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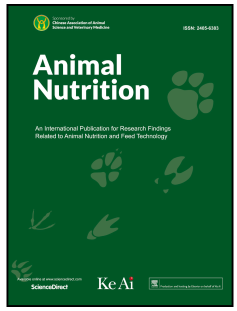

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Animals as sources of food-borne pathogens: A review

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Abstract

Food-producing animals are the major reservoirs for many foodborne pathogens such as *Campylobacter* species, non-Typhi serotypes of *Salmonella enterica*, Shiga toxin-producing strains of *Escherichia coli*, and *Listeria monocytogenes*. The zoonotic potential of foodborne pathogens and their ability to produce toxins causing diseases or even death are sufficient to recognize the seriousness of the situation. This manuscript reviews the evidence that links animals as vehicles of the foodborne pathogens *Salmonella*, *Campylobacter*, Shiga toxigenic *E. coli*, and *L. monocytogenes*, their impact, and their current status. We conclude that these pathogenic bacteria will continue causing outbreaks and deaths throughout the world, because no effective interventions have eliminated them from animals and food.

Keywords: Animal food; Foodborne pathogens; Zoonosis; Enteropathogens

1. Introduction

Food-producing animals (e.g., cattle, chickens, pigs, and turkeys) are the major reservoirs for many foodborne pathogens such as *Campylobacter* species, non-Typhi serotypes of *Salmonella enterica*, Shiga toxin-producing strains of *Escherichia coli*, and *Listeria monocytogenes*. The zoonotic potential of foodborne pathogens and their ability to produce toxins causing diseases or even death are sufficient to recognize the seriousness of the situation. Foodborne pathogens cause millions of cases of sporadic illness and chronic complications, as well as large and challenging outbreaks in many countries and between countries. The magnitude of this problem is demonstrated by the significant proportion of the 1.5 billion annual diarrheal episodes in children less than 3 years of age that are caused by enteropathogenic microorganisms, which results in more than 3 million deaths per year (EFSA-ECDC, 2016). Surveys estimate that in the United States alone, bacterial enteric pathogens cause 9.4 million episodes of foodborne illness in humans, 55,961 hospitalizations, and 1,351 deaths each year (Scallan et al., 2011). However, it is estimated that the reported incidence of food-borne disease represents less than 1% to 10% of the real incidence (Scallan et al., 2011). The importance of food-producing animals as carriers of pathogenic bacteria is real; for example, beef is reported to be the vector of 7% of the 1.7 million cases of foodborne disease that was recorded during 1996 to 2000 in England and Wales (Anderson et al., 2009).

The increase of human population and urbanization, the per capita income, the globalization, the changes on consumer trends (more protein in the diet) have increased the consumption of animal products (Dhama et al., 2013). Estimations suggest that consumption of these products will rise to 376 million tons by 2030 (Dhama et al., 2013).

This high demand of animal products provokes intensive animal production and processing of products, with an increased movement of foods globally. This situation could conduce to defective processing practices and an augment of the risk of contamination by foodborne pathogens at any point of the farm to fork chain.

Animal and animal products contamination is a serious concern because it is difficult to control. Many factors could be involved in contamination, including these from the environment (associated fauna, water from different sources, and animal manure disposal, etc.), and human related animal handling (slaughtering and processing practices, and storage procedures, etc.) (Sofos, 2008).

Microbial pathogens can cause disease by consumption of the animal products contaminated with microorganisms or their toxins. This paper reviews the evidence that links animals as vehicles of the foodborne pathogens *Salmonella*, *Campylobacter*, Shiga toxigenic *E. coli*, and *L. monocytogenes*, their impact, and their current status.

2. Salmonella

Salmonella is found naturally in the environment and in both domestic and wild animals including cats, dogs, amphibians, reptiles, and rodents. It is commonly found in the entrails of poultry, where in some cases could affect the health of the bird (McMullin, 2004; Park et al., 2017). Bacteria are acquired through parents or from the environment (Park et al., 2017). This bacterium causes salmonellosis and other diseases.

Salmonellosis is one of the most common foodborne diseases worldwide, accounting around 93.8 million foodborne illnesses and 155,000 deaths per year worldwide (Eng et al., 2015). Reports in the United States account for more than one million people sickened by *Salmonella* each year, and in approximately 20% of these cases, poultry was the pathogenic vehicle (Hoffmann et al., 2015). Data from 2000 to 2008 give an estimated average cost in health care of this foodborne illness of $55.5 to $93.2 billion, in the United States (Scharff, 2015). Reports from the EU in 2015 showed 94,625 confirmed cases of salmonellosis in humans and 126 deaths (EFSA-ECDC, 2016). The picture is obscure because of the emergence of multi-drug-resistant *Salmonella* serotypes, having a large impact on the efficacy of antibiotic treatment, and an increase in the prevalence of these resistant strains may lead to an increase in mortality caused by *Salmonella* infections (Eng et al., 2015).

The genera *Salmonella* is a member of *Enterobacteriaceae* family, and it includes Gram-negative, flagellated, non-sporulating, and facultative bacteria that grow well between 35 and 37 °C (Ricke et al., 2013). Members of *Salmonella* are commonly classified in 2,579 serotypes according to the Kauffman-White scheme, considering differences in flagellar (H), capsular (k), and somatic (O) antigens (Lamas et al., 2018). Additionally, *Salmonella* serotypes can be subdivided by molecular subtyping methods or by phage typing (Ricke et al., 2013). This bacterium has the ability to induce localized gastroenteritis in humans and some animals, but the range of infections in the host varies depending on the bacterial virulence factors and the immunity and host-resistant capability. The signs and symptoms could evolve from nausea, vomiting, and diarrhea to septicemia or bacteremia, and reactive arthritis as a post-infection sequela that has been reported (Ricke et al., 2013).

There are 2 major species of *Salmonella: S. enterica* and *Salmonella bongori*. *S. bongori* comprises 22 serotypes that are mainly associated with cold-blooded animals, and human infections are uncommon (Lamas, et al 2018). *S. enterica* is divided into 6 subspecies (*enterica*, *salamae*, *arizonae*, *diarizonae*, *houtenae*, and *indica*) because of the differences in biochemical characteristics (Grimont and Weill, 2007). The subspecies *enterica* is responsible for more than 99% of human salmonellosis, and it includes 1,531 serotypes among which are *Salmonella* Typhimurium and *Salmonella* Enteritidis (Lamas et al, 2018). Humans are the only reservoir of typhoid *Salmonella*, produced by *Salmonella* Typhi and *Salmonella* Paratyphi. The rest of *Salmonella* serovars are known as non-typhoid, where the animals are the major reservoir (Eng et al, 2015). *S. enterica*, subsp. enterica serotypes, are principally related to warm-blooded animals whereas the other non-enterica subspecies are more related to cold-blooded animals, although some exceptions have been found (Lamas et al., 2018). The incidence of diseases caused by non-typhoid *Salmonella* varies between countries; for example, it is estimated to cause 690 cases per 100,000 population in Europe, while in Israel, non-typhoid *Salmonella* infection is around 100 cases per 100,000 annually (Eng et al., 2015).

S. Typhimurium is the most dominant serovar around the world, and it is associated with foodborne outbreaks in both developing and high-income countries (Mohammed, 2017). *Salmonella* serovar Newport is mainly isolated in Latin American, North American, and European countries; *Salmonella* Infantis is found globally; *Salmonella* Virchow is found more frequently in Asian, European, and Oceanic countries; *Salmonella* Hadar is found in European countries; and *Salmonella* Agona is found in Latin American, North American, and European countries (Hendriksen et al., 2011). Although there are differences in the most commonly isolated serovars among regions, the differences are not significant between countries within the same region (Hendriksen et al., 2011).

The transmission of non-typhoid *Salmonella* infection to humans can occur through the ingestion of food or water contaminated with waste of infected animals, by direct contact with infected animals or by consumption of food from infected animals (Eng et al., 2015). This bacterium has been isolated from a wide range of animals: poultry, ovines, porcines, fish, and seafood and their food products, and also from some other cold blooded animals (Nguyen et al., 2016; Flockhart et al., 2017, Zajac et al., 2013). Traditionally poultry, meat products, and eggs are the food sources most commonly identified as responsible for outbreaks of salmonellosis (Sanchez et al., 2002), although the microorganism has also been found in other foodstuffs. In the United States, outbreaks with a known vehicle that was associated with beef peaked at 30% in 1981, dropped to 4% in 1982, and after that it has been rising gradually. The proportion of *Salmonella* outbreaks caused by chicken and eggs also increased from 1973 to 1987 (Beat and Griffin, 1990).

Salmonella Thyphimurium has been linked mainly to consumption of undercooked meat or ground beef and dairy products, and especially raw eggs. Outbreaks by *Salmonella* Enteritidis and *Salmonella* Heidelberg have been mainly associated with consumption of raw eggs, whereas outbreaks caused by *Salmonella* Newport have been linked to uncooked ground beef, runny scrambled eggs, or omelets (DuPont, 2007). One important characteristic of *Salmonella* Enteritidis is its ability to contaminate the contents of intact egg shells (DuPont, 2007).

3. Campylobacter

The *Campylobacter* genus was established in 1963, but it was not until 1972 that it was shown to be related to febrile hemorrhagic enteritis (Garcia and Heredia, 2013). The illness caused by these bacteria is named campylobacteriosis, which is characterized by acute onset of diarrhea, abdominal pain, and fever, and it is usually self-limiting (Kaakoush et al., 2015). However, a range of other serious conditions within the gastrointestinal tract has been reported, including intestinal bloody diarrhea, esophageal diseases, periodontitis, functional gastrointestinal disorders, celiac disease, cholecystitis, and colon cancer. Approximately 3 out of 10,000 cases of campylobacteriosis will develop Guillain–Barré syndrome (severe demyelinating neuropathy, Sharp et al., 2016). It is estimated that each case of campylobacteriosis costs $920, mainly because of medical expenses and lost productivity (Silva et al., 2011).

The problem is getting worse because the number of cases of campylobacteriosis has dramatically increased in North America, Europe, and Australia, and data from some African, Asian, and Middle East countries indicate that the disease is endemic, especially in children (Kaakoush et al 2015). It is estimated that *Campylobacter* is responsible for 400 to 500 million cases of infection each year worldwide (García and Heredia, 2013), and together with *Salmonella*, it is the most frequently isolated foodborne pathogen.

Campylobacter is a member of the family *Campylobacteriaceae*, which also includes the genera *Arcobacter*, and the species *Bacteroides ureolyticus*. The genus *Campylobacter* consists of 26 species, 2 provisional species, and 9 subspecies (Kaakoush et al., 2015). They can be divided into more than 600 penner serotypes (heat-stable antigens) and more of 100 Lior serotypes (heat-labile antigens), and only the thermotolerant species have clinical importance (García and Heredia, 2013).

The members of genus *Campylobacter* are small, curved or spiral-shaped Gram-negative bacilli that exhibit rapid and corkscrew-like motion via a polar flagellum, and grow optimally between 37 to 42 °C. For *in vitro* growth, these bacteria need partial oxygen tension (2% to 10%), but generally, *Campylobacter* spp. can be found in diverse environmental conditions because of their high genetic, metabolic, and phenotypic diversity in their population (Garcia and Heredia, 2013). Although several *Campylobacter* species (*C. jejuni, C. coli, C. upsaliensis, C. lari, C. concisus, C. fetus, C. hyointestinalis, C. helveticus, C. insulaenigrae, C. mucosalis, C. rectus, C. sputorum, and C. ureolyticus*) and *Arcobacter butzleri* have been reported to cause gastroenteritis (Butzler, 2004; Kaakush et al., 2015), *C. jejuni* was the species that was most frequently isolated from man and retail poultry, and *C. coli* was generally the second most frequently isolated species. However, the ratio of *C. coli* to *C. jejuni* was considerably different in different countries such as Thailand and South Africa, where *C. coli* was the dominant species isolated from retail poultry (Suzuki and Yamamoto, 2009).

Analysis showed that international travel was the most important risk factor for campylobacteriosis, followed by consumption of undercooked chicken, environmental exposure, and direct contact with farm animals (Kakkus, 2015). It is well documented that poultry products, unpasteurized milk, and water are the main vehicles for *C. jejuni* and *C. coli* infection (Butzer, 2004). Poultry is recognized as the primary source of food-related *Campylobacter* species transmission to humans (Kaakus et al., 2015), probably because of their higher body temperature. Handling, preparation, and consumption of broiler meat may account for 20% to 30% of human campylobacteriosis cases, while 50% to 80% may be attributed to the chicken reservoir as a whole (EFSA, 2010). However, bacterial prevalence in poultry and the contamination level of poultry products varies greatly among countries. For example, an average of 58.8% of retail poultry meats and 60.3% of poultry by-products, were contaminated with *Campylobacter* spp. in Japan (Suzuki and Yamamoto,

2009) whereas 77.3% and 70.7% of poultry at retail was contaminated in the United Kingdom and the United States, respectively (Kramer et al., 2000, Zhao et al., 2001).

Several risk factors such as flock size, age of birds, environmental water supplies, insects and air quality can be linked to colonization and transmission of *Campylobacter* spp. in broiler flocks (Horrocks et al., 2009). Once colonization occurs, the intestinal tract of the chicken (cecum and colon) can harbor large amounts of *Campylobacter* and can contaminate the skin of the carcass during slaughtering if an intestinal leak or rupture occurs (Silva et al., 2011).

Cattle have also been associated with cases of campylobacteriosis. Bacteria prevalence varies greatly from 6% to nearly 90% (Kaakush et al., 2015). The species detected in cattle include *C. jejuni, C. coli, C. lari,* and *C. lanienae,* which show higher levels in feedlots (64% to 68%) compared to adult pastured cattle (6.3% to 7.3%; Horrocks et al., 2009). *Campylobacter* species are also prevalent in pigs and piglets (from 32.8% to 85.0% depending the age of the animal). Bacteria can colonize piglets 24 h after birth, because of exposure to contaminated feces (Kaakush et al., 2015).

Sheep and goats have also been reported to carry *Campylobacter* species, with a prevalence from 6.8% to 17.5% (Kaakush et al., 2015). In addition to all the risks described, contact with domestic pets also presents another exposure pathway for human infection (Silva et al., 2011). Up to 58% of healthy dogs and 97% of diarrheic dogs have been determined to be positive for *Campylobacter* species (Kaakush et al., 2015).

4. Shiga-toxigenic *E. coli* (STEC)

E. coli is the predominant nonpathogenic flora of the human intestine with the exception of anaerobic bacteria, and it helps in the production of vitamins, and competes with and suppresses pathogenic bacterial growth (Feng, 2013). However, some strains have developed the ability to cause disease in the gastrointestinal, urinary, or central nervous system by the acquisition of virulence factors that have allowed them to adapt to new niches (Farrokh et al., 2013).

E. coli is a Gram-negative, facultative anaerobe, non-sporulating rod within the family *Enterobacteriaceae*. It has the ability to ferment different sugars, but lactose fermentation (with production of acid and gas) is a characteristic of the species (Feng, 2013).

The species *E. coli* is divided into serogroups and serotypes according to its antigenic composition, based on the Kauffman classification scheme (somatic or O antigens for serogroups and flagellar or H antigens for serotypes) (Feng, 2013). There are 174 *E. coli* O and 53 *E. coli* H antigens that have been recognized (Croxen et al., 2013).

Most *E. coli* strains are commensal in the intestine, but a small group harbor virulence factors known as *E. coli* pathotypes, or pathogenic, diarrheagenic, or enterovirulent *E. coli*. These include enteropathogenic *E. coli* (EPEC), Shiga toxin-producing *E. coli* (STEC), enteroinvasive *E. coli* (EIEC), enteroaggregative *E. coli* (EAEC), diffusely adherent *E. coli* (DAEC), and enterotoxigenic *E. coli* (ETEC), as well as a new pathotype, adherent invasive *E. coli* (AIEC) (Croxen et al., 2013). Enterohemorrhagic *E. coli* (EHEC) is a subset of pathogenic STEC strains (Feng, 2013).

The presence of the gene encoding Shiga toxins (stx 1 or stx 2), generally acquired via a lambdoid bacteriophage, classifies the strain as Shiga toxin-producing *E. coli* (STEC) or verocytotoxin-producing *E. coli* (VTEC, Croxen et al., 2013). Shiga toxin-producing *E. coli* (STEC), including O157 and many non-O157 serogroups, are important causes of foodborne diseases. Although many outbreaks throughout the world have been attributed to O157:H7, approximately 400 STEC serotypes are considered to be implicated in the disease (Karmali et al., 2010).

The most common STEC serogroup implicated in severe illness in humans is O157, but serogroups O26, O45, O103, O111, O121, and O145 (also known as the Big 6), are the most commonly found non-O157 STEC strains (Croxen et al., 2013). Prevalence of STEC serogroups differs geographically; for example in Australia, non-O157 STEC strains corresponded to 42% of all STEC isolates, where O111 and O26 were the most commonly found serogroups (Croxen et al., 2013), whereas in the EU, O157, O26, O111, O103, and O145 are the serogroups of major concern, but not O45 and O121 (Feng, 2013). Additionally, the importance of serogroup O182 is increasing, showing a larger increment between 2011 and 2013 in EU (EFSA, 2013).

Shiga-toxigenic *E. coli* typically causes severe hemorrhagic colitis in humans, which is accompanied by acute abdominal cramping and vomiting (Anderson et al., 2009). However, several STEC strains are of serious public health concern because their association with large outbreaks and hemolytic uremic syndrome (HUS), which is a sequela in 3% to 7% cases overall, and is the leading cause of acute renal failure in children (Feng, 2013). Reports have estimated that STEC causes 2,801,000 acute illnesses annually worldwide and leads to 3,890 cases of HUS, 270 cases of end-stage renal disease, and 230 deaths in the United States, costing more than $1 billion each year in direct and indirect costs (Majowicz et al., 2014).

The modes by which STEC infection is transmitted in human populations include foodborne transmission, environmental transmission from contaminated animals or water, and transmission through person-to-person contact (Du Pont 2007). It is estimated that animal contact constitutes 8% of non-O157 and 6% of O157:H7 STEC illnesses in the United States (Croxen et al., 2013). In 2013, a total of 73 outbreaks caused by STEC were reported in the EU, of which the main food vehicle was bovine meat and its products (EFSA, 2015).

Cattle and other ruminants are considered to be the major reservoirs for STEC; however, isolation of this bacterium from other animals has been reported (Terajima et al., 2017). The frequency of STEC in animals is variable. For example, reports from Germany indicated that STEC strains were isolated from 28.9% of sampled animals, most frequently from sheep (66.6%), goats (56.1%), and cattle (21.1%), and in a lower proportion from pigs (7.5%), cats (13.8%), and dogs (4.8%), but STEC strains were not found in chickens (Beutin et al., 1993). However, a study in Belgium reported viable O157 isolates in 37.8% of the farms analyzed (Farrokh et al., 2013). In the United States, *E. coli* O157 has been reported in 10% to 28% of cattle (Karmali et al., 2010). A lower incidence of STEC O157 was reported in Japan, with 6.4% of beef cattle in 28% of beef farms analyzed, and this serogroup was not detected in any dairy cows tested (Terajima et al., 2017).

The farm environment plays an important role in STEC colonization and recirculation. However, it is known that most range-fed beef calves are exposed to bacteria by the time of weaning; however, after colonization and survival in the gut, cattle can eliminate bacteria over several months via fecal elimination (Karmali et al., 2010). However, some cows and sheep may be high shedders or super shedders, discharging more than 10^4 colony forming units per gram of feces, and increasing the risk of widespread transmission and contamination. Specific reasons why some animals are in the special shedder stage remain unknown (Callaway et al., 2013; Baker et al., 2016).

5. Listeria

Members of the *Listeria* genera belong to the Firmicutes division, and are currently classified into 17 species: *L. monocytogenes, L. seeligeri, L. ivanovii, L. welshimeri, L. marthii, L. innocua, L. grayi, L. fleischmannii, L. floridensis, L. aquatica, L. newyorkensis, L. cornellensis, L. rocourtiae, L. weihenstephanensis, L. grandensis, L. riparia,* and *L. booriae*. Only 2 of these species, *L. monocytogenes* and *L. ivanovii*, are considered to be pathogenic (Orsi and Wiedmann, 2016).

The species in the *Listeria* genera are divided in 2 groups based on the relatedness of species to *L. monocytogenes*: 1) *Listeria* sensu strictu, which includes *L. monocytogenes, L. seeligeri, L. marthii, L. ivanovii, L. welshimeri,* and *L. innocua*; and 2) *Listeria* sensu lato, a group that includes the other *Listeria* species (Orsi and Wiedmann, 2016).

L. monocytogenes is the most important and representative species of the genera. It is a small, a Gram-positive rod-shaped, facultatively anaerobic, flagellated, ubiquitous, and intracellular pathogen that grows between −0.4 and 50 °C (Donelly and Diez-Gonzalez, 2013). This bacterium is the causative organism of several outbreaks of foodborne disease. Although *L. monocytogenes* is responsible for sporadic cases, its importance lies as a leading cause of death related to foodborne illness (up to 24%) (Farber and Peterkin, 1991), which causes a considerable economic impact for society and the food industry.

L. monocytogenes infection can be non-invasive or invasive (Orsi and Wiedmann, 2016). The invasive illness is characterized by severe symptoms such as meningitis, septicemia, primary bacteremia, endocarditis, non-meningitic central nervous system infection, conjunctivitis, and flu-like illness (Donelly and Diez-Gonzalez, 2013). The non-invasive form of listeriosis is characterized by febrile gastroenteritis. The immunocompromised stage and presence of chronic disorders determine the intensity of the *Listeria* infection (Buchanan et al., 2017).

L. monocytogenes is widely present in plant, soil, and surface water samples, and it has also been found in silage, sewage, slaughterhouse waste, milk from normal cows and cows with mastitis, and in human and animal feces (Donelly and Diez-Gonzalez, 2013). Thus, it is virtually impossible to permanently eradicate *L. monocytogenes* from food environments (Buchanan et al., 2017).

L. monocytogenes had caused episodes of human listeriosis throughout the world and has been found on all the continents, with isolates reported in North and South America, Europe, Africa, Asia, and Oceania (Orsi and Wiedmann, 2016). Although control measures have been implemented, there has been no change or even an increase in the trend of listeriosis cases over time. For example, the EU reported a 8.6% increase in listeriosis in 2013 compared with 2012 (Buchanan, 2017). The United States exhibited no change in the number of outbreaks caused by consumption of dairy products, but foods considered to be of moderate or low risk (vegetables or ice cream) have been implicated in several listeriosis outbreaks. An increase of the frequency of *L. monocytogenes* in fishery products at processing plants (mainly smoked fish) has been reported in the United States and the EU (EFSA, 2015).

Food vehicles for *L. monocytogenes* include crustaceans, shellfish, mollusks and related products, cheese, meat and meat products, pig meat and related products, vegetables, juices and related products, such as mixed salads (Buchanan et al., 2017). Soft cheeses made from pasteurized milk were reported to be vehicles in 5 of 12 listeriosis outbreaks between 2009 and 2011 in the United States (CDC, 2013).

Sporadic cases of listeriosis have been reported in workers in contact with diseased animals (Farber and Peterkin, 1991). *L. monocytogenes* has been isolated from cattle, sheep, goats, and poultry, mainly on their surface, but various reports also showed that this bacterium was present inside muscle, although at low proportions (Buchanan, 2017). In beef and dairy calves, evidence shows a low prevalence of this bacterium in very young calves (<2 months), but its presence increases in the next few months of life, and declines after weaning (Rhoades et al., 2009).

The fecal prevalence of *L. monocytogenes* on United States farms was found to be of 29.4%; 82% of feed samples harbored *Listeria* spp. and 62% had *L. monocytogenes*. *Listeria* spp. was detected in 67% and *L. monocytogenes* in 28% of minced beef samples processed at a farm. The prevalence in fecal poultry samples was 33% for *Listeria* spp. and 33% *for L. monocytogenes* (Skovgaard and Morgen, 1988).

Although the presence of *L. monocytogenes* has been demonstrated in animals, *Listeria* contamination of processed foods is most likely a function of post-processing recontamination.

6. Prevention and control measures

Although it is not easy, it is possible to prevent and get control of enteropathogens carried by animals. Some basic measures are known to be effective to reduce the risk of contamination (Bean, 1990; Dhama et al., 2013; DuPond, 2007; EFSA, 2013; Sofos, 2008); and it is imperative that these are applied in farms and processing plants: 1) reduction of the infection burden in farms by increasing the hygiene and separating the sick animals from healthy ones, 2) since most enteropathogens are killed by chilling, it is necessary to increase the monitoring of this condition after slaughter, 3) avoid the cross-contamination, 4) take precautionary measures to check for pathogen spread in the farm and processing environments 5) judicious use of antibiotics for treating animal diseases, 6) application of sublethal multiple hurdles in the food processing and preservation, 7) proper cooking of the food products, and 8) avoid the consumption of raw/uncooked animal products.

7. Conclusion

We conclude that the pathogenic bacteria described here will continue causing outbreaks and deaths throughout the world, because no effective interventions have eliminated them from animals and food. Further research is imperative to develop effective strategies against these bacteria, and these strategies can be a combination of practices and technologies that already exist or that are being developed.

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486 Table 1. Characteristics of four foodborne bacteria frequently carried by animals or animal products.

Bacteria	Principal species involved	Reservoir animal	Food vehicle	Transmission mode	Disease in humans	Principal signs and symptoms in humans
Salmonella spp.	*Salmonella* Typhimurium	Poultry, bovines, ovines, porcines, fish, and seafood, and some other cold blooded animals	Poultry meat products, and eggs, undercooked meat or ground beef, and dairy products	Ingestion of food or contaminated water, direct contact with infected animals or consumption of food from infected animals	Localized gastroenteritis in humans and some animals	Nausea, vomiting, diarrhea, septicemia or bacteremia, and reactive arthritis as a post-infection sequela
Campylobacter spp.	*C. jejuni* *C. coli*	Poultry, cattle, pigs and piglets, domestic pets	Poultry products, unpasteurized milk, and water	Ingestion of contaminated food or water, direct contact with infected animals or consumption of food from infected animals	Campylobacteriosis	Acute diarrhea, abdominal pain, fever, intestinal bloody diarrhea, esophageal diseases, periodontitis, functional gastrointestinal disorders, celiac disease, cholecystitis, and colon cancer
Shiga toxigenic *E. coli*	Serogroup O157 is most common, but O26, O45, O103, O111, O121, and O145 are also important	Cattle, sheep, goats, and in a lower proportion pigs, cats, and dogs, and other ruminants	Undercooked ground meat, raw milk, raw vegetables, fruits, water, cheese, curd, and juice	Ingestion of contaminated food or water, direct contact with infected animals or consumption of food from infected animals and person-to-person	Severe hemorrhagic colitis in humans	Hemorrhagic diarrhea, acute abdominal cramping and vomiting, and hemolytic uremic syndrome (HUS), as a sequela

				contact		
Listeria spp.	*L. monocytogenes*	Cattle, sheep, goats, and poultry	Crustaceans, shellfish, mollusks, cheese, beef, pork, vegetables and juices, and milk products	Ingestion of food or water contaminated, direct contact with infected animals or consumption of food from infected animals and person-to-person contact	Listeriosis	1) Invasive illness: meningitis, septicemia, primary bacteremia, endocarditis, non-meningitic central nervous system infection, conjunctivitis, and flu-like illness 2) Non-invasive: febrile gastroenteritis

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