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Food systems and antimicrobial resistance: impacts on food safety, animal production and trade

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Summary

Antimicrobial resistance (AMR) in bacteria originating from food-producing animals constitutes a significant challenge for food safety, public health, animal production and international trade. The acquisition of AMR genes by bacterial populations in both animals and humans obscures the inference of gene transfer directionality and complicates the assessment of selective pressures imposed by antimicrobial use.

Zoonotic food-borne pathogens, such as *Salmonella* species, are key agents in transmitting AMR directly to humans via food. These pathogens frequently exhibit multidrug resistance, and their prevalence in food indicates a substantial public health risk. The application of antimicrobials in livestock production for therapeutic, prophylactic and growth promotion purposes is a recognised contributor to the emergence of resistance, although regulatory interventions have reduced these practices.

Commensal and animal-specific pathogenic bacteria contribute to the indirect transfer of AMR genes, potentially affecting both animal and human health. Animal-derived food is a major reservoir for AMR pathogens; further research on contamination of plant-based food with AMR bacteria is crucial to assess its impact.

Risk analysis of AMR is hindered by insufficient data, especially on AMR’s effects on animal health and production. Certain bacterial infections in animals have become more difficult to treat; however, untreatable infections are not yet widespread. The lack of international trade regulations regarding AMR bacteria in food complicates future policy creation and implementation.

Enhanced surveillance, comprehensive risk analysis and international collaboration are therefore essential to mitigate the risks associated with AMR in food. Addressing these challenges is critical to safeguard food safety and animal health and maintain the integrity of global trade.

Keywords

Animal pathogen – Animal production – Antimicrobial resistance – Food safety – Public health.

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Introduction

Antimicrobial resistance (AMR) in bacteria from food-producing animals has been regarded as one of the major problems in food safety as well as for public health [1]. However, with the current technical possibilities in science offered by next-generation sequencing, opinions on the influence of food on the transfer of resistance from animals to humans have become better informed. Nevertheless, it has not been possible to make a full risk analysis on the role of antimicrobial-resistant bacteria (AMRB) in food and the impacts on food safety and ultimately public health [2]. This is mainly because the resistance genes have a common origin and have been integrated into both animal and human bacteria, masking the direction of transfer as well as the influence of the selective pressure of using antimicrobials in the different ecosystems [3,4].

This article will analyse available data and situations in selected zoonotic, commensal and animal pathogenic bacteria. This separation is warranted because these groups differ markedly in their implications for food safety. Zoonotic food-borne bacteria are transmitted directly to humans via the food chain and can cause clinical disease, whereas commensal and animal pathogenic bacteria most often do not establish in humans and therefore contribute to AMR mainly through indirect transfer of resistance determinants from animal to human bacterial populations. Animal pathogenic bacteria additionally affect animal health, with downstream consequences for animal production and food security. Although the focus is mainly on animal-derived food products, vegetables can also be contaminated by AMRB. However, fewer data are available for vegetables, and the origin of these resistant bacteria is often difficult to ascertain.

The article further reviews existing risk analysis of food-borne AMR and summarises current conclusions and remaining data gaps. Examples are provided to illustrate reduction in resistance among animal-derived bacteria leading to a reduction in food-borne isolates and, subsequently, in human infections; these serve as inverse examples to assess the impact on food safety. From a One Health standpoint, these interconnected pathways illustrate how resistance in one sector can impact others, emphasising the need for integrated surveillance and policy responses.

The impact of AMR on food production should mainly be sought in bacterial infections that become more difficult to treat or untreatable. Fortunately, the latter has not been described in veterinary medicine as yet, but it is an increasing thread in human medicine. Unfortunately, there are also few data available on AMR in animal pathogens, which makes it difficult to estimate potential impact on animal production. This article will analyse the current literature for indications of effects on production and identify gaps [5].

Finally, the broader implications of AMR in food systems and trade, both national and international, remain largely unexplored. The extent to which consumers are aware of AMR in foods, and whether such awareness influences purchasing and consumption behaviour, has not been systematically investigated. Similarly, there is limited understanding of how the presence of resistant bacteria in food products affects international trade and market access. Although current sequencing technologies would potentially enable the identification and tracking of resistant bacteria to their possible sources, the translation of such knowledge into regulatory or management action remains limited. While specific rules exist for certain food-borne pathogens, no equivalent international standards currently address AMRB in foods, highlighting a major gap in global food safety governance.

Antimicrobial resistance in food products

Antimicrobial resistance in food products is a significant public health challenge with implications for food safety and security on a global scale [6]. Unsafe food causes an estimated 600 million illnesses and 420,000 deaths annually, resulting in 33 million lost healthy life years (measured in disability-adjusted life years, or DALYs). Alarmingly, 125,000 of these deaths represent children aged under five, highlighting the critical importance of food safety [7]. However, the role of food and AMR transmission is not always clear, especially in commensal bacteria. The situation is different for food-borne pathogens, for which the direct transmission of AMRB can be demonstrated. The prevalence of AMR food-borne pathogens in food samples was shown to be greater than 10%, and those resistant bacteria were frequently multidrug resistant [8]. This widespread presence of resistant microorganisms represents a fundamental shift in the microbial ecology within our food system, driven by selective pressures from antimicrobial usage in modern agriculture. Antimicrobials have been used extensively to intensify livestock production and raise more food to meet growing consumer demands [9,10].

The next sections will therefore provide a detailed examination of food-borne pathogens, first focusing on those found in animal sources and then exploring those from non-animal sources. This critical analysis is essential for developing effective strategies and research directions in order to mitigate the risks associated with AMR in the food chain.

Antimicrobial resistance in zoonotic pathogens

Livestock production contributes an average of 40% of the total agricultural gross domestic product across developing countries [11], playing a significant role in society. Despite the benefits and growing market of livestock farming, there are various challenges, particularly concerning AMR. One major factor that has contributed to the emergence of AMR is the use of antibiotics in livestock farming. Livestock production systems frequently employ antimicrobials to treat and prevent disease and, in some places, they are used as growth promoters [12]. However, overall use has decreased substantially in some countries, is banned in several countries and is under scrutiny in others [13].

Animal-derived food products constitute a significant reservoir of antimicrobial-resistant pathogens that can cause clinical disease in humans[1]. The World Organisation for Animal Health has identified several key species of zoonotic food-borne pathogens associated with AMR, including *Salmonella* species, *Campylobacter* species and emerging bacterial pathogens such as methicillin-resistant *Staphylococcus aureus* (MRSA). These pathogens can develop resistance to critical antimicrobial agents, limiting treatment options for human infections and leading to severe clinical outcomes [6].

Salmonella enterica subspecies *enterica* serotypes

Salmonella enterica serotypes are widely distributed among food animals such as poultry, pigs and cattle, and humans are typically exposed through the consumption of contaminated animal-derived foods or through cross-contamination during food preparation [14].

Non-typhoidal *Salmonella* infections are a leading bacterial cause of food-borne diseases worldwide, with an estimated global burden of 93 million enteric infections and 155,000 deaths each year [15]. In sub-Saharan Africa, however, they are also a major cause of bacteraemia, presenting an increased risk for individuals infected with HIV or

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[1] https://www.cdc.gov/food-safety/foods/antimicrobial-resistance.html

malaria [16,17]. Surveillance of AMR in *Salmonella* is well established in many developed countries, and it has been shown that resistance is quite serotype specific, with certain serotypes rarely resistant and others multidrug resistant. In *Salmonella*, 279 unique AMR alleles have been found, with genes for aminoglycoside, tetracycline and sulfonamide resistance being the most abundant [18]. While resistant *Salmonella* are almost equally found in terrestrial animals and food, animal isolates contain a higher number of AMR genes compared to non-animal samples. This indicates that multidrug-resistant *Salmonella* outbreaks are more likely to occur due to the consumption of animal-derived foods compared to other sources [19].

In addition to the burden of food-borne pathogens, antimicrobial-resistant *Salmonella* infections are associated with disease severity, e.g. hospitalisation rates, invasive infections and treatment failure, especially when multidrug-resistant strains are implicated [20]. These results highlight the clinical significance of resistance patterns in food-associated *Salmonella* and also emphasise the need for surveillance data linking resistance profiles to public health significance. The development and persistence of multidrug-resistant *Salmonella* are strongly associated with antimicrobial use in food-producing animals, especially intensive poultry, pig and cattle production systems [21]. This selective pressure facilitates maintenance and dispersion of resistant serotypes. Resistant *Salmonella* strains have been consistently reported in globally exchanged foods such as meat and animal products, and food trade has become an important factor [22]. While plant-based foods in particular can serve as vehicles for *Salmonella* transmission through contamination during manufacture or production, animal-produced foods continue to be the main source of multidrug-resistant *Salmonella* diseases linked with human disease. This distinction is particularly important in today’s global trade context, where the resistant strains of some animals brought into production systems are also being passed on by others across regions, facilitating international spread of AMR.

Campylobacter species

Campylobacter species are recognised as one of the leading causes of bacterial gastroenteritis globally, with *Campylobacter jejuni* being the predominant species, causing most infections in humans. In second place comes *Campylobacter coli*, which also represents a significant pathogen, accounting for up to 25% of *Campylobacter*-associated infections in humans [23-25].

Campylobacter spp. were linked to approximately 6.27 million DALYs in 2019, representing a significant health burden [26]. This burden was particularly high in children under the age of five, who are disproportionately affected by *Campylobacter* infections. *Campylobacter* species are commonly found in most warm-blooded animals, including poultry, cattle, pigs, sheep, and companion animals such as cats and dogs [27]. The primary route of human infection is through the consumption of undercooked or raw meat of mainly poultry origin, or cross-contamination with those products and contaminated dairy products. Contaminated water and ice can also serve as sources of infection, and less commonly, transmission can occur through contact with animals and person to person via the faecal–oral route [27]. Antimicrobial resistance in *Campylobacter* has emerged as a significant public health threat, complicating treatment and increasing the risk of severe outcomes.

In general, antibiotic therapy is not recommended as the infection is typically self-limiting and resolves without antibiotics. However, it may be necessary in cases of severe and prolonged disease, or in immunocompromised patients [28]. The most common prescription is macrolides, such as erythromycin, for cases confirmed by laboratory analysis. This is due to *Campylobacter*'s relatively low rates of erythromycin resistance [29].

Resistance to fluoroquinolones is primarily driven by spontaneous point mutations in the quinolone resistance determining region or the *gyrA* gene, which reduces antibiotic binding affinity [29,30]. In general, resistance to fluoroquinolones as well as other antibiotics is more common in *C. coli* compared to *C. jejuni* [29]. While the reasons are not fully understood, it has been suggested that *C. coli* may be better able to tolerate resistance-associated fitness costs, such as point mutations in the *gyrA* gene, aiding the persistence of *C. coli* with fluoroquinolone resistance [31,32].

Resistance to fluoroquinolones is widespread globally and has been steadily on the rise since the late 1980s [33,34]. However, in Canada, there was a decreasing trend in resistance to ciprofloxacin in human isolates from 2017 to 2021, from 32% to 24% [35], while fluoroquinolone-resistant *Campylobacter* isolates from broiler chickens, feedlot cattle, pigs, turkeys and layers have generally increased over recent years. In the United States of America, *C. jejuni* showed an increase in resistance rates to fluoroquinolones from 2013 to 2019, from 22.6% in 2013 to 33.54% in 2019 [36]. In Europe, 69.1% of *C. jejuni* and 70.6% of *C. coli* isolates from human clinical samples were resistant to fluoroquinolones, though this difference is mainly due to differences in breakpoints between the Clinical and Laboratory Standards Institute and the European Committee on Antimicrobial Susceptibility Testing [37,38]. The increased trends in fluoroquinolone resistance are similarly observed in livestock, due to the increased use of fluoroquinolones in intensive animal farming for food production [39,40]. In Asia, fluoroquinolone resistance in human *Campylobacter* isolates and poultry isolates is notably high. For example, in Thailand, fluoroquinolone resistance in human *Campylobacter* isolates increased from virtually 0% before 1991 to 84% by 1995 [39], while more recently resistance levels against quinolones ranged from 75.4% to 94.8% in human-related isolates and from 71.6% to 88.7% in chicken isolates [41]. In Africa, data are limited but indicate a high burden of resistant *Campylobacter* infections, particularly in children. In Ethiopia, a high prevalence of *Campylobacter* infection in children under five showed notable resistance to ciprofloxacin and doxycycline; the same study highlighted the presence of *Campylobacter* in backyard poultry and dogs associated with these children, suggesting household-level transmission and underscoring the significant public health burden of resistant *Campylobacter* infections in Africa [42]. The frequent asymptomatic carriage of *Campylobacter* in endemic regions further facilitates silent transmission of resistant strains [43].

Macrolides are currently the gold standard for treating *Campylobacter* infections where antibiotic treatment is required. Globally, resistance to macrolides in *Campylobacter* remains relatively low. Surveillance data from Europe, North America and parts of Asia consistently show macrolide resistance rates typically below 10%, with *C. jejuni* exhibiting lower resistance than *C. coli* [36,39-43]. This relatively low level of resistance can be largely explained by the nature of the resistance mechanisms involved. Macrolide resistance in *Campylobacter* primarily arises from point mutations in the peptidyl-encoding region in domain V of the 23S rRNA gene, which disrupts antibiotic binding [44]. These mutations often have a significant fitness cost to the bacteria, reducing their growth and competitive ability in the absence of antibiotic pressure [45,46]. Additionally, the comparatively lower use of macrolides in intensive poultry production reduces selective pressure, further contributing to the sustained low resistance rates observed globally [39].

Methicillin-resistant *Staphylococcus aureus*

Global deaths attributable to MRSA doubled from an estimated 57,200 in 1990 to 130,000 in 2021 [47]. Methicillin-resistant *Staphylococcus aureus* is classically recognised as a major hospital-acquired (healthcare-associated MRSA) infection but has since expanded beyond the healthcare setting and is currently also prevalent in community environments (community-acquired MRSA) and livestock (livestock-associated MRSA, or LA-MRSA) [48,49]. While the impact is still debated, MRSA has been regarded as a zoonotic pathogen with implications for both human and animal health [50]. The ability of certain MRSA clones to transmit between humans and animals, coupled with MRSA's multidrug resistance, indicates its importance as a pathogen that threatens public health: though not immediately causing a substantial number of infections, it has been shown that these clones may acquire virulence genes such as the toxin Panton–Valentine leukocidin [51]. An integrated One Health approach is needed in order to effectively prevent and control MRSA [48]. While the transmission through direct contact with positive animals is clear, its role as food-borne pathogen is less so [52]. Nevertheless, LA-MRSA has been shown to be present in foods of animal origin, including turkey, chicken, pork, beef and veal [53-55]. The potential that such foodstuff may serve as reservoirs for clinical infections therefore cannot be ignored.

The most prevalent LA-MRSA clonal complex in Europe is CC398, particularly sequence type (ST) 398. ST398 primarily colonises pigs and veal calves but can also be found in poultry and horses [56]. LA-MRSA CC398 in Europe typically carries SCC*mec* types IVa and V, showing multidrug resistance to several microbial classes, including trimethoprim, tetracycline, macrolides, lincosamides, macrolide–lincosamide–streptogramin B, pleuromutilin–lincosamide–streptogramin A, phenicols, aminoglycosides and mupirocin [57]. Resistance genes and mobile genetic elements such as SCC*mec* and Tn916 are maintained across livestock hosts and geographic regions in a stable manner [58]. Other clonal complexes such as CC1 and CC97 have been reported in European livestock, with reports of CC1 strains spreading to pigs and dairy cows in Italy, Denmark, Belgium and Norway [59,60]. Interestingly, Norway documented MRSA CC1 (spa-type t177) in pigs during a 2008–2016 outbreak. Whole genome sequencing revealed a distinct cluster linking isolates from pigs, a sheep herd and exposed humans, potentially indicating a transmission link between livestock and humans. Epidemiological data suggest introduction by a farm worker and subsequent spread via pig trade. This provides molecular and epidemiological evidence of zoonotic transmission of CC1 MRSA in Norwegian livestock, and the potential of spread within Europe [61].

Livestock-associated MRSA has been shown to be mainly present in pigs and veal calves [62]. In Europe, LA-MRSA prevalence in pig farms ranges widely, from 1.3% and 13% in Switzerland and Denmark to as high as 81% and 90% in the Netherlands and Belgium, respectively. In addition, within countries and farm types, differences exist according to the region, such as in Germany, where rates vary between 21% and 70% depending on farm type and region [63-65].

There are major differences in the epidemiology of MRSA between Europe and Asia. While the predominant clone is ST398 in Europe, Asia exhibits a more diverse and complex LA-MRSA landscape [57]. While in the past, methicillin-susceptible *S. aureus* ST398 was quite prevalent in human infections in Asia, the situation may change rapidly with the introduction of the MRSA ST398 lineage into Asia, and this seems to be in connection with the LA-MRSA ST398 clones recently introduced in livestock [66-69]. The spread of the European LA-MRSA ST398 lineage and other lineages raises concerns about the potentials shifts in dominant strains and their associated risks.

In Asia, the dominant LA-MRSA clonal complex is CC9, which is prevalent in pigs and poultry and genetically differs from CC398, which is prevalent in Europe [10,68-69]. CC9, particularly sequence type 9, is found in the People's Republic of China, HKSAR[2], Sri Lanka, Bangladesh, Malaysia and Thailand [10,69-71]. CC9 isolated in Asia carries a variety of distinct SCC*mec* types, mainly III, IV, V and IX, with SCC*mec* III being the most common in China (People's Rep. of). The CC9/ST9 strains are often associated with *spa* type t899 and confer multidrug resistance to more than 15 antibiotics, including but not limited to erythromycin, ciprofloxacin, gentamicin, tetracycline and clindamycin [54]. Epidemiological studies show that livestock farmers and workers in close contact with livestock have a significantly higher prevalence of CC9 MRSA carriage compared to non-exposed controls [72]. While CC9 strains remain predominant, there are sporadic detections of the European-associated ST398 lineage detected in swine farms, abattoirs and pork products [73,74]. Similar sporadic cases of ST398 detection have been reported in Japan, the Republic of Korea, Thailand and Malaysia [66,69,75-77]. One study suggests Pakistan may present a unique case in the epidemiology of LA-MRSA in Asia, with a high overall prevalence of LA-MRSA (63%) found in slaughterhouses and meat shops [78]. However, the study was not very detailed, and it is even uncertain whether the strains isolated were LA-MRSA.

There is thus a critical need for country- and even region-specific surveillance and targeted interventions based on local LA-MRSA prevalence, types and epidemiology. However, as the current LA-MRSA strains are in general of low pathogenicity to humans, vigilance is necessary to monitor virulence, as they may acquire virulence genes from other staphylococci. Additionally, the current LA-MRSA generally lacks immune evasion

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2. HKSAR: Hong Kong, Special Administrative Region of the People's Republic of China

gene clusters, which allow the bacteria to evade the immune system, thus limiting their capacity to establish a persistent infection in humans [74,79]. This may also change in the near future, however, as demonstrated in an LA-MRSA ST9 strain in China (People's Rep. of) that has gained an immune evasion cluster-carrying βC-Φ prophage, which is found in clinical human *S. aureus* [80].

Antimicrobial resistance in commensal bacteria

Although antibiotic resistance in pathogenic bacteria poses major medical concerns, it is more prevalent in commensal bacteria, some of which can also act as facultative pathogens [81] and as reservoirs for AMR genes [22,82-84]. As commensal bacteria are continuously present, they are exposed to any antibiotic application, which facilitates the selection and accumulation of antibiotic-resistant bacteria [85]. Therefore, monitoring programmes focused on the effects of antimicrobial use and the consequences for AMR selection make use of commensal bacteria, as they can provide more accurate data [86]. Bacteria acquiring AMR genes through horizontal gene transfer occur more often in microbial-rich communities like the gut. In addition, the gut microbiota of both humans and animals are repeatedly exposed to orally administered antimicrobials. It has been estimated that the average level of horizontal gene transfer within the gut is 25 times higher than in soil or any other microbe-rich niche [87]. It is undeniable that the use of antibiotics in both humans and animals is a major contributing factor in the selection of AMRB [88]. Farm animals are considered a critical reservoir of resistant bacteria [89]. Several studies have demonstrated the relationship between antibiotic usage, both for growth promoter use and clinical use, and the selection of AMRB in animals [90]. Reducing antibiotic use by nearly 80% from the index year clearly demonstrated that lower antimicrobial usage results in reduced resistance levels in commensal bacteria [91]. However, the significance of the human health threat posed by these farm-associated bacteria remains unclear.

Transmission of commensal resistant bacteria from food-producing animals to humans can occur through a variety of routes, including direct contact between animals and humans. A more important pathway, however, could be through food, whereby people consume animal products contaminated with resistant microbes or vegetables fertilised with animal manure containing resistant bacteria [7]. Moreover, the composition of resistant bacteria or the resistome in the gut can be influenced by dietary changes and geographical locations. These variations are likely driven by differences in diet, antibiotic use, agricultural practices and environmental factors across regions. For instance, even short-term travel to regions such as Southern Asia and Northern Africa can alter an individual’s gut resistome [92]. Therefore, not only animal farms but also the whole food-producing environments where both animal and non-animal sources are produced or processed play an important role in the transmission and persistence of AMRB.

Monitoring and surveillance of antibiotic resistance from farm to fork have been executed mainly on commensal bacteria, and this along the entire food chain, including processing, packaging and retail [93]. The focus has been mainly on *Escherichia coli*, *Enterococcus faecium* and *Enterococcus faecalis*. These bacteria present in nearly all animal species and are relatively easy to isolate, and their susceptibility is straightforward to determine [94,95]. Over the years such surveillance (mainly in Europe) has remained more or less the same, with modifications according to changing insights or demands. An important change is the selective isolation of resistant bacteria, whereby the number of animals carrying a specific resistant bacterium, like extended-spectrum beta-lactamase (ESBL)-carrying *E. coli* or LA-MRSA, is monitored [96]. Next to continuous national surveillance programmes, there are several point prevalence studies. The target animal species to monitor can vary by country, as can the food monitored [93]. Moreover, *E. coli* and *Enterococcus* spp. can be found in vegetables as well as in the environment [97]. Animal manure and wastewater are considered hotspots for the spread of resistant bacteria and resistance genes to humans and the environment [98]. The AMR profiles and resistome of livestock vary between animal species, farms and countries; for example, sulfonamide resistance genes were almost absent in pigs but frequently found among veal calves, broilers and turkeys in European livestock farms. Quinolone resistance genes were core components in Spanish and German turkey flocks, while French flocks lacked these but instead had trimethoprim resistance genes [99,100].

Pork is the most consumed meat globally, accounting for 36% of the world’s meat intake, followed by poultry at 35% and beef at 22% [101]. These are recognised as important reservoirs for AMRB such as MRSA, ESBL-producing Enterobacteriaceae, vancomycin-resistant *Enterococcus* and ‘ESKAPE’ pathogens (*E. faecium*, *S. aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa* and *Enterobacter* spp.) [102-104]. A meta-analysis covering food samples produced in or imported into Switzerland between 1996 and 2016 found that meat products accounted for the majority of AMRB in food (60.1%), especially raw meats (cuts, ground, meatballs), followed by seafood and cheese [105]. The same study found that AMRB isolates were mainly detected in food products from North America (>45%), followed by Europe (33%) and Asia (29.6%), with very few from South America, Africa and the Caribbean, though the number of samples from those areas was very limited. Resistance against tetracyclines, aminoglycosides, penicillins, cephalosporins and fluoroquinolones was the most prevalent in Gram-negative bacteria, while resistance to macrolides, glycopeptides, nitrofurans and lincosamides was found in Gram-positive bacteria. In contrast, *E. coli* from food products at farmers' markets and retail stores in the USA showed a multidrug resistance rate of 11.6%, mainly resistance against streptomycin (39.1%), ampicillin (20.7%) and tetracycline (14.9%) [106]. It is thus clear that studies may not always be comparable and may not provide an accurate view of what is circulating at national level. At the retail level, a high frequency of multidrug resistance was detected in coagulase-negative staphylococci (43.5%, or 37 of 85 isolates) in ready-to-eat foods served in bars and clubs in Poland, indicating the importance of hygiene in food handling [107].

The European Union's ban on antimicrobials as growth promoters in livestock has reduced resistance against these antibiotics substantially, to the extent that resistance against them could no longer be detected [108]. Concurrent reduction of therapeutic use, despite an increase in pig production in Denmark, further lowered the levels of AMR [109]. In the same country, two years after stopping cephalosporin use in 2009, a decline in ESBL *E. coli* in slaughtered pigs was noticed [110]. A 2017 report by the European Food Safety Authority shows a decrease in the prevalence of ESBL-producing *E. coli* between 2015 and 2017 in pork across 28 EU Member States, with declines of 11.1% in Malta and 8.2% in Portugal and none detected in Luxembourg, Sweden, Finland, the United Kingdom, Iceland and Norway. However, missing data from six EU countries in 2015 and varying import capacities between countries make it difficult to establish a direct link between resistance in pigs and pork meat [86]. Likewise, a 2021 report by the Animal and Plant Health Agency on *E. coli* in beef and pork in the United Kingdom found that less than 1% of beef samples and under 4% of pork samples contained ESBL or AmpC-producing *E. coli*. Over seven years of monitoring (2015–2021), no carbapenem-resistant *E. coli* were detected in UK beef and pork samples, and only one isolate of non-EU-origin beef showed resistance to colistin [111]. But the most remarkable decline in use and concurrent resistance was seen in the Netherlands, where antimicrobial use is down to just over 20% compared to the index year 2009, with a concurrent reduced prevalence of resistance against most antibiotics [91,112]. In North America, the National Antimicrobial Resistance Monitoring System and the Canadian Integrated Program for Antimicrobial Resistance Surveillance report on AMR in *E. coli* and *Enterococcus* species found in retail meats and animal caecal contents. Both programmes observed either a reduction or stabilisation of AMR, except in retail pork, in which rates increased from 16% to 22%. Significant decreases in gentamicin-resistant *E. faecalis* were noted among turkeys and chickens, with similar reductions observed in retail chicken and turkey products [113].

One should also take into account, however, that variations in resistant bacterial contamination rates across regions are influenced not only by antibiotic use but also by socio-economic status, hygiene practices and policies governing antibiotic use in agriculture [114]. Poverty, overcrowded farming and weak food safety regulations in low- and middle-income countries (LMICs) are major causes of a higher prevalence of AMR bacterial contamination in food products [115]. A large study on *E. coli* from retail pork markets in the border area of Thailand, Cambodia, Laos and Myanmar demonstrated prevalence of colistin resistance was above 10%, and ESBL production was detected in more than 6% of the *E. coli* isolated [116]. A high prevalence of resistance against ampicillin, tetracycline and aminoglycosides in *E. coli* from poultry meat was also reported in Bangladesh, Ethiopia and Vietnam [117-119]. In Ghana, *E. coli* from diverse meat products displayed high resistance to tetracycline (73.3%) and ampicillin (71.67%) [120]. A selection of surveillance studies on AMR in the food chain across various LMICs is shown in Table I.

Through selective isolation using antibiotics to capture resistant strains, more resistant strains are found. In Asia, high prevalence of ESBL *E. coli* was found on poultry meat in Singapore and Malaysia wet markets (48–50%) [121,122], and up to 88.8% prevalence was found in HKSAR [123]. In Europe, in general, prevalence is lower than in Asia, with some countries nevertheless having similar levels [124]. *E. faecium* and *E. faecalis* have a high potential for horizontal transfer of resistant genes such as vancomycin-resistant *vanA* and erythromycin-resistant *erm* genes (*ermA*, *ermB* and *ermC*), among others [125]. Since the ban on growth promoters, the interest in surveilling animal *enterococci* has, however, largely lessened, and the latest resistance levels are no longer so high, with the exception of tetracycline and erythromycin [124]. There are no continuous national surveillance programmes on these species in food – only specific point prevalence studies, whereby in general observations are made but the resistance percentages are lower [126-128].

Antimicrobial resistance in animal pathogens

Antimicrobial-resistant animal pathogenic bacteria have been isolated from food-producing animals including aquaculture, livestock and poultry [129,130]. Those resistant bacteria can remain in the food chain, rendering them a potential threat to food safety, as resistant bacteria or their resistance genes can be transmitted to human bacteria via direct contact, the food chain or environmental routes, aligning with the One Health framework [131]. However, they most probably cause revenue loss for farmers due to treatment failures and reduced productivity. Animal pathogens vary widely in their resistance profiles, depending on species, antibiotic exposure, farming systems and geography [132]. While some bacterial species have been extensively studied for their role in AMR, others remain understudied, making it difficult to determine their current and future threat levels. This highlights the importance of expanding surveillance beyond commonly monitored bacteria to include emerging or regionally significant bacterial species in animal health.

In food-producing animals, AMR is most frequently observed in animal pathogenic *E. coli, Mannheimia haemolytica*, *K. pneumoniae*, *P. aeruginosa* and *Streptococcus suis*, all of which are considered problematic in veterinary medicine [56,129,133]. These pathogens, especially in poultry and swine, often show resistance to commonly used antibiotics such as tetracyclines, beta-lactams and fluoroquinolones. On the other hand, some pathogens such as *Actinobacillus pleuropneumoniae*, typhoidal *Salmonella*, *S. aureus*, *Pasteurella multocida* and *Mycoplasma bovis*, although widespread, remain by and large susceptible to several commonly used antibiotics [134,135]. The reasons for this remain obscure but must be related to bacterial lifestyle or genetics.

Animal health may be directly affected by AMR. A well-studied case is *M. haemolytica*, associated with bovine respiratory disease (BRD) and the number one cause of morbidity, mortality and the use of antibiotics in cattle production [136]. The control of BRD is mainly antimicrobial, with macrolides most frequently used to treat BRD and for metaphylaxis. The emergence of macrolide-resistant *M. haemolytica* has caused great concern in relation to the effectiveness of conventional disease management practices in animal husbandry [137]. The acquisition of resistance resulted in decreased treatment success, with negative effects on welfare and productivity. This subsequently led to an increase in antimicrobial use. Such dynamics illustrate how AMR can strengthen further selection pressure. This illustrates that AMR in food systems is a multifaceted issue, since food safety, public health and animal health will be affected. The response to AMR thus demands integrated strategies that take into account resistance selection and transmission in animal communities, transnational chains of food production, and international trade networks within a One Health framework [96].

In LMICs, weak surveillance systems as well as limited regulatory frameworks and quality control further complicate efforts to understand and combat AMR in animal pathogens [138]. Despite increasing data on AMR in livestock pathogens, major gaps remain in understanding of resistance trends in aquaculture and companion animals, as well as the role of lesser-known pathogens in AMR dissemination.

Antimicrobial resistance in non-animal-derived food products

The consumption of vegetables has increased in recent years across different regions, with Asia being the highest consumer, followed by Europe, Northern America, Oceania and Africa [139]. AMRB and resistance genes from non-animal-derived food production relate to human, animal and environmental sources. These AMRB are primarily introduced to agricultural environments through faecal contamination. The application of manure as fertiliser on vegetable farms, along with its subsequent spread via irrigation and surface water, serves as a major source of transmission [12]. Enteric bacteria and resistant genes from manure can persist in soil for several weeks following the application of manure [140]. Generally, the manure used for fertilisation is treated by anaerobic digestion and aerobic composting to eliminate pathogens prior to application [141,142]. Composting chicken litter eliminates 50–70% of bacteria loads compared to raw litter [143]. However, shotgun metagenomic analysis showed that sulphonamide resistance genes (*sul1*) and aminoglycosides (*aadA* and *aph(3')-I*) may increase after composting of manure [144,145]. A study comparing the effects of raw and composted litter on vegetable resistomes found that vegetables grown in soil with raw litter had a higher abundance of antibiotic resistance genes than those with composted litter [143].

In Africa it was shown that irrigation water and the soil environment were the main sources of antimicrobial-resistant bacteria on lettuce [146]. In South Africa, bacteria on vegetables were more resistant than those in irrigation water and soil [147]. However, vegetables grown in environments without manure or wastewater also contain resistant bacteria [97]. Therefore, it is assumed that wild animals and farm workers may contaminate vegetables with resistant bacteria. Further, fruits and spices, mainly originating from Asia, Egypt, Cameroon, Nigeria and Ghana, may contain bacteria with important resistance as ESBL-producing Enterobacteriaceae and MRSA strains [148]. In Europe, vegetables can also be highly contaminated with resistant bacteria, up to 25% in Ukraine [149] and half of the local vegetables in Switzerland, where ESBL-producing Enterobacteriaceae and even carbapenem-resistant isolates were found [150]. In the United Arab Emirates, up to 20% of the *E. coli* from fresh vegetables were resistant, with 13.79% displaying multidrug resistance phenotypes [151]. Bacteria and fungi can also cause plant diseases and production losses globally, particularly in LMICs, with climate change expected to worsen this issue [152]. Some of the antimicrobials that are applied in human and veterinary medicine, such as streptomycin, tetracyclines and triazoles, are also used to treat and prevent plant diseases [153]. The implications of this antibiotic usage on plants remain largely unknown as research on the subject is scarce. The extent of contamination by antimicrobial-resistant organisms to non-animal-derived food products in relation to the global emergence of AMR remains unclear.

The public health impact of antimicrobial resistance in food

Risk analysis models

Several risk analysis models, quantitative and not, have been developed for food-borne pathogens, among them ComBase (https://combase.errc.ars.usda.gov), which is a quantitative method that allows estimation of the contamination. This level of contamination can then be related to a certain risk of infection, though the dose–response relationship is not always clear, and several methodologies exist to determine this [154] and allow one to estimate potential risk with quite some uncertainty. Multiple quantitative microbial risk assessment models for AMR in food have been developed, though they face challenges due to data limitations and context-specific requirements. Based on this, a tentative risk model has been developed for assessing human exposure to third-generation cephalosporin resistant *E. coli* [154], carrying its own limitations but showing that at the quantitative level, the risk may not be too large. Other studies based more on molecular analysis have shown that direct contact with positive animals may bring a higher risk of acquiring resistance [155]. A distinction must be made between AMR in food-borne pathogens and AMR in commensal non-pathogenic bacteria. As for the food-borne pathogens, in addition to the risk of infection, there is an increased health risk due to treatment failures, similar to other pathogens of importance for public health.

The advent of whole genome sequencing has brought new insights into the transmission of AMR genes, and this can aid in the prediction of microbial behaviour, leading to more precise quantitative microbial risk assessments [156-158]. However, these analyses have more utility when dealing with food-borne pathogens. Nevertheless, it aids in determining the location of the genes and thus enables deciphering of their potential mobility and thus risk of transferring to other bacteria [159]. Large-scale country studies have identified several potential sources of transmission and have refined the analysis somewhat, albeit coming to different conclusions [160].

Future developments with the inclusion of metagenomics may lead to new risk analysis models, though the main problem is to determine the impact of AMR on public health. This will remain a major issue given that the presence of a resistance gene cannot indicate origin because they are present in all ecosystems. Statistical analysis on proportions present in each ecosystem may, however, give indications.

The public health impact of resistance in animal bacteria

To determine whether AMR in animal-derived bacteria impacts public health, two key bacterial groups must first be distinguished: zoonotic food-borne pathogens and commensal bacteria [161]. For food-borne pathogens, resistance may influence public health, as infections caused by these bacteria may warrant treatment, and if the bacteria are resistant, the treatment will be compromised. The current status of resistance in these bacteria has been outlined above. Their transmission is well recognised and has been demonstrated repeatedly. Moreover, with the advancement of molecular techniques, resistant strains can now be reliably traced back to their sources.

Resistance in bacteria other than those causing food-borne or zoonotic infections remains hard to determine, as discussed above. Several studies with different designs have been conducted and came to conflicting results. Early studies suggested that a substantial proportion of human ESBLs may have been acquired through meat consumption [162,163], although these findings were not quantitatively substantiated. Subsequent work in the Netherlands [164] offered a more refined analysis of potential transmission pathways, concluding that the contribution of food-producing animals and meat to human ESBL carriage was relatively limited, estimated at close to 20%. Other studies conducted during the same time found no epidemiological linkage between livestock and the general community-acquired ESBL strains, concluding that food may not play an important role in the transmission of ESBL/AmpC resistance. Another indication of lesser importance was given by whole genome sequencing-based studies, which suggested that ESBLs are spread through different plasmids in humans and animals and that the transfer is thus not very large [165], although occasional exceptions have been reported [166].

The Netherlands achieved a nearly 80% reduction in antimicrobial use in food-producing animals [167], accompanied by subsequent reduction in AMR in bacteria from animal origin and in meat [168]. It is not clear whether this has already resulted in a reduction in AMR in human bacteria; a recent study indicated that a reduction in ESBLs in hospital carriage may be ongoing, although the authors did not establish a causal link and noted challenges in proving attribution [169]. This effect cannot be ruled out as a potential outcome of concurrent control measures in human medicine.

Transfer of AMR has also been evaluated in some LMICs and non-intensive farming. Studies in Vietnam repeatedly detected limited to no transfer between animals, food and humans [170-172]. This is surprising given the closer human–animal contact and potentially weaker hygiene controls, which might intuitively suggest higher transmission risks. It is clear that understanding of AMR transmission between different ecosystems remains limited, and that there are unknown factors influencing its potential spread.

An example of reduced resistance in animals and impact on food products and public health

The first documented recommendations on the use of antimicrobials in food-producing animals were presented in the Swann report of 1969. The advice in this report focused primarily on the use of growth-promoting antibiotics, now largely prohibited in many countries, though not eliminated worldwide. At that time, the use of antimicrobials as growth promoters was widely accepted, and it was only in 2006 that European legislation fully prohibited the use of antimicrobials for growth promotion. Nevertheless, several antibiotics had already been restricted prior to that date [173]. One of the main antibiotics under scrutiny was avoparcin, an antibiotic of the glycopeptide group, use of which stopped in the late 1990s, and which generated significant controversy at the time due to conflicting study results [174]. After the ban of avoparcin, there was a clear reduction in glycopeptide-resistant enterococci in animals, though no improvement was observed in human medicine, where problems with infections persisted and in some cases worsened. This raises questions about the public health impact of vancomycin-resistant enterococci (VRE) originating from animal sources. It became clear that the vancomycin-resistant *Enterococcus faecium* was a specific lineage (CC17) carrying a pathogenicity island and the *esp* virulence gene [175,176]. Importantly, this observation does not undermine the broader evidence linking antimicrobial use in food-producing animals to resistance selection but rather highlights the complexity of the resistance transmission pathways and the need to consider multiple reservoirs and selective pressures within a One Health framework. It was also clear that, though there was no reduction in clinical infection, there was a reduction in intestinal carriage of VRE in the general population [177], indicating at least a temporary colonisation of humans with animal VRE. Nevertheless, the use of growth promoters should be banned, as their use may compromise animal health through the co-selection of resistance and may also compromise the effectiveness of new and existing antimicrobials due to potential co- and cross-resistance. On the other hand, action is needed in human medicine to reduce VRE as they remain a problem in hospitals, and in some cases the problem is increasingly present [178].

Antimicrobial resistance and food production

Food production encompasses the entire process of growing crops, raising animals and harvesting aquatic organisms to provide food for human consumption. It is a critical component of global food security and economic development [179]. However, the increasing use of antimicrobials in agriculture and aquaculture has raised concerns about the emergence and spread of antimicrobial-resistant organisms through food production. These resistant microbes can persist throughout the food production chain, from farm to fork [180]. Contamination of food products, water and the environment with resistant bacteria or resistance genes threatens public health and compromises food safety.

One of the primary contributors to AMR is the widespread use of antibiotics in agriculture, including animal husbandry and aquaculture, where it is often employed not only for therapeutic purposes but also for growth promotion and disease prevention. Indeed, the highest volume (abstracting of corrections for biomass) of antimicrobials is used in animals [181], and this volume is expected to increase as production of animals increases. This practice causes selective pressure on both pathogens and commensal microbes within host-associated microbiotas, thereby favouring the emergence and proliferation of antibiotic-resistant bacteria [182]. These resistant bacteria can be transmitted through the food production chain via direct contact with animals, bioaerosols – particularly those documented and modelled in agricultural settings where row crops and horticultural systems are located near confined animal feeding operations – as well as contaminated food products and exposure to contaminated water and soil [183]. Addressing AMR in food production requires a One Health approach and responsible antibiotic stewardship at every stage.

Antimicrobial resistance affects health, and as such one can assume that it also affects animal health and consequently animal production [6]. Thus, knowledge of resistance in animal pathogens is necessary, and a summary of this is given in the previous section. While for some bacteria there is a high prevalence of resistance, for others resistance is negligible. It should be noted, however, that knowledge on resistance in animal pathogens is minimal. There is a lack of studies demonstrating that AMR in animal pathogens creates treatment problems and, in turn, has an impact on food production [184].

Antimicrobial resistance and trade

International trade and spread of resistance

Antimicrobial resistance is a global silent pandemic, as borders are crossed not only by food, but also by human travel and, importantly, wildlife, especially migratory birds. There is emerging evidence that international food trade can contribute to the spread of AMR through both animal- and plant-based products, facilitating the movement of resistant bacteria and resistance genes across regions [185]. However, the importance of food trade as a driver of AMR dissemination remains difficult to quantify. An epidemiological analysis of resistance patterns in food products in relation to international trade routes could provide further insights, although such analyses should be done with caution due to the likelihood of incomplete data. An additional dimension is international travel, whereby AMR may be imported through the consumption of food with potential resistant bacteria. While it has been demonstrated that travel is a risk factor for infection with multidrug-resistant organisms, it remains unclear to what extent this risk can be attributed to food consumption [186].

Legislations on antimicrobial resistance with influence on trade

While there are national food control systems that can impose trade restrictions, there are no restrictions specific to AMR, and existing trade restriction measures vary by country. The Codex Alimentarius is instrumental in guiding regulation on food; however, its implementation is voluntary, and it does not contain explicit provisions addressing AMR or its regulation. Nevertheless, the programme’s task force on AMR has issued several guidelines: guidelines on integrated monitoring and surveillance of food-borne AMR (CXG 94-2021), guidelines for risk analysis of food-borne AMR (CXG 77-2011) and a code of practice to minimise and contain food-borne AMR (CXC 61-2005). Indeed, it would be difficult to set standards on what level of AMR bacteria food can carry, as there is no clarity on the impact of AMR in food on human health [187]. Regulations are warranted, though whether they will prove feasible remains to be seen. One of the more feasible measures may be issuing regulations on the use of growth-promoting antimicrobials, as these cannot be seen as essential for animal health and their abolishment will reduce the presence of resistant bacteria in food. This may be hampered by the international trade regulations of the World Trade Organization (WTO). However, as stated in a shared World Health Organization, World Intellectual Property Organization and WTO document on antimicrobial resistance, ‘WTO trade law ultimately can support the implementation of international standards for appropriate use of antibiotics, including in the area of animal husbandry' [188].

Conclusion and future directions

Quantifying the burden of AMR in food remains challenging, particularly for commensal bacteria, as transmission estimates vary widely across studies and distinguishing food-borne from direct contact routes is difficult. Advances in sequencing technologies and epidemiological modelling provide opportunities to clarify the role of food as a vehicle for AMR transmission. Despite persistent knowledge gaps, effective antimicrobial stewardship, including reductions in use of up to 80%, remains essential. Complementary strategies such as the use of antibiotic alternatives (for example, probiotics and phage therapy), enhanced biosecurity and improved farm management practices are also necessary to limit disease spread and resistance selection.

Les systèmes alimentaires et la résistance aux antimicrobiens : effets sur la sécurité sanitaire des aliments, la production animale et les échanges internationaux

N.O. Khine, L.Y.S. Tong, B.O. Oluwarinde & P. Butaye

Résumé

La présence et propagation de bactéries devenues résistantes aux agents antimicrobiens chez les animaux servant à la production de denrées alimentaires constitue un défi majeur pour la sécurité sanitaire des aliments, la santé publique, la production animale et le commerce international. L'acquisition de gènes de la résistance survient dans les populations de bactéries présentes chez les humains comme chez les animaux, d'où la difficulté de déterminer clairement dans quelle direction s'effectuent les transferts de gènes et quelles sont les pressions sélectives exercées par l'utilisation des agents antimicrobiens.

Les agents pathogènes zoonotiques d'origine alimentaire tels que les espèces de *Salmonella* jouent un rôle clé dans la transmission directe de la résistance aux antimicrobiens (RAM) aux humains par les aliments. Nombre de ces agents étant multi-résistants, leur détection fréquente dans les denrées alimentaires indique un risque important pour la santé publique. Le recours aux antimicrobiens dans les élevages, à des fins thérapeutiques, prophylactiques ou en tant que stimulateurs de croissance est un facteur reconnu d'émergence de résistances, même si ces pratiques font désormais l'objet de mesures réglementaires visant à les réduire ou à les interdire.

Les bactéries commensales et les pathogènes spécifiques aux animaux participent au transfert indirect de gènes de résistance, ce qui constitue une menace potentielle pour la santé animale et humaine. Les produits alimentaires d'origine animale sont un réservoir majeur de pathogènes résistants ; pour ce qui est des aliments d'origine végétale, il est essentiel de poursuivre les recherches sur leur contamination par des bactéries porteuses de gènes de résistance, afin d'en évaluer l'impact.

L'analyse des risques liés à la RAM est entravée par l'insuffisance des données, notamment concernant les effets de la RAM sur la santé et la production animales. Certaines infections bactériennes affectant les animaux sont devenues plus difficiles à traiter, mais à ce jour les infections totalement intraitables sont encore rares. L'absence d'un cadre réglementaire international couvrant spécifiquement la question des bactéries résistantes dans les denrées alimentaires faisant l'objet d'échanges internationaux complique l'élaboration et la mise en œuvre de politiques futures.

Il est donc indispensable de renforcer la surveillance, de mener des analyses de risque exhaustives et de soutenir la coopération internationale pour atténuer les risques associés à la RAM dans les systèmes de production alimentaire. Il s'agit d'un défi crucial pour la préservation de la sécurité sanitaire des aliments, la santé animale et l'intégrité du commerce mondial.

Mots-clés

Agent pathogène d'origine animale – Production animale – Résistance aux antimicrobiens – Santé publique – Sécurité sanitaire des aliments.

Sistemas alimentarios y resistencia a los antimicrobianos: repercusiones en la seguridad sanitaria de los alimentos, la producción animal y el comercio

N.O. Khine, L.Y.S. Tong, B.O. Oluwarinde & P. Butaye

Resumen

La resistencia a los antimicrobianos (RAM) en bacterias procedentes de animales destinados a la producción de alimentos representa un reto importante para la seguridad sanitaria de los alimentos, la salud pública, la producción animal y el comercio internacional. Debido a la adquisición de genes de RAM por poblaciones bacterianas, tanto en animales como en humanos, se dificulta la determinación de la direccionalidad de la transferencia genética y se complica la evaluación de presiones selectivas impuestas inherentes al uso de antimicrobianos.

Los patógenos zoonóticos transmitidos por los alimentos, como las especies de *Salmonella*, son agentes clave en la transmisión directa de la resistencia a los antimicrobianos (RAM) a los humanos a través de los alimentos. Suelen presentar multirresistencia y su prevalencia en los alimentos indica un riesgo considerable para la salud pública. La aplicación de antimicrobianos en la producción ganadera con fines terapéuticos, profilácticos y de promoción del crecimiento es un factor reconocido de la aparición de resistencia, a pesar de que estas prácticas han disminuido debido a intervenciones normativas.

Las bacterias comensales y patógenas específicas de animales contribuyen a la transferencia indirecta de genes de RAM, lo que puede afectar tanto a la sanidad animal como a la salud humana. Los alimentos de origen animal constituyen un importante reservorio de patógenos resistentes a los antimicrobianos; es fundamental realizar más investigaciones sobre la contaminación de alimentos de origen vegetal con bacterias resistentes a los antimicrobianos con el fin de evaluar sus repercusiones.

El análisis de riesgos de la RAM se ve obstaculizado por la insuficiencia de datos, especialmente relativos a sus consecuencias en la sanidad y la producción animal. Si bien algunas infecciones bacterianas en animales son más difíciles de tratar ahora que antes, las infecciones que no se pueden tratar aún no se han generalizado. Asimismo, la falta de reglamentaciones comerciales internacionales sobre bacterias resistentes a los antimicrobianos en los alimentos complica la formulación e implementación de políticas futuras.

Por consiguiente, una vigilancia reforzada, un análisis de riesgos completo y la colaboración internacional son esenciales para mitigar los riesgos asociados con la RAM en los alimentos. Abordar estos retos es fundamental para salvaguardar la seguridad sanitaria de los alimentos y la sanidad animal, y mantener la integridad del comercio mundial.

Palabras clave

Patógeno animal – Producción animal – Resistencia a los antimicrobianos – Salud pública – Seguridad sanitaria de los alimentos.

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Table I

Prevalence of antibiotic-resistant bacteria contamination and their main resistance profiles isolated from food sources in low- and middle-income countries

Country	Food source	Bacteria	Prevalence	Resistance profiles	References
Iran	Raw bovine milk (*n*=100)	*Escherichia coli*	78%	High resistance to amoxicillin, penicillin, cefalexin; *bla*TEM (50%), *bla*SHV (6.4%)	[189]
		Staphylococcus aureus	25%	*mec*A (20%), *bla*Z (12%)	
		Salmonella spp.	21%	*bla*TEM (28.5%), *bla*SHV (19%)	
Cuba	Various food samples (*n*=1,178 isolates)	*E. coli*	30%	40–53% showed resistance to tetracycline, nalidixic acid and ampicillin	[190]
		Vibrio cholerae	8.6%	High resistance to ampicillin (85.7%)	
		Staphylococcus	29%	Highest resistance to penicillin (41.5%) 20–27% resistance to tetracycline, ceftriaxone, oxacillin, erythromycin	
		Salmonella	32.3%	Highest resistance to tetracycline (59.3%), nalidixic acid (29.7%), ampicillin (23.3%)	
Malaysia	Dairy cattle (milk, *n*=71)	*E. coli*	16.9%	*bla*TEM, *bla*CTX-M	[191]
India	Raw poultry, fish, mutton, fruits, vegetables (*n*=100)	*E. coli, Klebsiella pneumoniae, Enterobacter* spp., *Pseudomonas* spp.	46.4%	*mcr*-1 (2.7% in *E. coli*)	[192]
Brazil	Chicken meat (*n*=41)	*E. coli*	19.5%	MDR (*mcr*-1, *bla*CTX-M, *bla*CMY-2)	[193]

Country	Food source	Bacteria	Prevalence	Resistance profiles	References
Pakistan	Chicken, beef, mutton (*n*=300)	MRSA	Chicken: 77% (23/30); beef: 63% (25/40); mutton: 50% (15/30)	*mec*A	[78]
Thailand	Raw meat from local markets (*n*=150)	*E. coli*	52%	*bla*TEM	[194]
	Ready-to-eat foods (*n*=150)	*Bacillus cereus*	21% (31/150)	97% resistant to ampicillin, 94% to amox-clav, 97% to penicillin	[195]
	Fermented pork (*n*=120)	*Enterococcus* spp.	MDR observed in 76.2%	Highest resistance to ciprofloxacin (97.5%), erythromycin (78.2%), tetracycline (67.2%)	[196]
	Eggs (*n*=750)	*E. coli*	91.2% of eggshell samples; MDR in 57.1% of isolates	High resistance to streptomycin, ampicillin, tetracycline	[197]
Thailand, Laos, Cambodia	Pig carcasses, pork	*E. coli*	Thailand: 3.5%; Laos: 6%; Cambodia: 14%	*mcr*-1, *mcr*-3, and *mcr*-5 were predominant	[198]
China (People's Rep. of)	Retail chicken and pork meat (*n*=290)	*E. coli*	Overall: 64.1%; chicken: 73.9%; pork: 42.9/%	High resistance to sulfonamides (87.4%), doxycycline (32.6%), gentamicin (29.7%), cephalosporins (44.6%); ESBL genes *bla*TEM-1D, *bla*CTX-M9, *bla*CTX-M-1, *bla*OXA-7 and *mcr-1*, *sul1*, *sul2*, and *sul3*	[199]

ESBL: extended-spectrum beta-lactamase
MDR: multidrug resistance
MRSA: methicillin-resistant *Staphylococcus aureus*