary research (Mekonnen *et al.,* 2021) have identified enormous zoonotic bacterial pathogens, among these were *Salmonella* species which are still a public health problem in Ethiopia.

According to numerous studies, most bacterial species of human, animal, food, and environmental origin are becoming more resistant to antimicrobials (Gemeda *et al.,* 2021). This resulted in the loss of valuable antimicrobials. According to a review study, the pooled prevalence of AMR bacteria from live food-producing animals was 20% (Asfaw *et al.,* 2022). High estimates of pooled AMR prevalence were found to be 29% for bacteria identified in milk and environmental samples and 28% for meat (Gemeda *et al.,* 2021). *Salmonella* species are reported to have higher MDR pattern in samples (meat and meat products, dairy and dairy products, poultry products, and food contact surfaces) (Belina *et al.,* 2021). Thus, interactions between humans-animals-ecosystems raise the risk of emerging and re-emerging antimicrobial resistance, which results in fatalities and financial losses each year (Erkyihun *et al.,* 2022).

Conclusion

Salmonella, food-borne pathogens, pose a formidable challenge to human and animal health and significant economic loss worldwide. An important factor in the emergence of MDR strains has been the indiscriminate use of antibiotics, especially as growth promoters and at sub-therapeutic dosages. As researchers prediction, by two or three decades, the global economy will lose $100 trillion and almost 10 million people would die as a result of antibiotic resistance if serious steps are not taken to address its impacts. Protecting the public's health, economy and food safety from the threat of common food-borne pathogens like MDR *Salmonella* requires the implementation of a One Health paradigm and ongoing cooperation in antibiotic stewardship between researchers, medical professionals, veterinarians, and policymakers.

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Competing Interests

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Author Contributions

All authors contributed equally to all the previous versions of the manuscript. All authors read and approved the final manuscript.

Ethical Consent

Ethical approval is not required for this type of work, since we did not test any material on human and animal subjects.

Consent to Participate

The consent to participate in this study was given by each author.

Consent to Publish

The consent of each author was obtained prior to the commencement of the publishing process.

Data Availability

The datasets addressed during the current review are available from the corresponding author on reasonable request.

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