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One Health and Food-Borne Disease: *Salmonella* Transmission between Humans, Animals, and Plants

CLAUDIA SILVA,[1] EDMUNDO CALVA,[1] and STANLEY MALOY[2]

[1]Departamento de Microbiología Molecular, Instituto de Biotecnología, Universidad Nacional Autónoma de México, Cuernavaca, Morelos 62210, Mexico; [2]Center for Microbial Sciences, San Diego State University, San Diego, CA 92182-1010

ABSTRACT There are >2,600 recognized serovars of *Salmonella enterica*. Many of these *Salmonella* serovars have a broad host range and can infect a wide variety of animals, including mammals, birds, reptiles, amphibians, fish, and insects. In addition, *Salmonella* can grow in plants and can survive in protozoa, soil, and water. Hence, broad-host-range *Salmonella* can be transmitted via feces from wild animals, farm animals, and pets or by consumption of a wide variety of common foods: poultry, beef, pork, eggs, milk, fruit, vegetables, spices, and nuts. Broad-host-range *Salmonella* pathogens typically cause gastroenteritis in humans. Some *Salmonella* serovars have a more restricted host range that is associated with changes in the virulence plasmid pSV, accumulation of pseudogenes, and chromosome rearrangements. These changes in host-restricted *Salmonella* alter pathogen-host interactions such that host-restricted *Salmonella* organisms commonly cause systemic infections and are transmitted between host populations by asymptomatic carriers. The secondary consequences of efforts to eliminate host-restricted *Salmonella* serovars demonstrate that basic ecological principles govern the environmental niches occupied by these pathogens, making it impossible to thwart *Salmonella* infections without a clear understanding of the human, animal, and environmental reservoirs of these pathogens. Thus, transmission of *S. enterica* provides a compelling example of the One Health paradigm because reducing human infections will require the reduction of *Salmonella* in animals and limitation of transmission from the environment.

INTRODUCTION

There are >2,600 recognized serovars of *Salmonella enterica*. Many of these *Salmonella* serovars have a broad host range and can infect a wide variety of animals, including mammals, birds, reptiles, amphibians, and insects. In addition, *Salmonella* can grow in plants and can survive in protozoa, soil, and water. Hence, reducing human infections will require the reduction of *Salmonella* in animals and limitation of transmission from the environment.

SALMONELLA IN ANIMALS AND HUMANS

The species *S. enterica* is subdivided into seven subspecies, designated by roman numerals. The majority of *Salmonella* human pathogens belong to subspecies I isolates, whereas the other subspecies are mainly associated with cold-blooded vertebrates (1, 2). There are >2,600 serovars of *S. enterica*. The serovars differ widely in their ability to infect different mammals and birds, and can be divided into three groups based upon their host range: broad-host-range or generalist, host-adapted, and host-restricted serovars (3–5). Host-restricted serovars are associated exclusively with one particular host species. For example, *S. enterica* serovars

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Correspondence: Stanley Maloy, smaloy@mail.sdsu.edu

Typhi, Paratyphi A, Paratyphi C, and Sendai cause disease only in humans; Abortusovis is restricted to goats and sheep; Gallinarum and Pullorum are restricted to poultry; Typhisus is restricted to swine; and Abortusequi is restricted to horses. Other serovars are adapted to a particular host but retain the ability to cause disease in alternative hosts. For example, *S.* Choleraesuis and *S.* Dublin are host-adapted serovars associated with severe systemic disease in cattle and pigs, respectively, but they infrequently cause disease in other mammalian hosts, including humans. The host-restricted and host-adapted serovars produce systemic infection in their natural hosts, but there is limited or no evidence of gastroenteritis. These serovars migrate rapidly from the intestine to the reticuloendothelial system, where they reside in intracellular niches (e.g., macrophages) and often persist in the host to produce a carrier state. The establishment of a chronic infection in the carrier permits shedding of a relatively low bacterial load for an extended period of time. In contrast, broad-host-range serovars, such as *S.* Typhimurium and *S.* Enteritidis, can infect a wide range of animals, from insects to reptiles, birds, and mammals. Although capable of causing systemic disease in certain animals, broad-host-range serovars usually induce a self-limiting gastroenteritis in infected hosts (6).

Only about 50 of the subspecies I serovars are isolated as animal and human pathogens (6). Most human salmonellosis cases are food borne, often derived indirectly from animal or human fecal contamination. However, infections are also acquired through direct or indirect animal contact in homes, veterinary clinics, zoological gardens, farm environments, or other public and private settings. Clinically sick animals may pose the greatest risk to humans because they are more likely to shed *Salmonella* organisms at higher concentrations than are apparently healthy animals. However, asymptomatic carriers can shed *Salmonella* organisms for long periods of time. A recent review (6) describes the variety of sources of *Salmonella* transmission from mammals, birds, reptiles, amphibians, fish, and invertebrates to humans; the distribution of the most common human *Salmonella* serovars among animals; and the distribution of these infections in different geographic regions.

Salmonella organisms occur naturally in the gastrointestinal tract of many reptiles as a part of their normal intestinal microbiota and are commonly shed in their feces (6). Although reptiles often carry *Salmonella* subspecies II, III, and IV, other serovars of subspecies I commonly associated with human salmonellosis, notably *S.* Typhimurium and *S.* Enteritidis, also occur in reptiles. The overwhelming majority of reptiles that carry *Salmonella* are asymptomatic. Human salmonellosis attributable to reptile exposure was first documented in the 1940s, and a large number of case reports have since described zoonotic transmission of *Salmonella* from reptiles. A substantial number of human salmonellosis cases have been linked to contact with turtles, terrapins, snakes, and lizards (6).

IDENTIFICATION AND SURVEILLANCE

The wide variety of *Salmonella* serovars, coupled with potential confusion among infections with different food-borne pathogens, provides a challenge for characterizing the source of an outbreak. However, a number of genetic differences among serovars can be exploited for precise identification of different *Salmonella* strains. To improve the accurate identification and comparison of food-borne pathogens, the U.S. Centers for Disease Control and Prevention (CDC) developed the International Molecular Subtyping Network for Foodborne Disease Surveillance, dubbed PulseNet (http://www.pulsenetinternational.org). This site presents the six regional networks and different protocols for the molecular subtyping of *Salmonella*. The website, supported by the World Health Organization, contains phenotypic and epidemiological information from the Global Salm-Surv *Salmonella* surveillance program (http://www.who.int/salmsurv/en/), including information on the major *Salmonella* serovars identified globally as well as antimicrobial resistance. The European Union performs *Salmonella* surveillance in all member countries. A description of *Salmonella*, epidemiological information, and related information about the international surveillance network for the enteric infections *Salmonella* and verocytotoxin-producing *Escherichia coli* O157 (Enternet) can be accessed through the United Kingdom Health Protection Agency website (http://www.hpa.org.uk). Additionally, the *Eurosurveillance* journal publishes information on infectious disease, epidemiology, prevention, and control (http://www.eurosurveillance.org/).

The genomes of many *Salmonella* serovars have now been sequenced (a current list and links to related sites are available at https://www.sanger.ac.uk/resources/downloads/bacteria/salmonella.html). Pairwise genome sequence comparisons between each of the serovars indicate that they have >96% DNA sequence identity between shared genes (7). Each serovar has many insertions and deletions (indels) relative to the other serovars, accounting for 500 to 600 kb of unique DNA in each serovar (10 to 15% of their approximately 4.8-Mbp genomes). The unique regions are distributed over many regions of the

chromosome and range in size from <1 kb to >50 kb. The success of rapid full-genome sequencing in response to the *E. coli* O104:H4 outbreak in Europe in 2011 (8), coupled with the increased availability and reduced cost of whole-genome sequencing, makes it likely that this approach will become more widely used for the identification of foodborne pathogens in the near future.

Because few cases are sufficiently severe to demand professional medical care, providing information to the public about *Salmonella* infections is essential for accurate reporting of outbreaks. General information about *Salmonella* can be accessed at the website of the CDC (http://www.cdc.gov/Salmonella/). This website describes *Salmonella* in language accessible to the general public. In addition, this site provides links to descriptions of *Salmonella* outbreaks. The website salmonella.org (http://www.salmonella.org/) provides general information about *Salmonella* and links to genome sequencing projects and to researchers working on *Salmonella* around the world, to information on transmission from reptiles, and to strain collections available to the research community.

SALMONELLA HOST SPECIFICITY

The genetic differences between the host-restricted, host-adapted, and generalist serovars provide insights into the bacterial characteristics that determine host range. Broad-host-range pathogens must persist in a wide variety of host niches with a diversity of physiological requirements, and thus are under considerable selective constraints. Even small impacts on fitness may prevent broad-host-range bacteria from competing with other bacteria in one of these niches. In contrast, host-specific pathogens persist in a restricted environmental niche and have fewer selective constraints—a lifestyle that sacrifices fast growth in a wide variety of environments for slower growth and persistence in a more protected environment. The slower growth and more uniform metabolic requirements of host-specific *Salmonella* serovars eliminate the potential impact of genetic changes that invoke a fitness cost in fast-growth conditions with fluctuating metabolic demands (9). The loss of selective pressure for many of these functions allows host-restricted serovars to acquire many more loss-of-function mutations (pseudogenes) than broad-host-range serovars (10, 11). Some of these pseudogenes actually benefit survival in certain hosts by preventing expression of gene products that stimulate an immune response.

In addition to changes in the chromosome of *Salmonella*, mobile genetic elements can also play a key role in determining host specificity (12). One noteworthy difference between host-restricted and generalist *Salmonella* serovars is the presence of the *Salmonella* virulence plasmid (pSV). A small fraction of the *S. enterica* subspecies I serovars contain pSV. This plasmid encodes the *spv* operon, which plays a role in the expression of the virulence of the serovars in their specific hosts (13–17). The nine *S. enterica* serovars in which a pSV has been found are Abortusovis, Abortusequis, Choleraesuis, Dublin, Gallinarum, Paratyphi C, Sendai, Enteritidis, and Typhimurium. With the exception of the broad-host-range serovars *S.* Enteritidis and *S.* Typhimurium, few broad-host-range serovars carry pSV. Moreover, the host-restricted *S.* Typhi lacks pSV. Despite many common properties shared by the pSVs of different serovars, each plasmid seems to be specific to its bacterial host, exemplified by a unique plasmid size in different serovars (18). Numerous virulence determinants involved in modulation of the host immune response to infection, such as *rck*, *rsk*, and *spf*, are carried on pSV. Most of the variation among serovars in the pSV is due to the presence or absence of the conjugal transfer operon (*tra*) and the *pef* or *fae* fimbrial operons (18, 19). The *spv* region is inserted into the chromosome in subspecies II, IIIa, IV, and VII (20).

Loss of the *spv* region abolishes the virulence phenotype of the serovars in their animal hosts, and often in the mouse model (14, 15, 21). On the other hand, the introduction of a pSV to a serovar that is naturally devoid of it does not increase the virulence properties of the strain (22–24), suggesting that other chromosomally encoded factors are responsible for the virulence phenotype. Not all the members of a serovar contain the pSV; often within the population some members carry the plasmid while others do not (23, 24). The prevalence of the pSV in *S.* Typhimurium isolates from pigs in Japan can be illustrative of this point: only 36% carried the pSV, but they were predominantly associated with systemically infected pigs (92%), in contrast to pigs with gastrointestinal symptoms (19%) or healthy pigs (17%) (25). Broad-host-range serovars display more genetic variability than host-adapted or host-restricted serovars, which may account for their abundance of genetic resources to produce diverse clinical outcomes (5).

EVOLUTION OF HOST RANGE OF VARIANTS

S. Typhimurium has been isolated from essentially all warm-blooded animals and reptiles and is the most frequently documented serovar implicated in transmission of salmonellosis from mammals to humans (6). This

serovar can infect some animal hosts without producing disease (asymptomatic carriers) while causing acute disease in others (5). Subtyping methods, such as phage typing, macrorestriction mapping via pulsed-field gel electrophoresis, and multilocus sequence typing, have been used to characterize the genetic variability within *S.* Typhimurium strains isolated from a wide range of hosts in different geographic regions, such as a recent study done by us in Mexico (12, 26, 27). These studies have revealed that although *S.* Typhimurium has been regarded as a broad-host-range serovar, some strains have a broad host range while other strains are closely associated with particular hosts.

The definitive phage type 104 (DT104) is an example of a broad-host-range *S.* Typhimurium strain. This clone emerged during the 1980s and rapidly spread around the world, infecting a wide variety of animals, including humans. DT104 acquired a genomic island carrying multidrug resistance determinants, making it a major public health threat (28).

On the other hand, certain *S.* Typhimurium strains have a narrow host range. *S.* Typhimurium DT40 and DT56v are commonly associated with passerine birds. These strains are rarely detected in other animals, but there have been reports of infection of livestock from wild birds and infection of cats that consumed infected birds (29). *Salmonella* can be isolated from birds that show symptoms of salmonellosis, but birds of the same species can also be asymptomatic carriers (29). In addition, Rabsch et al. (30) demonstrated that DT2 and DT99 (variant Copenhagen) were almost exclusively associated with pigeons for many decades and over a wide geographic range. These strains produce fatal systemic disease in pigeons, similar to other highly host-adapted or host-restricted *Salmonella* serovars, although they retain the ability to cause disease in BALB/c mice. Host adaptation is often associated with increased survival in macrophages of the preferred host (31). The pigeon-adapted *Salmonella* strains were tested for virulence in mammals and pigeons (30). The pigeon-adapted strains showed enhanced cytotoxicity in pigeon macrophages and led to the development of typhoid fever-like syndrome with a high mortality rate in pigeons, with higher bacterial counts in the internal organs.

These observations indicate that increased adaptation of a *Salmonella* serovar to a certain host is associated with increased virulence, systemic disease, and asymptomatic carriers that shed the pathogen over extended periods (3). Furthermore, the pigeon-adapted *S.* Typhimurium strain was found in the ovaries of infected pigeons, a characteristic of other known host-adapted and host-restricted *S. enterica* serovars, including Pullorum, Gallinarum, Abortusovis, and Dublin (5). This potential for vertical transmission may facilitate the maintenance of a host-adapted *Salmonella* serovar in the limited available population.

In certain cases the outcome of infection may result from a natural balance in which one serovar competitively excludes other members of the same serogroup. The natural balance may be disrupted by human intervention (4). This scenario was documented by the investigation of the epidemiological consequences of eradication of the avian-adapted *S.* Gallinarum from poultry in the United States and Europe (32). Infections with the two host-restricted strains, *S.* Gallinarum and *S.* Pullorum, cause severe disease with high mortality and considerable economic losses on poultry farms. Adult animals often develop a carrier state, with transovarian transmission to newly hatched chicks (33). Because *S.* Gallinarum and *S.* Pullorum are host restricted, they are not a risk to human health. Like *S.* Gallinarum and *S.* Pullorum infections, infections with *S.* Enteritidis are typically asymptomatic in adult poultry, but transovarian transmission of *S.* Enteritidis results in high mortality of newly hatched chicks. In addition, because *S.* Enteritidis is a broad-host-range serovar, rodents and other vectors can readily facilitate transmission between poultry facilities. National efforts to eliminate *S.* Gallinarum and *S.* Pullorum from poultry farms greatly reduced these serovars in the United States and Europe, but apparently *S.* Enteritidis filled this vacant ecological niche, because the dramatic increase in *S.* Enteritidis in poultry coincided with the eradication of *S.* Gallinarum and *S.* Pullorum (Fig. 1) (32). This example nicely illustrates how a better understanding of host adaptation may provide new insights into the emergence of infectious disease (4).

NONMAMMALIAN VECTORS FOR *SALMONELLA*

Salmonella has been isolated from a large number of vertebrate species, and outbreaks can often be linked to infected animals. Once excreted from an animal host, *Salmonella* faces limited nutrient availability, osmotic stress, large variations in temperature and pH, and predation (34, 35). The survival of *Salmonella* in the secondary habitat ensures its passage to the next host. *Salmonella* has been detected in several locations within farms and slaughterhouses, and long-term contamination of farms appears to be a widespread phenomenon.

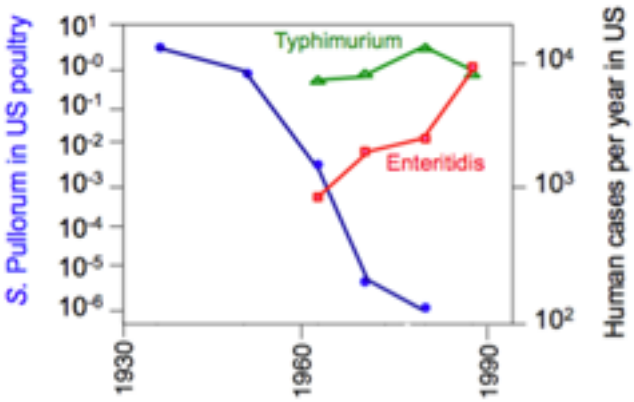

FIGURE 1 Changes in prevalence of *S. enterica* serovars Pullorum versus Enteritidis and Typhimurium in the United States. As the prevalence of Pullorum in U.S. poultry flocks decreased as a result of a U.S. Department of Agriculture program (blue line), the prevalence of Enteritidis in humans increased (red line). Transmission of Enteritidis to humans from chicken eggs increased coordinately with the increased prevalence in poultry. During the period when the incidence of Enteritidis infections in humans was increasing, the incidence of Typhimurium infections in humans (green line) was relatively unchanged. Figure redrawn from reference 65. See the original reference for precise numbers. doi:10.1128/microbiolspec.OH-0020-2013.f1

Insects and worms have been proposed as disease vectors for *Salmonella* on farms and agricultural fields, in animal feed, and in households. Biting mites have also been shown to efficiently transit *Salmonella* to chickens, and houseflies have been implicated in the transmission of typhoid fever vectors in military camps. Moreover, insects may represent reservoir hosts that play pivotal roles in *Salmonella* persistence. Birds, mice, litter beetles, and flies are important vectors for the rapid dissemination of *Salmonella* in the environment (6, 35, 36). Flies that come in contact with contaminated material, such as manure, food, and water, are capable of transmitting bacteria (37, 38). Association of *Salmonella* with insect vectors may be determined by specific adhesion-receptor interactions. Initial attempts at recovering *S.* Enteritidis from the surface of the houseflies by using an aqueous rinse were largely unsuccessful, but rinsing the flies with 0.5% detergent demonstrated that the flies were contaminated with high levels of bacteria. These results imply that *S.* Enteritidis was tightly associated with houseflies (37).

Salmonella has been collected from soil samples from both agricultural and recreational areas that serve as bacterial reservoirs and may aid transmission between hosts (39). Broad-host-range strains effectively cycle through ecosystems, and there are more environmental reservoirs where they can multiply than previously thought. Semenov et al. (40) designed long-chain experiments to follow bacteria through abiotic habitats (dung and soil), plant habitats (fodder and oats), and animal digestive tracts (snails, mice, and chicken), where the organisms underwent significant shifts in temperature, pH, oxygen, substrate availability, grazing by predators, and exposure to parasites like phages and amebae. They concluded that the population density of the enteric pathogens in these different habitats is sufficiently high (ca. 10^3/g) to cause disease in humans (40).

Salmonella is adapted to survive in host macrophages, so it is not surprising that it can also survive in protozoa in nature. *Salmonella* can survive in the vacuoles of protozoa, providing another niche for *Salmonella* in the environment (41–43). *S.* Thompson is expelled from *Tetrahymena* in vesicles containing a high density of bacteria, and the surrounding membrane may help protect bacteria from desiccation and disinfectants such as chlorine. Furthermore, it has been recently proposed that *Salmonella* organisms from rumen protozoa display a hypervirulent phenotype due to the hyperactivation of virulence gene expression, and that this environment provides a venue for conjugal transfer of antibiotic resistance plasmids (44, 45). Indeed, it has been postulated that protozoan predation may be the selective pressure maintaining O-antigen diversity among *Salmonella* organisms (46, 47).

SALMONELLA-PLANT INTERACTIONS AND THE FOOD CHAIN

Fresh fruit and vegetables are now recognized to be a major route of entry for pathogenic enterobacteria into the food chain. *Salmonella* and *E. coli* are among the most prevalent food-borne bacterial pathogens in the developed world and are able to enter the food chain at any point from farm to table (48). Changes in farming practices, food production, consumer habits, and improved surveillance are all possible factors in the increased prevalence of pathogenic enterobacteria in fresh produce. However, recent studies have demonstrated that *Salmonella* can interact specifically with plants, indicating that plants can serve as alternative hosts for the transmission of disease (49).

A wide range of fresh fruit and vegetable products have been implicated in *Salmonella* infection, most commonly lettuce, sprouted seeds, melons, and tomatoes (50). Plants may experience high concentrations of

Salmonella when infected animals defecate in farmland or as a result of fertilization of farmland with animal manure. Thus, *Salmonella* transmission from plants was initially thought to be simply due to surface contamination. However, it is now clear that enteric pathogens have acquired mechanisms to enter plants and reproduce inside of plants (51, 52), a discovery that explains the failure of sanitizers to efficiently eradicate food-borne pathogens in produce.

Similar strategies are required for bacteria to colonize both animal and plant hosts. The details of the initial adherence, invasion, and establishment differ depending on the specific interaction, but there are striking parallels between the processes (49, 53). A combination of bioinformatic approaches and molecular techniques has been used to study mechanisms of plant colonization by pathogenic enterobacteria. It was initially thought that the unique factors required for plant infections could be identified by genome comparisons between bacteria that are frequently or exclusively associated with plants and those that are only associated with human or animal hosts (49). However, many factors involved in infection of animals are also required for successful infection of plants, including type 3 secretion systems that modulate host cell responses, and suppression of the host immune response (53, 54).

Bacterial adherence to host tissue is a prerequisite of both animal and plant infection. Bacteria encode a large number of adherence factors with diverse receptor-binding capability. Among the better-known examples are adhesins of the chaperone-usher family, generally located on the ends of long hair-like structures termed fimbriae, and surface-associated afimbrial adhesins. These adhesins often recognize a range of glycosylation patterns that decorate surface proteins of eukaryotic cells. Among enterobacteria, different isolates commonly encode specific sets of adhesin gene clusters that confer tropism to a particular host tissue type. Other fimbriae-like structures contribute to functions in pathogenesis.

Bacterial adherence to biotic and abiotic surfaces is often due to a combination of factors rather than the action of a single adhesin. For example, Barak et al. (55) showed that the pilus curli (encoded by *agfB*), thin, coiled, fimbriae-like fibers that mediate cell-cell interactions in biofilms and binding to animal cell surfaces, play an important role in adhesion of *S.* Enteritidis and *S.* Newport to alfalfa sprouts. However, they also found that deletion of *agfB* did not completely prevent leaf attachment, indicating that other adhesins likely play a role as well. Likewise, the O-antigen capsule and cellulose synthesis play a role in adhesion of *S.* Enteritidis to plants (56). Curli and cellulose also facilitate transfer of *S.* Typhimurium from contaminated water to parsley (57). Curli and cellulose form a cellular matrix that promotes formation of biofilms. *Salmonella* strains that form extensive biofilms were found to have stronger adhesion to romaine lettuce leaves and greater persistence than weak biofilm-producing strains (58). Not surprisingly, curli, cellulose, and capsule are regulated by a common regulatory gene, *agfD*, which may play a major role in environmental fitness of *Salmonella* organisms (59).

In comparison with bacterial attachment to plant surfaces, the internal movement and translocation of *Salmonella* in plants is less well understood. Many animal-pathogenic enterobacteria preferentially invade plant root tissue rather than foliage (49), but recent reports show that *Salmonella* can invade leaves and developing fruit. The ability of *Salmonella* to penetrate plant cells has been demonstrated in *Arabidopsis thaliana* by tracking fluorescently marked *S.* Typhimurium cells. Colonization of foliage was found to be less extensive than root colonization, and bacteria that were artificially internalized into the leaves did not appear to spread systemically from the point of infiltration. However, bacteria could be detected in newly formed leaves 1 month after introduction (60). The initial entry is not a passive process: *S.* Typhimurium invades iceberg lettuce leaves through the stoma during active photosynthesis but not in the dark (61). The results indicate that *Salmonella* undergoes active chemotaxis toward metabolites produced by photosynthesis.

Studies on the invasion of tomato plants have shown that *Salmonella* can colonize developing fruit. When tomato plants were inoculated by injecting stems or brushing flowers with *Salmonella*, the bacteria remained viable during fruit development, surviving within the ripened fruit (62, 63). Not surprisingly, some strains are more effective at infecting plants than others. For example, *S.* Montevideo appeared to be more adapted to survival within tomatoes and was recovered from 90% of the fruit screened, providing a potential explanation of the narrow range of *Salmonella* serovars associated with *Salmonella* outbreaks linked to tomatoes. *Salmonella* can move inside tomato plants and colonize fruits at high levels without inducing any symptoms, except for a slight reduction in plant growth (64). The results indicate that direct transmission of *Salmonella* can occur between plants (49).

The study of the microbial ecology of food-borne pathogens associated with produce may allow the development of evidence-based policies, procedures, and

TABLE 1 Some sources of *Salmonella* outbreaks

Animal products	Pets	Plant products
Poultry	Turtles	Alfalfa sprouts
Beef	Reptiles	Bean sprouts
Pork	Dogs	Melons
Fish	Cats	Marijuana
Milk	Birds	Lettuce
Cheese	Ducks	Onions
Chocolate	Hedgehogs	Tomatoes
Eggs	Pet food	Peppers
Ice cream	Pet treats	Cilantro
		Spinach
		Cucumber
		Cereal
		Rice
		Flour
		Nuts (almonds, peanut butter, pistachios, hazelnuts)
		Spices (pepper, celery seed, basil, sesame seeds)

technologies aimed at reducing the risk of contamination of fresh produce. For instance, better understanding of the competitive interactions of enteropathogens with the naturally occurring microbiota in the rhizosphere and phyllosphere suggests that there is potential for the naturally occurring microbiota to be used as biocontrol agents to prevent the establishment of enteropathogenic pathogens in plants (50–52).

CONCLUDING REMARKS

Salmonella can be transmitted by a wide variety of food products and environmental sources (Table 1). Thus, transmission of *S. enterica* provides a compelling example of the One Health paradigm, with reservoirs of pathogens in humans, animals, plants, and the environment. Furthermore, the secondary consequences of efforts to eliminate the poultry-restricted *Salmonella* serovars demonstrate that basic ecological principles govern the environmental niches occupied by pathogens, making it impossible to thwart *Salmonella* infections without a clear understanding of One Health.

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