

Understanding the Complexities of Food Safety Using a “One Health” Approach

KALMIA E. KNIEL,¹ DEEPAK KUMAR,² and SIDDHARTHA THAKUR³

¹Department of Animal and Food Science, University of Delaware, Newark, DE 19716; ²Department of Veterinary Public Health & Epidemiology, College of Veterinary and Animal Sciences, Govind Ballabh Pant University of Agriculture & Technology, Pantnagar, Uttarakhand-263145, India; ³Department of Population Health and Pathobiology, College of Veterinary Medicine, North Carolina State University, Raleigh, NC 27607

ABSTRACT The philosophy of One Health is growing in concept and clarity. The interdependence of human, animal, and environmental health is the basis for the concept of One Health. One Health is a comprehensive approach to ensure the health of people, animals, and the environment through collaborative efforts. Preharvest food safety issues align with the grand concept of One Health. Imagine any food production system, and immediately, parallel images from One Health emerge: for example, transmission of zoonotic diseases, antibiotic residues, or resistance genes in the environment; environmental and animal host reservoirs of disease; challenges with rearing animals and growing fresh produce on the same farm; application and transport of manure or diseased animals. During a recent celebration of #OneHealthDay, information was shared around the globe concerning scientists dedicated to One Health research systems. An ever-growing trade and global commerce system mixed with our incessant desire for food products during the whole year makes it all the more important to take a global view through the One Health lens to solve these growing challenges. The recent explosion of Zika virus around the globe renewed the need for assessing transmissible diseases through the eyes of One Health. It is not good enough to know how a disease affects the human population without a thorough understanding of the environment and vector reservoirs. If 60 to 75% of infectious diseases affecting humans are of animal origin, the need for better One Health research strategies and overdue solutions is imperative.

INTRODUCTION

The term “One Health” describes a discipline, a theory, and a way of thinking that bring together human, animal, and environmental health. A majority of infectious

diseases critical to food safety in humans are zoonoses. In fact, the Centers for Disease Control and Prevention (CDC) states that scientists estimate that more than 6 out of every 10 known infectious diseases in people are spread from animals and that 3 out of every 4 new or emerging infectious diseases in people are spread from animals (<https://www.cdc.gov/onehealth/index.html>). Through the broad One Health concept, scientists can probe solutions and develop a better understanding of how to address the growing problems concerning human medicine, animal medicine, and environmental sciences. Educational advances in One Health are occurring quickly through many undergraduate, graduate, and professional programs across agricultural sciences and veterinary medicine, as well as in public and human health. Traditionally, human health has been managed separately from animal health, and the health of the environment has been considered less than the latter. This is even more true in the recent past given

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Correspondence: Kalmia E. Kniel, kniel@udel.edu

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the increase in specializations in human medicine, such as personalized medicine. Large government agencies and numerous private programs and companies work to protect human and animal health; therefore, clinicians, veterinarians, and environmentalists must all join together to fully address One Health.

One Health is certainly not a new concept: the Greek physician Hippocrates (460 to 370 BCE) recognized the impact of environmental conditions on human health in his *On Airs, Waters, and Places*, in which he wrote about how stagnant water and swampy environments were more likely to make people sick (1, 2); thousands of years later scientists would connect mosquitoes and malaria to those same environments. In the 1960s, Calvin Schwabe coined the term “One Medicine,” which initiated the alignment of human and animal medicine (3). Over the past decade, in light of growing scientific interest in climate change and in the protection of global health, One Health has gained traction and recognition. While a myriad of chapters and books have covered various aspects of One Health, including political and social implications, here we discuss two issues relevant to preharvest food safety in connection with each other. The first is the daunting issue of antimicrobial resistance (AMR), and the second some consider equally as formidable, that is, disease spread and occurrence associated with *Salmonella* spp. The shift in thinking through the One Health paradigm is critical to our approach to targeting these two subjects. Not only does One Health bring together the necessary experts and scientists to solve the problems, but this multidisciplinary approach is critical to educational programs and for continued learning about these broad issues. Lonnie King described this interconnectivity of people, animals, and their products as being embedded in a threatened environment which results in an unprecedented 21st-century mixing bowl (4). Our impacts on each other now cannot be separated. The interaction of these forces, as described by King, are similar to the dynamics of Newton’s third law of motion, which states that for every action there is an equal and opposite reaction. If this is true, then each action in any of the three domains has multiple consequences on the other.

ANTIMICROBIAL RESISTANCE SURVEILLANCE

To promote effective use of antibiotics, scientists and physicians are engaged in a One Health approach of integrated surveillance of antibiotic resistance in foodborne bacteria. This includes efficient reductions in

use and only diligent use of antibiotics to treat humans and nonhuman animals raised for agriculture. Integrated surveillance of AMR in foodborne pathogens involves collection, validation, analysis, and reporting of relevant microbiological and epidemiological data on AMR in foodborne bacteria from humans, animals, and food and data on relevant antimicrobial use in humans and animals (http://www.who.int/foodsafety/publications/agisar_guidance2017/en/). The focus of an integrated approach is to monitor the patterns of AMR, including the development of novel resistance mechanisms in pathogens isolated from foods (including foods of animal and plant origin) destined for human consumption and food animals, and to monitor the use of antimicrobials in humans and food animals. The WHO Advisory Group on Integrated Surveillance of Antimicrobial Resistance (AGISAR), in its recent guidelines, has outlined the basic requirements for countries to establish integrated surveillance of antibiotic resistance in foodborne bacteria. AGISAR guidelines give a detailed view of various steps such as the need for standardized and validated antimicrobial susceptibility testing methods, harmonized zone or MIC interpretive criteria, and monitoring and collection of antimicrobial consumption and use data in humans and animals.

The first component of the WHO guidelines for integrated surveillance of AMR in foodborne bacteria involves monitoring and interpretation of AMR in pathogens isolated from food-producing animals, foods, and humans. The focus of this section is to develop comparable epidemiological and microbiological methods for unbiased comparison of antimicrobial susceptibility results between different areas, countries, and regions. Specific guidelines on sampling sources (humans, retail meats, and food animals), target organisms (*Salmonella*, *Campylobacter* spp.), sampling design, and laboratory testing methodologies have been proposed. Laboratory testing methodologies includes bacterial culture identification and characterization, standardized antimicrobial susceptibility methods, testing of recommended antimicrobials for particular bacteria, and the use of uniform susceptibility standards such as those from CLSI and EUCAST for result interpretation. A final part of these guidelines is data management, validation, analysis, and reporting. Establishing a common set of comparable programs for integrated surveillance is difficult due to the differences in public health infrastructure, agricultural production systems, food supply systems, and veterinary practices. Hence, to achieve this objective, a minimum set of requirements has been proposed in the WHO guidelines; these include (i) the

presence of appropriate medical and veterinary infrastructure allowing routine collection and microbiological analysis of human and animal clinical samples; (ii) the availability of established human, veterinary, and food safety laboratory facilities and workforce; (iii) a quality management system for laboratories; and (iv) the capacity to analyze and report AMR surveillance data.

The second component of the WHO guidelines for integrated surveillance of AMR involves monitoring the use of antimicrobials in humans and food animals at national and international levels. Surveillance of antimicrobial use and consumption in humans and animals can be divided into three main activities, viz., measuring the quantity of different antimicrobials sold, obtaining information on the prescription practices for antimicrobials in human and veterinary medicine, and collecting information on the actual intake of antimicrobials by humans and animals. Various approaches are available to monitor the use of antimicrobials in humans and animals, which vary in methodology and output reporting. Strategies recommended for surveillance of antimicrobial usage in humans include monitoring of national antimicrobial sales data, point prevalence surveys on antimicrobial use in hospitals, and longitudinal studies of antimicrobial use in hospitals and the community. However, collecting data on antimicrobial usage in animals is more difficult than in humans due to variation in antimicrobial consumption across different species and production types (e.g., for meat or milk). Nevertheless, similar approaches, such as surveillance of national antimicrobial sales data and longitudinal studies at the farm level, have been recommended to monitor antimicrobial usage in animals. Additionally, collection of species-wide consumption data of antimicrobials is recommended.

Inappropriate prescription of antimicrobials in humans and animals is another important issue related to antimicrobial surveillance (5). According to the authors of a recent study, the American Medical Association has diagnosed the prevalence of prescriptions and estimates for the use of antibiotics that may be inappropriate in adults and children in the United States (5). The outcome of this study suggested that in 2010 to 2011 there was an estimated antibiotic prescription rate of 506 per 1,000 population; however, only 353 antibiotic prescriptions were likely appropriate during this time. This is an indication that antibiotic misuse is not only a problem associated with the treatment of animals. The authors suggest that a 15% reduction in overall oral antibiotic prescriptions would be necessary to meet the goal of

the White House National Action Plan for Combating Antibiotic Resistant Bacteria of reducing inappropriate antibiotic use (5). The situation is far more threatening in middle- and low-income countries such as India, where no control on the sale and use of antimicrobials exists. In countries like India, many antimicrobials can be purchased without a medical prescription. A recent study estimates that in India during 2007 to 2012, increases of 73% and 174% were recorded in the sale of watch group and reserve group antibiotics, respectively, compared to a 20% increase in key access antibiotics (6). The steep rise in sales of watch group and reserve group antibiotics was mainly attributed to the rampant use of fixed-dose combinations that contain watch group antibiotics. Apart from government inactivity in implementing strict antibiotic control regulations, the unauthorized and unscientific use of antibiotics by quacks and the prescription of reserve antibiotics by medical doctors for financial benefits are the major causes of the emergence of AMR in India. The prescription of higher-end or high-generation antibiotics is known to carry higher financial margins.

ANTIMICROBIAL USE IN HUMANS

According to the CDC, at least 2 million people become infected and at least 23,000 die annually due to antimicrobial-resistant bacteria in the United States alone (<https://www.cdc.gov/drugresistance/index.html>). A report recently concluded that if unchecked, the number of annual deaths due to drug-resistant pathogens will swell to 10 million by 2050 and could cost \$100 trillion in terms of lost global production (7). We are witnessing a steep increase in the global consumption of antimicrobials. For example, Van Boeckel and coworkers reported a substantial increase of 35% in global antibiotic consumption between 2000 and 2010 (8). Seventy-six percent of the overall increase in the global consumption of antimicrobials between 2000 and 2010 was attributed to BRICS nations (Brazil, Russia, India, China, and South Africa) (8). Interestingly, during these years BRICS countries had only a 31% share in the global increase in the human population. Among all nations, India ranked first in the consumption of antibiotics in 2010, with 12.9×10^9 units (10.7 units/person) followed by China (10.0×10^9 units and 7.5 units/person) and the United States (6.8×10^9 units and 22.0 units/person). The increase in the global consumption of antimicrobials has resulted in the emergence of a high frequency of resistance in bacterial pathogens/strains that were previously considered susceptible (9).

USE OF ANTIMICROBIALS IN FOOD ANIMALS

The emergence of AMR in foodborne pathogens is one of the most important aspects of preharvest food safety, which is mainly attributed to the irrational use of antimicrobials in food animals. Prolonged use of subtherapeutic doses of antimicrobials in food animals for growth promotion and disease prevention results in the development of multidrug resistance in bacterial pathogens. Subtherapeutic doses of antimicrobials are used on these farms for rapid growth of animals and disease prevention. Antimicrobials in low doses kill the majority of the gut microbiota, but some resilient bacteria are able to survive and become resistant over time. Extensive usage of important antibiotics in production animals speeds up this process and creates selective pressure on bacteria that eventually develop resistance to survive. These farms become a reservoir for the selection of new AMR bacteria that can be exchanged between animals and humans (10). The resistant bacteria originating from production systems can travel to surrounding human dwellings and slaughter and processing units and transfer antimicrobial-resistant determinants to the native microbial population. Domestic sales and distribution of antimicrobials approved for use in food animals in the United States in 2015 amounted to approximately 15.6 million kg, of which tetracyclines alone constituted 6.86 million kg (44%) (11). Moreover, it has been reported that 30 to 90% of the antimicrobials consumed by animals are released into manure and urine (12). Animal manure has been shown to contaminate the environment with antibiotic-resistant bacteria and genes (13).

People working and living close to animal feeding operations are at greater risk of acquiring AMR infections. Recently, a study evaluated differences in occupational risks of methicillin-resistant *Staphylococcus aureus* (MRSA) for farm workers working in industrial livestock operations (ILOs) and antibiotic-free livestock operations (AFLOs) (10). Although the prevalence of *S. aureus* and MRSA was similar among workers on both ILO and AFLO farms, *S. aureus* clonal complex (CC) 398, which is a livestock-associated MRSA clone, was predominately detected among ILO workers compared to AFLO workers. Moreover, only ILO workers carried *scn*-negative MRSA CC398 and *scn*-negative multidrug-resistant *S. aureus* CC398 strains, which confirms the presence of livestock-associated MRSA in ILO workers. Another study reported a higher risk of community-associated MRSA, skin, and soft-tissue infection in human populations living close to high-density swine

production operations in Pennsylvania (14). The outcomes of these studies highlight the extent of the danger posed by the irrational use of antimicrobials in food animal farms and the environmental route of transmission of such organisms to the human population.

ENVIRONMENTAL AMR

AMR is inextricably linked to the three basic domains of One Health—that is, human, animal, and environmental health. While AMR affects human, animal, and environmental health equally, human health and to some extent animal health get the spotlight. Environmental health is the least-explored domain of One Health. While our overall knowledge of soil microbes is limited, genes encoding antibiotic resistance are not a new phenomenon in response to extensive use of antimicrobials in humans or animals. Within the 1% of all soil microbes that have been identified, there appears to be a global “resistome” (2, 15, 16). Selective pressures placed on environmental bacteria forced these bacteria to express resistance genes to survive. Resistance genes are known to persist in nature and can be transmitted that way among bacteria in sewage, soil, water, and waste. Perhaps humans can learn from the environment since antibiotic resistance genes are ancient, predating the selective pressure of modern antibiotic use. Such genes have been identified in Alaskan permafrost sediments that date back to the Late Pleistocene era. Microbes that are metabolically active readily have the potential for evolving or acquiring resistance genes (17).

In most low- and middle-income countries, the use of antibiotics for animal growth promotion and treatment is unregulated, which results in the high proportion of antimicrobial-resistant bacteria, antimicrobial resistance genes (ARGs), and antimicrobial residues in foods of animal origin and farm waste. Resistant bacteria and genes emanating from food animal farms are a public health threat. These resistance genes could enter the human food chain through water, soil, and manure. In particular, manure is known to harbor various AMR bacteria and genes. Despite the huge volumes of antimicrobials used on food animal farms, very little information is available regarding the presence of AMR genes in manure and soil around these farms. The dissemination of manure on soil increases the risk of resistance gene exposure to crops, surface water bodies, groundwater, and human populations living close to the farms (18–20). Few studies have explored the presence of AMR bacteria or ARGs in soil/manure samples and their persistence in the outside environment (21–23). In one

such study, various *Salmonella* serotypes were found to persist in the soil outside swine farms for up to 21 days post-manure application (22). The authors confirmed the role of manure as a reservoir in the dissemination and persistence of antimicrobial-resistant bacteria in the environment. Recently, another study detected 149 unique resistance genes at three large-scale (10,000 animals per year) commercial swine farms in China. The 63 most prevalent ARGs were enriched 192-fold up to 28,000-fold compared to the antibiotic-free manure or soil controls. The diversity and abundance of ARGs reported in this study is alarming and clearly indicates that unmonitored use of antibiotics and metals on swine farms has expanded the diversity and abundance of the antibiotic resistance reservoir in the farm environment (23).

Another major environmental reservoir of ARGs is the wastewater effluents from drug industries and municipalities. It is known that a large proportion of the antimicrobials consumed by humans are excreted in their bioactive form in feces and urine (24). These biologically active components in wastewaters exert selective pressure and force bacteria to develop resistance. The presence of antibiotic resistance genes and antibiotics in wastewater effluent selects for novel combinations of AMR. These resistance determinants can be transferred to susceptible microorganisms by horizontal gene transfer via plasmids, integrons, and transposons (25).

ONE HEALTH, PREHARVEST FOOD SAFETY, AND SALMONELLA

As a foodborne pathogen, nontyphoidal *Salmonella* results in an estimated 1.2 million illnesses, 19,000 hospitalizations, and 370 deaths each year (26). There are over 2,600 recognized serovars of *Salmonella enterica* that have a broad range of hosts and can infect a wide variety of animals, as well as grow or survive in plants, protozoa, soil, and water. These serovars can be divided into three general groups based on host range: broad host range or generalist, host adapted, and host restricted (27). Selective pressures and the science behind host range evolution and specific reservoirs are not well understood. *Salmonella* has a complex environmental life cycle in multiple host species (mammals, reptiles, birds, and insects) that is affected by many factors of the external environment (sunlight, nutrients, temperature, moisture) (28).

The large number of possible *Salmonella* strains, coupled with their ability to be supported by a myriad of hosts, likely contributes to the continuing growth and potential for contamination by *Salmonella* in our food

supply. The public health impact of *Salmonella* continues to grow, because we missed the mark on significant decreases for the Healthy People 2010 goal and remain a distance from the Healthy People 2020 goal at this time (https://www.cdc.gov/nchs/healthy_people/hp2020.htm). With the increasing use of whole-genome sequencing, more information is documented and shared about the presence of specific *Salmonella* strains in the environment as well as those isolated from animals and human clinical strains. The U.S. Food and Drug Administration supports the GenomeTrakr Network, where isolates from foodborne outbreak investigations and federal- and state-funded research projects are identified and maintained in public databases. Similar databases are supported by the World Health Organization, with information from the Global Salm-Surv *Salmonella* surveillance program, including AMR information. These types of data are being used to approach *Salmonella* One Health integration programs around the globe. For example, a Canadian surveillance program from 2005 to 2012 determined how integrated surveillance can identify an issue in an exposure source and link it to trends in human disease (29).

In their analysis of the impact of *Salmonella* on contaminated foods, the Centers for Disease Control and Prevention ranks *Salmonella* contamination of poultry among the top contributors to outbreaks and *Salmonella* on vine-stalk vegetables as the second-highest contributor to outbreak-associated hospitalizations; fruit and nut contamination with *Salmonella* is a leading cause of outbreak-associated deaths (30). *Salmonella* is consistently challenging the dogma of foodborne disease and food microbiology with its ability to persist and cause illness associated with a large range of foods, including peanut butter, dried spices, and other powders. *Salmonella* plays a unique role in preharvest food safety because it is a concern for all commodities. *Salmonella* can cause disease in foods due to its complicated association with the three domains of One Health.

HUMAN AND ANIMAL DOMAIN INTERFACE

Numerous case studies have explored the interactions of zoonotic *Salmonella*. Perhaps the longest history is human salmonellosis linked to live poultry, which is historic but also is an increasing public health concern. In 2012 to 2013, an investigation traced *Salmonella* Branderup infections to a mail-order hatchery in the United States (31). The authors describe 8 unrelated outbreaks of human salmonellosis linked to live poultry contact which resulted in more than 517 illnesses. In this

study, a case was defined as an infection with the outbreak strain determined by pulsed-field gel electrophoresis with onset from 25 July 2012 to 27 February 2013. Epidemiological evidence supported an environmental investigation of one hatchery where sampling yielded the outbreak strain. The investigation concluded that improved sanitation and pest control were warranted. The authors state that similar to other outbreaks, industry knowledge and involvement are needed to solve outbreaks. Nakao et al. state that in this case a “One Health” approach leveraged the necessary expertise in human, animal, and environmental health (31).

The type of outbreak described above is not rare. The CDC stated in a 2016 report by the National Center for Emerging and Zoonotic Infectious Diseases that backyard flocks caused a record number of illnesses, with 900 human infections associated with keeping live chickens and ducks in backyard flocks. Of these 900, 200 people were hospitalized. In 2017, 10 separate multistate outbreaks of human *Salmonella* infection resulted in the largest number of illnesses linked to contact with live poultry ever recorded in the United States, affecting 48 states. According to the CDC, 1,120 people were infected, 249 of which were hospitalized, and 1 death was reported from North Carolina. These *Salmonella* outbreaks occurred between 4 January and 22 September 2017. Epidemiological and laboratory investigations linked the 10 outbreaks to contact with live poultry in backyard flocks. Importantly, 70% of the ill people reported contact with live poultry a week before their illness (<https://www.cdc.gov/Salmonella/live-poultry-06-17/index.html>). The CDC response to these events included education for flock owners and industry about staying healthy while maintaining a backyard flock. It is essential to educate individuals about the potential for the transmission of *Salmonella* as well as about the acute and chronic symptoms associated with salmonellosis.

ENVIRONMENTAL DOMAIN INTERFACE

A wide variety of bacteria have close relationships with plants and in some cases promote plant growth and nitrogen uptake. The study of human pathogens on plants has become increasingly popular and important over the past 20 years (32). Agricultural crops may become contaminated with bacterial and viral pathogens that are a threat to human health but not necessarily to plant health. Research has shown that plants can become contaminated with human pathogens in the preharvest environment through a variety of outlets, including soil, irrigation water or water used to apply pesticides and

fertilizers, dust, insects, land-applied manures and biosolids, and directly from wild or domestic animals (33). In particular, manure from food animal farms is a major reservoir of antibiotic-resistant *Salmonella*. Plants may receive higher concentrations of *Salmonella* if the farm-generated manure is contaminated with *Salmonella*. Leafy greens are considered a high-risk food crop because they have been epidemiologically linked to foodborne illness (34) and they are commonly consumed in their raw state, with little or no processing taking place to reduce contaminants. Leafy greens are not all the same when it comes to potential contamination. For example, spinach forms a canopy that may serve as a trap for zoonotic pathogens if the plants become contaminated. The outer leaves of lettuce plants may provide a reservoir for pathogens, but this route of contamination may not lead to illness. Herbs may be cultivated differently, and some have smooth leaf surfaces while others have rougher structures.

Addressing safer ways to manage crop growth and harvest is essential to minimizing microbial contamination (35). It is important to determine the type of relationships that human pathogens have with plants, whether they be symbiotic, endophytic, or antagonistic (32). *Salmonella* is a classic human pathogen that has a unique environmental niche and the potential for fierce and continuous interactions with plants. Schikora et al. suggested that human pathogenic *S. enterica* serotype Typhimurium infects and intracellularly proliferates within tissues of *Arabidopsis thaliana* through both the root and shoot of the plant (36). These same researchers noted that *Salmonella* infection may result in disease symptoms in the plants, including wilting, chlorosis, and death of infected plant organs (36). *Arabidopsis* plants responded immunologically similarly to *Salmonella* as they would to the plant pathogen *Pseudomonas syringae* (DC3000), by induction of the mitogen-activated protein kinase cascades as well as by enhanced expression of pathogenesis-related genes (36). Numerous studies have focused on *A. thaliana*, a small flowering plant that is widely used as a model organism in plant biology, demonstrating that bacteria normally pathogenic to humans and other mammals can infect plants including *S. enterica*, *Pseudomonas aeruginosa*, *Burkholderia cepacia*, *Erwinia* spp., *S. aureus*, *Escherichia coli* O157:H7, and *Listeria monocytogenes* (37–41).

A wide range of plants and agricultural produce have been linked with *Salmonella* infection in the past. Notably, the 2017 multistate outbreak of *Salmonella* in the United States linked to Maradol papayas imported from Mexico highlights the importance of fresh produce contamination and the risk of *Salmonella* infection.

Several *S. enterica* serotypes such as Urbana, Newport, Infantis, Anatum, Thompson, and Agona were identified from Papayas imported from Mexico. According to the CDC, this outbreak resulted in 251 illnesses and 2 deaths (1 each in New York and California) across 26 states. Four farms located in Mexico were implicated in this *Salmonella* outbreak. Recalls were issued after the *Salmonella* strains from papayas and human cases matched. In 2016, two separate *Salmonella* outbreaks were linked to the consumption of contaminated alfalfa sprouts. In the first outbreak, 26 people in 12 states were infected with the outbreak strains of *S. enterica* Muenchen (25 people) or *S. enterica* Kentucky (1 person). The outbreak resulted in the hospitalization of 8 people. The second *Salmonella* outbreak resulted in 36 illnesses and 7 hospitalizations in 9 states. Outbreak strains of *S. enterica* serotypes Reading and Abony were involved. No deaths were reported in either outbreak. Infected people in both of these outbreaks reported eating or possibly eating alfalfa sprouts in the week before the illness started. [Table 1](#) summarizes the various food commodities and *Salmonella* serotypes involved in multiple *Salmonella* outbreaks during 2006 to 2017.

Salmonella is a resilient bacterium, surviving extremely successfully in the outside environment and finding its

way into the food chain. However, it is not clear how *Salmonella* survives so efficiently in the outside environment. To understand this, Bleasdale and coworkers demonstrated that amoebae living freely in the environment are a potent reservoir of *S. Typhimurium* (42). The authors highlighted the role of *Salmonella* pathogenicity island 2 in the survival of *S. Typhimurium* inside amoebae (*Acanthamoeba polyphaga*). They concluded that amoebae may be a major source of *Salmonella* within the environment and could play a significant role in the transmission of *Salmonella* to humans and animals.

CONCLUSION

The One Health approach is the best way to comprehensively address preharvest food safety issues such as AMR and foodborne salmonellosis. It is important to understand that there cannot be a single solution to the problem of AMR that is applicable to all nations. Regulating antibiotic use in humans may not be the only solution for middle- and low-income countries, where people need easy access to the cheap life-saving antibiotics and where antibiotics are often used as an alternative in the absence of basic healthcare and sanitation facilities. Putting a complete ban on the prescription of antibiotics will not work in such nations. Instead, a holistic approach embodying the principles of One Health is needed which includes judicious and unbiased antibiotic prescription in humans, regulation of antibiotic use in food animals, and prevention and monitoring of antibiotic resistance in environmental reservoirs. Similarly, foodborne salmonellosis can be transmitted by a wide variety of food and environmental sources. Foods of animal origin (meat, milk, and their products) and fresh produce (lettuce, papaya, cucumbers, and sprouts) have been implicated in several *Salmonella* outbreaks in the past. Also, efficient survival of *Salmonella* in the adverse environmental conditions in a variety of reservoirs is a well-known fact. Hence, a One Health approach addressing *Salmonella* in humans, animals, and the environment is envisaged.

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TABLE 1 Listing of select multistate outbreaks associated with fresh produce where preharvest contamination was suspected from 2006 to 2017^a

Year	Commodity	<i>S. enterica</i> serotype
2017	Maradol papayas	<i>S. Urbana</i> , <i>S. Newport</i> , <i>S. Infantis</i> , <i>S. Anatum</i>
2016	Cucumbers	<i>S. Oslo</i>
2016	Alfalfa sprouts	<i>S. Reading</i> , <i>S. Abony</i> , <i>S. Muenchen</i> , <i>S. Kentucky</i>
2015	Cucumbers	<i>S. Poona</i>
2014	Bean sprouts	<i>S. Enteritidis</i>
2013	Cucumbers	<i>S. Saintpaul</i>
2012	Mangoes	<i>S. Branderup</i>
2012	Cantaloupe	<i>S. Typhimurium</i> , <i>S. Newport</i>
2011	Papayas	<i>S. Agona</i>
2011	Alfalfa and spicy sprouts	<i>S. Enteritidis</i>
2011	Cantaloupe	<i>S. Panama</i>
2010	Alfalfa sprouts	<i>S. I 4,[5], 12:i:</i>
2010	Alfalfa sprouts	<i>S. Newport</i>
2009	Alfalfa sprouts	<i>S. Saintpaul</i>
2008	Jalapeno peppers, serrano peppers, tomatoes	<i>S. Saintpaul</i>
2008	Cantaloupe	<i>S. Litchfield</i>
2006	Tomatoes	<i>S. Typhimurium</i>

^aAdapted from reference 32 and original source (<http://www.cdc.gov/foodsafety/outbreaks/multistate-outbreaks/outbreaks-list.html>).

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