



## Comparative meta-analysis of antimicrobial resistance from different food sources along with one health approach in Italy and Thailand

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### ARTICLE INFO

#### Keywords:

Antimicrobial resistance (AMR)  
Antibiotics  
Multi-drug resistant (MDR)  
Surveillance  
One health

### ABSTRACT

Antimicrobial resistance (AMR) is increasing worldwide due to overuse, misuse and incomplete treatment of antibiotics. Many countries are facing the excessive issue due to the spreading of AMR not only in humans and animals, but also in water and agri-food sector. Our main aim was to perform a competitive meta-analysis of surveillance-resistant microbes and their antimicrobial superintendence in Italy and Thailand. Data have been collected from reports published for the period 2012–2021. A total of 9507 and 11,753 food samples contained 3905 (41.07%) and 3526 (30%) AMR bacteria in Italy and Thailand, respectively. In Italy, the highest microbial prevalence was  $\beta$ -lactam and tetracycline, while in Thailand mostly isolates showed resistance to cephalosporin and aminoglycoside. Our findings contribute to highlighting the increment of AMR related to different microbes with tendency to become multidrug resistant.

### 1. Introduction

The emergence of antimicrobial resistance (AMR) is one of major public health concerns in the 21st century. According to the World Health Organization (WHO) more than 670,000 persons are infected each year by antibiotic resistant bacteria of which approximately 33,000 succumb [1]. Studies on antimicrobial resistance spread predict that annually 10 million people will succumb because of drug-resistant infections within 2050 with a huge economic burden of USD 60 to 100 trillion [2–4]. Antibiotic-resistant bacteria found in food, environment, animals and their products in developing and developed nations. In Developed nations such as European Union [5] and Norway [6], it was found that, MDR-E.coli are majorly prevalent, in similar way, in European Union MDR-Salmonella Infantis and in Norway Vancomycin resistance Enterococcus are also widespread in some regions, In addition to it Denmark [7] and United States [8] MDR-Salmonella spp. and E.coli are highly prevalent. In developing nations such as in China [9] Plasmid mediated colistin resistant E.coli are highly prevalent, in Vietnam [10],

Brazil [11] and South Africa [12] MDR-E.Coli and colistin resistant E. coli are highly common, whereas in Algeria [13] MDR- Salmonella spp. showed most prevalence rate. As per our finding Staphylococcus spp. showed highest prevalence rate in both Italy (a developed nation) and Thailand (a developing nation).

Although the large-scale production of antibiotics, started eighty years ago, delivered various advantages to humans in the battle against infectious diseases, the extensive use of antibiotics led to an increasing number of resistant bacterial strains in humans, livestock, poultry and environment [14–16]. Multiple environment reservoirs, such as soil, water, industrial wastewater, take part in antibacterial resistance spreading, and may additionally introduce resistance genes into the food chain as illustrated in Fig. 1.

Different mechanisms enable a microorganism to acquire genetic material providing resistance to antimicrobials, such as transformation, transposition and conjugation (horizontal gene transfer—HGT), and mutations on genes related to drugs such as antibiotic-modifying enzymes [17,18]. An improper consuming of antibiotics by overuse,

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<https://doi.org/10.1016/j.onehlt.2022.100477>

Received 23 October 2022; Received in revised form 20 December 2022; Accepted 20 December 2022

Available online 22 December 2022

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misuse, or incomplete dosing increases the chance of developing antibiotic resistance since it increases the mutation rate. Moreover, multi-drug resistant (MDR) microorganisms are emerging in some regions in the world and spreading globally [19] making AMR a “silent pandemic” that risks to hardly affect us in the upcoming years [20,21]. The presence of MDR bacteria in the environment, food and animals suggests that agro-food sector should be thoroughly monitored for the AMR presence. Particularly, the food chain has to be investigated for causing foodborne diseases related to the microorganisms resistant to the most used antimicrobials [22].

The WHO plays a major role in surveillance of antibiotic use and provides the specified data to fight against AMR. Several global plans introduced by the WHO aim to combat AMR, such as, at the global level “The Global Action Plan (GAP)” [23] and “Global Antimicrobial Resistance and Use Surveillance System (GLASS)”, and regionally “Central Asian and European surveillance of AMR (CAESAR)” network and “European AMR surveillance network (EARS-Net)”. These plans are based on One Health concept that connects human and animal health with their ecosystems [24]. The WHO recommends investigations that link health, food, environment and economy at regional, national, and international level in a multidisciplinary, multi-sectorial approaches. Moreover, WHO surveillance techniques have also been adopted by the ESAC-Net and WHO regional centers [21]. At the moment, WHO runs the GAP project [3] that surveilles the use of antibiotics 65 countries. The detail description of two of these programs in Italy and Thailand is given in Table 3. As illustrated, the One Health approach includes implementing and designing policies, legislation and research to connect multiple sectors, which can work together. Different government associations and organizations collect and provide data on antibiotic consumption in human beings and animals [21] [3] [25–27]. Five main strategies are recommended to tackle AMR: 1) a judicious use of antibiotics; 2) greater efforts to prevent infections and to facilitate antibiotics alternatives; 3) enhanced knowledge to improve target measures; 4) sharing information and guidance on resistance and transmission, and 5) a strong international cooperation to minimize the development of antibiotic resistance (Fig. 8) [28].

In this context, we performed a systematic research and meta-analysis on AMR presence in food samples in two representative countries: Italy (a developed country) and Thailand (a developing country) using data published for the period 2012–2021. Out of 190 papers, 56 papers were selected as fitting the criteria (Fig. 2). In Italy, there is an increasing prevalence of AMR and MDR not only in hospitals but also in the community [29] regardless the application of several measures to

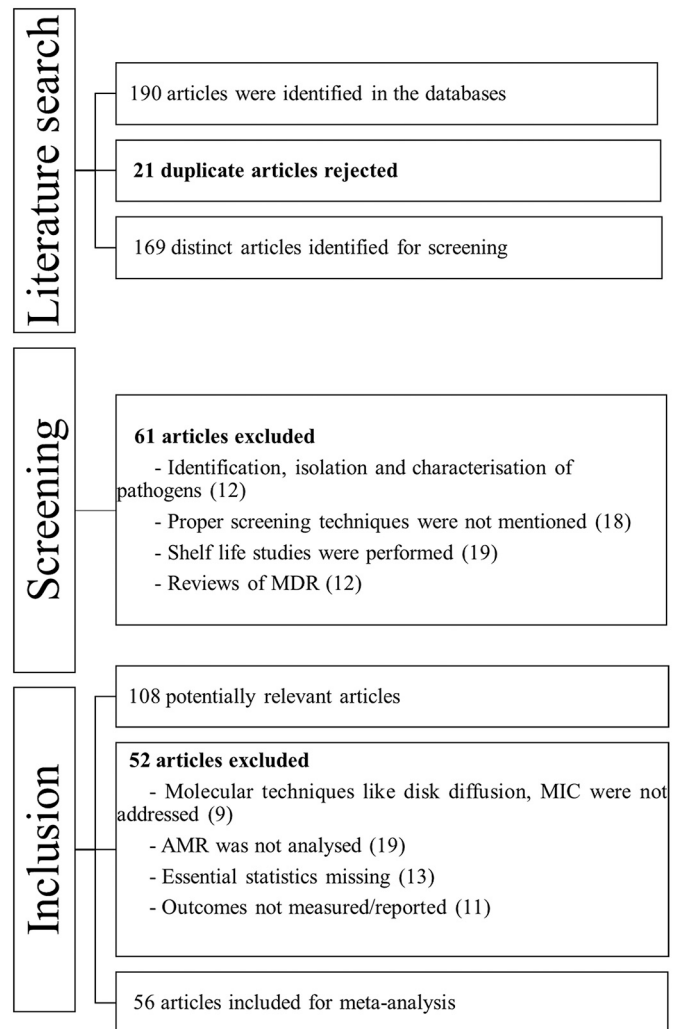


Fig. 2. An approach for identifying, screening, and incorporating data from various food sources and their AMR in meta-analyses.

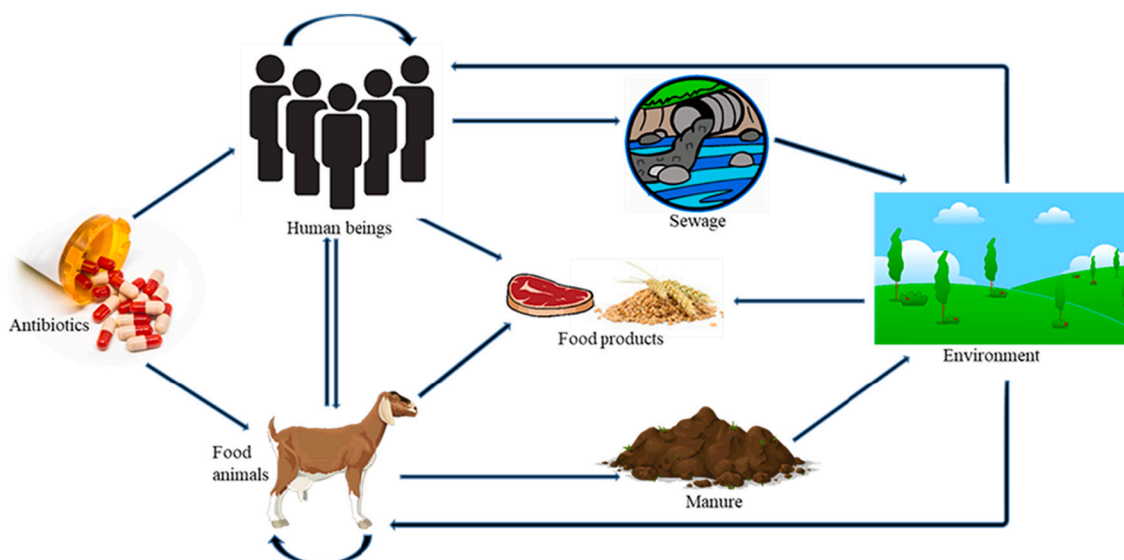


Fig. 1. Relationship between animal-human-environment in spreading of AMR by different sources.

control AMR spreading. In Thailand, fresh foods sold at open markets such as meat, eggs and sea-food represent an important source of foodborne diseases due to their easy contamination by pathogens [30–34]. The food conservation at environmental temperature, without strict hygienic and temperature control, favors cross-contamination in storing facilities and distributing channels like shipping from slaughterhouse to the markets [35,36]. Consequently, Taiwan and India has adapted several plans to limit AMR and MDR spreading. We, thus, investigated the prevalence of different foodborne bacterial pathogens and related it to the category of contaminated food and presence of specific AMR genes.

## 2. Materials and method

### 2.1. Search stratagem

Data from different websites such as PubMed, Google Scholar and Science Direct were used to retrieve relevant published articles from January 2012 to December 2021. The retrieving data were followed by the preferred reporting items for systematic reviews and meta-analysis (PRISMA) guideline (<http://www.prisma-statement.org/>) and the relevant medical subject heading (MeSH) term was also used to retrieve below-listed data. For e.g. “AMR from different food sources”, “AMR Spreading from Different pathogens”, “Multi drug resistance”, “Drug susceptibility tests of different pathogens isolated from different food sources”, “AMR assessment method”, “MDR”, “Italy”, “Thailand” are the keywords and the MeSH terms that were used [37]. The “AND” and “OR” Boolean operators were employed while applying the search queries. The full search plan for the PubMed/MEDLINE database was provided for Table 1 and Table 2 in the supplementary file.

### 2.2. Data extraction criteria

A total of 56 papers were selected to retrieve data and for the addition or rejection of data. Following criteria were applied: 1) availability of the article full text and abstract, 2) reported food pathogen and AMR, 3) mention of the method of analysis for pathogens, 4) sample sources (animal and vegetable food origins, dairy products, environmental samples, food handlers, slaughter houses etc.), 5) AMR assessment

method, including different molecular techniques, disk diffusion, minimum inhibitory concentration (MIC), and 6) sample size and susceptible/ resistant organism, multidrug resistant (MDR).

### 2.3. Data extraction and evaluation

Data obtained for different food type, microorganism, and their AMR were summarized in a single sheet using Excel® (Microsoft® office excel 2013) and pre-tested before full extraction. The extracted data included year of publication, source and size of samples, author names, publication system (focused on animal food source), date of publication (2012–2021), number of positive samples (for prevalence calculation), and microorganism species. Data were scrutinized and the data related to AMR were represented in a pie chart, and the cited papers by using Mendeley (version 1.19.8) [17].

### 2.4. Food category

The food categories taken into account are chicken, pork, turkey, raw beef, fish (shrimp, seafood), pig, dairy products (including milk, cheese, yoghurt), ready-to-eat, vegetables (sprouted seeds), barbecue, egg, animal (fox, mustelids, wild cat, wolf, cocks, bulls, horses) and bird are reported in Table 1 and Table 2.

## 3. Results

Prior to analyze data published on AMR in Italy and Thailand we compared their national programs applied to reduce AMR spreading.

### 3.1. One health and AMR training programs in Italy

Italy is one of the European countries which have the highest concerns about the spreading of MDR bacteria [3]. Reasons that can be considered responsible for this problem are: 1) inappropriate prescription of antibiotics; 2) lack of guidelines and recommendations in daily clinical practices; 3) lack of application of Antimicrobial Stewardship Programs (ASPs) and guidelines in hospitals and clinics [38]. The Italian Medicines Agency (AIFA) and the European Center for Disease Prevention and Control (ECDC) are organizing training programs to tackle the

**Table 1**  
Prevalence of different microbes in different Food sources in Italy from 2012 to 2021.

Microorganism	Chicken Total n = 4162	Turkey Total n = 253	Raw beef Total n = 280	Pig Total n = 1188	Dairy products Total n = 1706	Fish Total n = 1277	Animal Total n = 263	Bird Total n = 378	Total n = 9507
	n and (%)	n and (%)	n and (%)	n and (%)	n and (%)	n and (%)	n and (%)	n and (%)	n and (%)
<i>Escherichia coli</i>	531 (12.76)	85 (33.60)	21 (7.5)	–	181 (10.61)	–	–	101 (26.72)	919 (9.67)
<i>Enterococcus</i> spp.	440 (10.57)	–	–	–	296 (17.35)	–	–	–	736 (7.74)
<i>Vibrio</i> spp.	–	–	–	–	–	624 (48.86)	–	–	624 (6.56)
<i>Staphylococcus</i> spp.	–	–	–	–	92 (5.39)	50 (3.92)	–	–	142 (1.49)
<i>Streptococcus</i> spp.	–	–	–	–	29 (1.70)	–	–	–	29 (0.30)
<i>Yersinia enterocolitica</i>	–	–	–	55 (4.63)	–	–	–	–	55 (0.58)
<i>Campylobacter</i> spp.	262 (6.30)	40 (15.81)	–	–	25 (1.47)	311(24.35)	–	–	638 (6.71)
<i>Salmonella</i> spp.	52(1.25)	–	–	–	28 (1.64)	84 (6.58)	–	–	164 (1.73)
<i>Enterobacter</i> spp.	–	–	–	–	–	–	225 (85.55)	–	225 (2.37)
Other	3 (0.07)	4 (1.58)	–	–	162 (9.50)	204 (15.97)	–	–	373(3.92)
Total infected	1288 (30.95)	129 (50.99)	21 (7.5)	55 (4.63)	813 (47.66)	1273 (99.69)	225 (85.55)	101 (26.72)	3905 (41.07)

n: number of isolates; (%) of isolates.

**Table 2**  
Prevalence of different microbes in different Food sources in Thailand from 2012 to 2021.

Microorganism	Chicken Total n = 3589	Pork Total n = 758	Bird Total n = 32	Pig Total n = 3721	Fish Total n = 28	Retail Total n = 1099	Vegetable Total n = 1133	Milk Total n = 227	Water Total n = 68	Barbecue Total n = 226	Egg Total n = 750	Animals Total n = 122	Total n =
	n and (%)	n and (%)	n and (%)	n and (%)	n and (%)	n and (%)	n and (%)	n and (%)	n and (%)	n and (%)	n and (%)	n and (%)	n and (%)
<i>Escherichia coli</i>	506 (14.10)	368 (48.55)	26 (81.25)	611 (16.42)	–	77 (7.01)	5 (0.44)	–	60 (88.24)	–	91 (12.13)	–	1744 (14.84)
<i>Salmonella</i>	532 (14.82)	111 (14.64)	–	–	–	250 (22.75)	24 (2.12)	–	–	–	–	–	917 (7.80)
<i>Staphylococcus</i> spp.	208 (5.80)	–	–	–	0 (0)	–	41 (3.62)	–	–	36 (15.92)	–	41 (33.61)	326 (2.77)
<i>Bacillus</i> spp.	–	–	–	–	–	81 (7.37)	31(2.74)	53 (23.35)	–	–	–	–	165 (1.40)
<i>Yersinia</i> <i>enterocolitica</i>	–	–	–	–	–	3 (0.27)	–	–	–	–	–	–	3 (0.03)
<i>Cronobacter</i>	–	–	–	–	–	6 (0.55)	–	–	–	–	–	–	6 (0.05)
<i>Enterococcus</i> spp.	–	96 (12.66)	–	135 (3.63)	–	57 (5.19)	–	–	–	–	–	–	288 (2.45)
<i>Listeria</i> spp.	–	–	–	–	–	7 (0.64)	–	–	–	–	–	–	7 (0.06)
<i>Campylobacter</i> spp.	61 (1.70)	–	–	–	–	–	–	–	–	–	–	–	61 (0.52)
<i>Klebsiella</i> spp.	–	–	–	–	–	–	9 (0.79)	–	–	–	–	–	9 (0.08)
Total infected	1307 (36.42)	575 (75.86)	26 (81.25)	746 (20.05)	0 (0)	481 (43.77)	110 (9.71)	53 (23.35)	60 (88.24)	36 (15.92)	91 (12.13)	41 (33.61)	3526 (30)

n: number of isolates; (%) of isolates.

MDR strains in the food. EARS-Net, AIFA and Agenzia Italiana del Farmaco play major role in raising awareness at the political level, among public health workers regulating the drug uses. Moreover, plans like National Action Plan on Antimicrobial Resistance (PNCAR) 2017–2020, Healthcare-associated Infections Surveillance Network (HAI-Net) had been applied for surveillances of AMR and antibiotic usage in Italy [Table 3] [39].

### 3.2. One health and AMR training programs in Thailand

Organizations and agencies such as ASEAN post-2015 Health Development Goals [40] had applied surveillance programs for AMR in Asian countries with the aim to increase and strengthen international

**Table 3**  
Vigilance of antimicrobial resistance and monitoring system of Italy and Thailand.

Country	Organizations	Role
Italy	European Antimicrobial Resistance Surveillance Network (EARS-Net) <a href="https://www.ecdc.europa.eu/en/">https://www.ecdc.europa.eu/en/</a>	Raising awareness at the political level, among public health workers regulating the drug uses.
	Italian Medicines Agency (AIFA, Agenzia Italiana del Farmaco) <a href="https://www.aifa.gov.it/en/">https://www.aifa.gov.it/en/</a>	Responsible for drugs regulation.
	Healthcare-associated Infections Surveillance Network (HAI-Net) <a href="https://www.ecdc.europa.eu/en/">https://www.ecdc.europa.eu/en/</a>	Surveillance on antibiotics usage.
Thailand	The Global Action Plan on Antimicrobial Resistance (GAP-AMR) <a href="https://www.emro.who.int/">https://www.emro.who.int/</a>	Improve awareness and understanding, strengthen knowledge, reduce infection, optimize the use of antimicrobial agents, ensures sustainable investments in countering AMR.
	ASEAN post-2015 Health Development Goals <a href="https://asean.org/">https://asean.org/</a> National Strategic Plan for Emerging Infectious Disease Preparedness, Prevention and Response (NSP-AMR) (2017–2021) <a href="https://rr-asia.woah.org/">https://rr-asia.woah.org/</a>	Consist of four clusters responding to common priority posed to Asian country. AMR is in 2nd cluster. Includes emergence of AMR.

cooperation and support capacity building in low and high ranking countries [3]. The Thai Health Promotion Foundation, Health Systems Research Institute of Thailand, and different programs like Global Action Plan on Antimicrobial Resistance (GAP-AMR) have the following objectives: 1) improving awareness and understanding of AMR; 2) strengthening knowledge; 3) reducing infection; 4) optimizing the use of antimicrobial agents, and 5) ensuring sustainable investments in countering AMR. Other plans dealing with vigilance on AMR are the ASEAN post-2015 Health Development Goals consisting of four clusters responding to common priority posed to Asian countries in which AMR is in the 2nd cluster, and the National Strategic Plan for Emerging Infectious Disease Preparedness, Prevention and Response (NSP-AMR) (2017–2021) [Table 3] [6] [41].

### 3.3. Comparative meta-analysis

The meta-analysis and systematic study included 56 articles (23 from Italy and 33 from Thailand) out of 190 eligible studies as shown in fig. 2. A total number of 21,260 AMR tests were collected for different microorganisms present in different food items, animals and environments (9507 from Italy and 11,753 samples from Thailand). Resistance to approximately 12 different antimicrobial agents/drugs and 14 different microorganisms were found. Tables 1 and Table 2 show sample sources, type of bacterial species and their proportion.

#### 3.3.1. Comparative meta-analysis in Italy

Out of 78 eligible studies related to pathogens carrying AMR in Italy from 2012 to 2021, 23 papers were selected for further examination [42–64]. They report 9507 total AMR isolates of which 3905 (41.07%) were represented by *E. coli* 919 (9.67%), *Enterococcus* spp. 736 (7.74%), *Vibrio* spp. 624 (6.56%), *Staphylococcus* spp. 142 (1.49%), *Streptococcus* spp. 29 (0.30%), *Yersinia enterocolitica* 55 (0.58%), *Campylobacter* spp. 638 (6.71%), *Salmonella* 164 (1.73%), *Enterobacter* 225 (2.37%) and others 373 (3.92%), (Fig. 3). It can be assumed that *Enterococcus* spp. and *E.coli* are the most prevalent in Italy. About 24% of AMR *E. coli* isolated in Italy originated from chicken, turkey and raw beef, followed by (20%) AMR *Enterococcus* spp. originated from chicken and dairy products, (17%) AMR *Campylobacter* spp. originated from chicken, turkey and dairy products, (17%) AMR *Staphylococcus* spp., *Vibrio* spp.

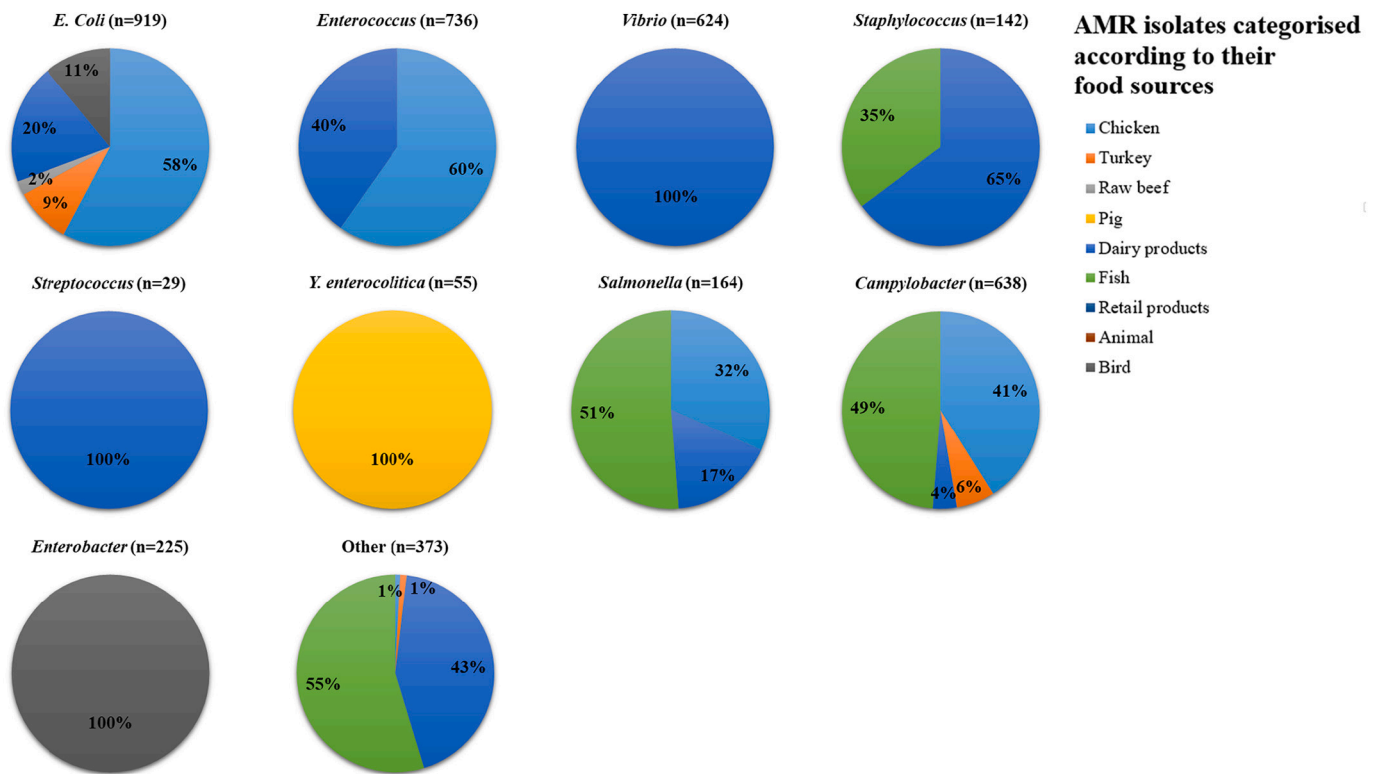


Fig. 3. AMR positive isolates from different food sources (n = 9507) in Italy, (n represent the number of isolates) from 2012 to 2021.

(7%), AMR *Enterobacter* spp. (6%), AMR *Salmonella* spp. (4%), (1%) AMR *Streptococcus* spp., (1%) AMR *Y. enterocolitica* (1%). (Fig. 5). Moreover, there were some bacteria identified primarily in specific food samples in Italy. For example, *Vibrio* spp. is highly abundant in fish

(about 6.56%), existing naturally in freshwater, estuary, and marine settings and producing “vibriosis.” [43,65] As agents of rare and epidemic foodborne diseases associated with the ingestion of raw or undercooked contaminated seafood or shellfish, *Vibrio* spp. poses a

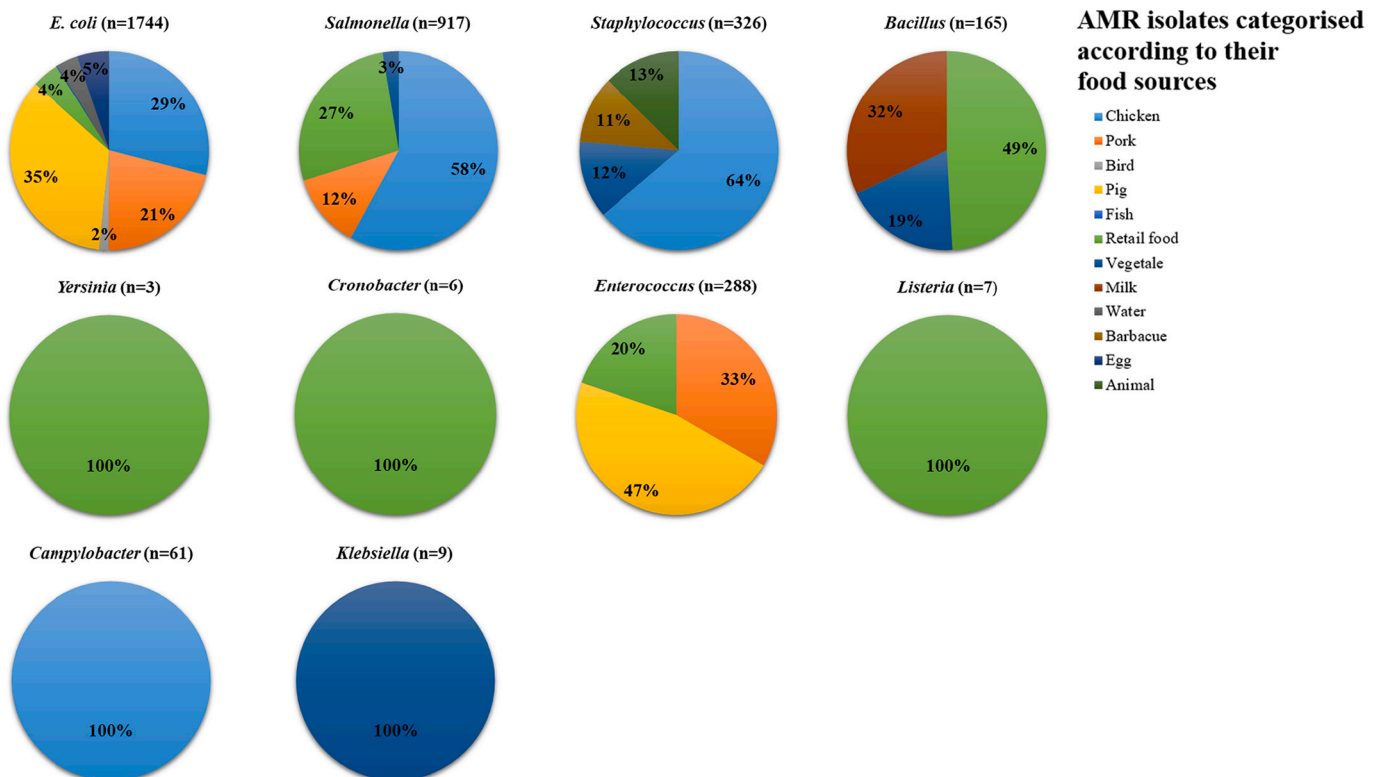


Fig. 4. AMR positive isolated microbes categorized in different food sources (n = 11,753) in Thailand, (n represent the number of isolates) from 2012 to 2021.



significant public health risk. [66] *Streptococcus* is quite common in dairy (about 0.30%), and this genus is one of the most common pathogens that cause cow mastitis. Mastitis is the most prevalent and costly disease in the dairy industry. It not only reduces economic profit owing to milk losses and therapy costs, but it also has a substantial impact on animal health and welfare. [67,68] Pigs are the principal reservoir of *Yersinia enterocolitica* (about 0.58%) and According to epidemiological research, the principal source of human infections is undercooked pork and other pig products and transported by infected finishing pigs. From farms to slaughterhouses, *Y. enterocolitica* has been found. [62]

### 3.3.2. Comparative meta-analysis in Thailand

Out of 112 research papers related to foodborne pathogens in Thailand from 2012 to 2021, 33 were considered for meta-analysis [4,31,34,35,69–97]. Among 11,753 AMR isolates 3526 (30%) were represented by *E. coli* 1744 (14.84%), *Salmonella* spp. 917 (7.80%), *Staphylococcus* spp. 326 (2.77%), *Bacillus* spp., 165 (1.40%), *Yersinia*, 3 (0.03%), *Cronobacter* 6 (0.05%), *Enterococcus* spp. 288 (2.45%), *Listeria* spp. 7 (0.06%), *Campylobacter* spp. 61 (0.52%), and *Klebsiella* spp. 9 (0.08%), as presented in Fig. 4. It can be assumed that *E. coli* (50%) and *Salmonella* spp. (26%) are prevalent in Thailand. Data from Thailand showed a high prevalence for *Staphylococcus* spp. (9%) followed by *Enterococcus* spp. (8%), *Bacillus* spp. (5%), *Campylobacter* spp. (2%) as illustrated in Fig. 5. In addition, there were some bacteria that were identified primarily in specific food samples in Thailand. For example, *Yersinia enterocolitica* is highly abundant in retail food (0.03%). *Cronobacter* is predominant in retail food (0.05%) and has been detected in a wide range of foods, including ready-to-eat foods, meat products, vegetables, herbs, and spices. [98] Moreover *Cronobacter* has been related to serious, frequently fatal infections such as meningitis, necrotizing enterocolitis, and septicemia in babies and newborns. [99] *Listeria* spp. is highly prevalent in retail (0.06%). This bacterium species can cause invasive listeriosis, which has been linked to various ready-to-eat (RTE) foods and can result in serious infections in humans. [100,101] *Campylobacter* spp. are quite common in chicken (0.52%), causing campylobacteriosis, which is typically spread by handling or consumption of infected food, particularly poultry products, and ingesting a few bacterial cells may cause mild to severe diarrhea. [102,103]

### 3.4. Comparison of AMR isolates in Italy and Thailand and their antimicrobial resistance

Comparison of AMR isolates in Italy and Thailand reported in Fig. 5

indicates the similar prevalence of *E. coli* in both countries. On the contrary, *Salmonella*, is the second most relevant AMR bacterium detected in Thailand with the 26%, but was found in only 4% of isolates in Italy. In addition, *Campylobacter*, reached 17% in Italy while 2% in Thailand. The *Salmonella* prevalence in Thailand is mainly related to the high consumption of pork and retails, while the presence of *Campylobacter* in Italy is related to the consumption of chicken. Similarly, the percentages of *Enterococcus* isolates can be related to the consumption of chicken and pork in the two countries.

An analysis of the antimicrobial agents found and the antibiotic resistances detected for each microbial isolate in Italy and Thailand is reported in Fig. 6 and Fig. 7 respectively. Multi drug resistant *Staphylococcus* spp. were found in both Italy and Thailand, while *Vibrio* spp., and *Campylobacter* spp. MDR strains were detected in Italy, and *E. coli*, and *Salmonella* MDR strains in Thailand. Microbes detected in Italy mainly possessed microbial resistance to  $\beta$ -lactams and tetracyclines followed by aminoglycosides and quinolones (Fig. 6), while microbial resistances mostly found in Thailand were for cephalosporin and aminoglycoside followed by tetracyclines (Fig. 7). It is worrying that most of the reported bacteria showed multidrug resistance.

## 4. Discussion

This work provides a comprehensive overview regarding the prevalence of foodborne pathogens and the occurrence of AMR genes in Italy and Thailand. The data published within last ten years were analyzed with the intention to relate the AMR prevalence with different microorganisms. Out of 190 papers, 56 papers were selected as fitting into the criteria. A designed follow-up AMR risk group assessment was performed at a variety of food sources such as retail food, chicken, pork, duck, turkey, raw beef, fish, shrimp, seafood, packed meat, dairy products, vegetables, sprouted seeds, and others.

The meta-analysis suggested that foods were highly contaminated with *E. coli*, and *Enterococcus* spp. in Italy, while *Salmonella* spp. was the prevalent bacterium detected in food in Thailand. The obtained data reflected that contamination occurred in the food mostly eaten in each country. The isolated bacteria showed resistance mainly to  $\beta$ -lactams, cephalosporin, aminoglycosides, fluoroquinolone, sulfonamides, tetracycline, phenicol, macrolides, quinolones, amphenicol, chloramphenicol, lincomycin. The large variety of resistance genes suggests that strains isolated from food may affect the animals-humans-environment. In Italy, out of 21,260 isolates, 9507 were positive for AMR (45%), by which 3905 (18%) isolated bacteria were  $\beta$ -lactam and tetracycline

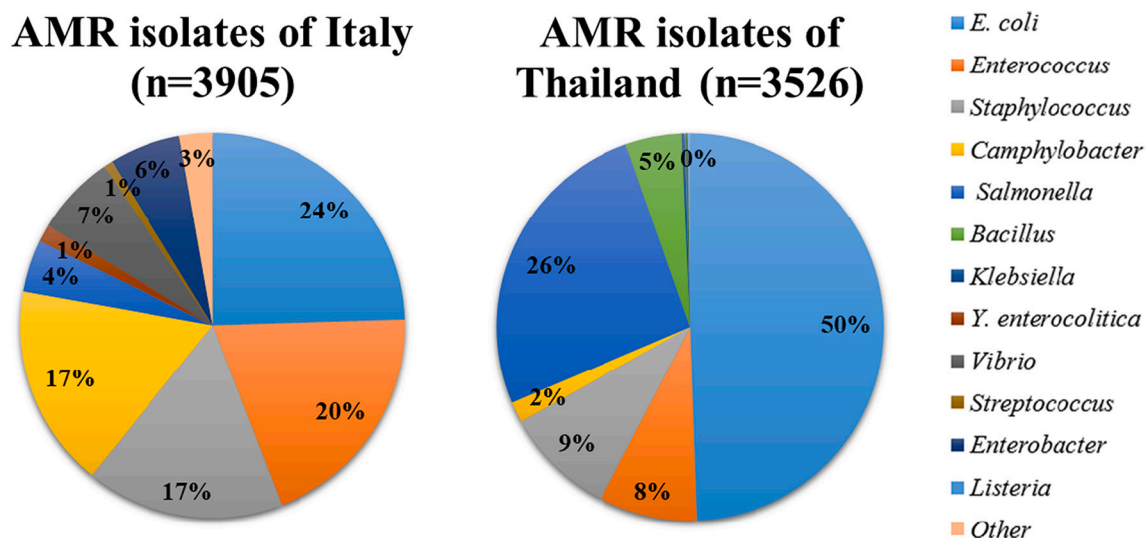


Fig. 5. Comparison between AMR isolates from different food sources in Italy ( $n = 3905$ ) and Thailand ( $n = 3526$ ) from 2012 to 2021.

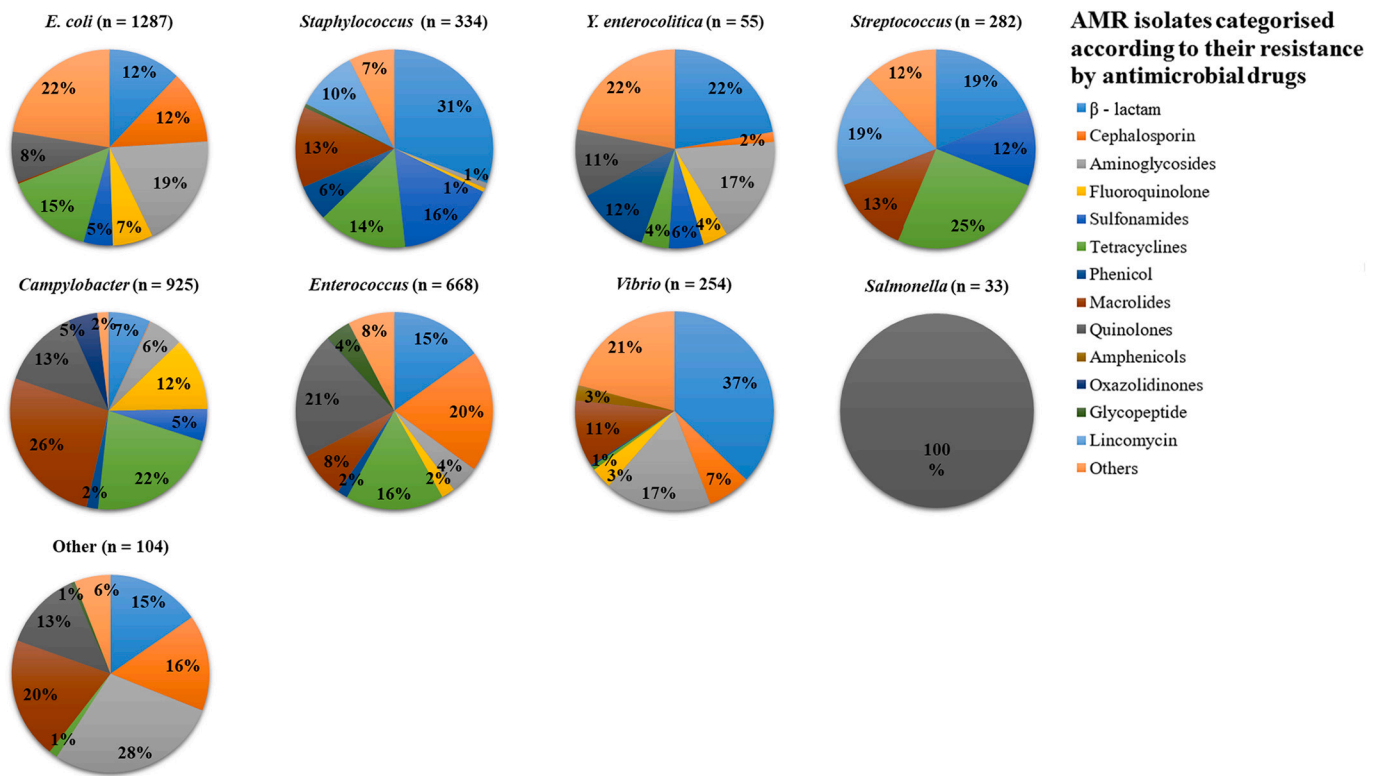


Fig. 6. Antimicrobials resistance prevalence for isolates (denoted by n) from foods of animal and non-animal origin (N = 3905) in Italy. Antimicrobial agents are represented by different colors in the pie charts.

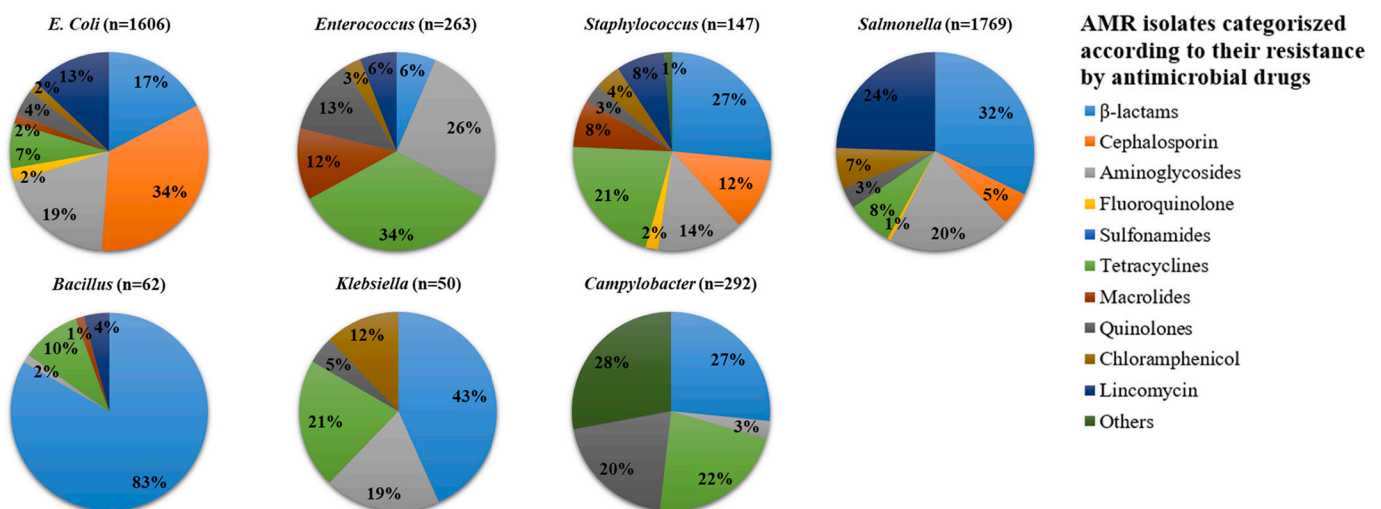


Fig. 7. Antimicrobials resistance prevalence for isolates (denoted by n) from foods of animal and non-animal origin (N = 3526) in Thailand. Antimicrobial agents are represented by different colors in the pie charts.

resistant. The resistance to aminoglycosides and quinolones had middle prevalence whereas cephalosporin, fluoroquinolone, sulfonamide, phenicol, macrolides, amphenicol, lincomycin showed low prevalence. In Thailand, out of 21,260 isolates, 11,753(55%) samples were positive for AMR by which 3526(17%) bacteria were isolates. Cephalosporin and aminoglycoside along with tetracycline showed the highest resistance occurrence, while beta-lactam shows middle prevalence and quinolones, chloramphenicol, fluoroquinolone, macrolides, lincomycin showed low prevalence. Differences in national policies on controlling antimicrobial prescription and use and their particular needs related to specific diseases may explain the observed differences in most prevalent AMR genes

in Italy and Thailand.

The population progression increases the food demand, which consequently contributes to AMR ubiquitous spreading [66]. Our meta-analysis indicated different food sources of resistant microbes (Tables 1 and Table 2). Many microorganisms can get suitable conditions for survival and acquire resistance to various drugs by mutation, horizontal gene transfer or other mechanisms. Recently, the European Food Safety Authority (EFSA) has assessed the role of food-producing environments in the emergence and spread of AMR in EU plant-based food production, terrestrial animals (poultry, cattle and pigs) and aquaculture [104]. Among the various sources and transmission routes identified, fertilizers

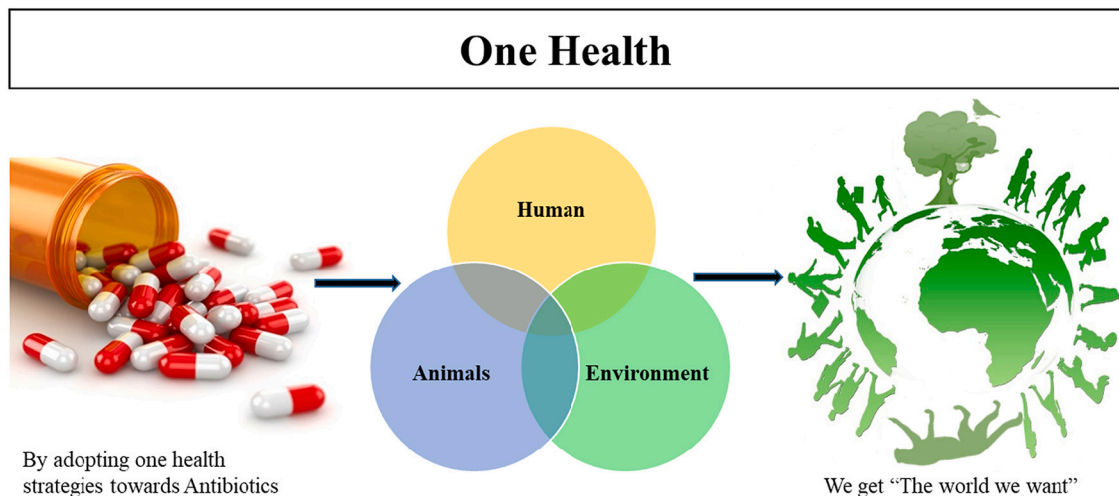


Fig. 8. One Health approach.

of fecal origin, irrigation and surface water were found to contribute mostly. Raw food are considered as highly risky to consumers because resistant bacteria survive in non-treated food. Minimal food processing and treatments may stress bacterial cells without killing them and in that way may trigger the AMR genes transfer [105].

The incidence of microorganisms becoming resistant to different antimicrobial agents could continue to grow [106] becoming a global threat if not appropriate strategies will be adopted. Therefore, there is urgent need to reduce the usage of antibiotics to minimize the burden related to antimicrobial resistance. This may be achieved through the One Health approach taking into account threats to animals-humans-environment in different countries that cause ineffective treatment of bacterial infections. Finally, the reduction of antibiotic resistance spreading requires a coordinated global effort and cooperation together with the sustained to chart a new course to address the urgent global challenge of antimicrobial resistance.

## 5. Conclusion

We presented, the current situation of AMR in food in one European and one Asian country obtained by the meta-analysis and systematic study, together with One Health programs carried in these countries to combat the AMR spreading. The primary agricultural production based on the utilization of antibiotics is an important cause of AMR selection in bacteria that may be found on foodstuffs. However, food may be contaminated by resistant bacteria during its processing, stocking and distribution. The cross-contamination occurs frequently when good agricultural practices cannot be achieved, which is the case with the open-air market. The implementation of One Health approach and guidelines to tackle AMR provided by different organizations should be followed to combat MDR microbes and most dangerous pathogenic bacteria such as *E. coli*, *Klebsiella* spp., *Streptococcus* spp., *Staphylococcus* spp., *Salmonella*, *Campylobacter* spp. Our study demonstrated the need for further analyses and harmonization in resistance incidence in different countries. The comparison between Italy and Thailand revealed the urgent need for controlled and lower use of antimicrobials, confirmed the necessity of the One Health approach and supports for measures should be provided at a global level.

## Funding

VtR Inc-CGU (SCRPD1L0221); DOXABIO-CGU (SCRPD1K0131), and CGU grant (UZRPD1L0011, UZRPD1M0081).

## Ethical consideration

Not Applicable.

## CRedit authorship contribution statement

**Gunjan:** Methodology, Writing – original draft. **Jasmina Vidic:** Data curation. **Marisa Manzano:** Writing – original draft. **V. Samuel Raj:** Investigation, Visualization. **Ramendra Pati Pandey:** Supervision, Validation. **Chung-Ming Chang:** Supervision, Writing – review & editing.

## Declaration of Competing Interest

Not Applicable.

## Data availability

Data will be made available on request.

## Acknowledgements

This work was supported through industry-academia collaboration projects, VtR Inc-CGU, R.O.C., project grant (SCRPD1L0221), DOXABIO-CGU, R.O.C., project grant (SCRPD1K0131), and also the CGU project grant (UZRPD1L0011, UZRPD1M0081).

## References

- [1] A.R. Collaborators, Articles Global Burden of Bacterial Antimicrobial Resistance in 2019 : A Systematic Analysis 399, 2022, [https://doi.org/10.1016/S0140-6736\(21\)02724-0](https://doi.org/10.1016/S0140-6736(21)02724-0).
- [2] *Antimicrobial Resistance: Tackling a Crisis for the Health and Wealth of Nations*, 2014.
- [3] F. Menichetti, M. Falcone, P. Lopalco, C. Tascini, A. Pan, L. Busani, B. Viaggi, G. M. Rossolini, F. Arena, A. Novelli, F. De Rosa, S. Iannazzo, J. Cohen, The GISA call to action for the appropriate use of antimicrobials and the control of antimicrobial resistance in Italy, *Int. J. Antimicrob. Agents* 52 (2018) 127–134, <https://doi.org/10.1016/j.ijantimicag.2018.05.010>.
- [4] P. Sornsenee, S. Chimplee, A. Arbubaker, S. Kongchai, H. Madimong, C. Romyasamit, Occurrence, antimicrobial Resistance profile, and characterization of extended-Spectrum  $\beta$ -lactamase-producing *Escherichia coli* isolates from minced meat at local Markets in Thailand, *Foodborne Pathog. Dis.* 19 (2022) 232–240, <https://doi.org/10.1089/fpd.2021.0059>.
- [5] The European Union summary report on trends and sources of zoonoses, zoonotic agents and food-borne outbreaks in 2016, *EFSA J.* 15 (2017), <https://doi.org/10.2903/J.EFSA.2017.5077>.
- [6] *Resistance, A, Norm - Vet*, 2015.
- [7] DANMAP\_2021\_version-1. (2021).



- [8] D. Administration, 2014 SUMMARY REPORT Antimicrobials Sold or Distributed for Use in Food-Producing Animals, 2015.
- [9] Y.Y. Liu, Y. Wang, T.R. Walsh, L.X. Yi, R. Zhang, J. Spencer, Y. Doi, G. Tian, B. Dong, X. Huang, L.F. Yu, D. Gu, H. Ren, X. Chen, L. Lv, D. He, H. Zhou, Z. Liang, J.H. Liu, J. Shen, Emergence of plasmid-mediated colistin resistance mechanism MCR-1 in animals and human beings in China: a microbiological and molecular biological study, *Lancet Infect. Dis.* 16 (2016) 161–168, [https://doi.org/10.1016/S1473-3099\(15\)00424-7](https://doi.org/10.1016/S1473-3099(15)00424-7).
- [10] M. Usui, S. Ozawa, H. Onozato, R. Kuge, Y. Obata, T. Uemae, P.T. Ngoc, A. Heriyanto, T. Chalemchaikit, K. Makita, Y. Muramatsu, Y. Tamura, Antimicrobial susceptibility of indicator bacteria isolated from chickens in southeast Asian countries (Vietnam, Indonesia and Thailand), *J. Vet. Med. Sci.* 76 (2014) 685–692, <https://doi.org/10.1292/JVMS.13-0423>.
- [11] M.R. Fernandes, Q. Moura, L. Sartori, K.C. Silva, M.P. Cunha, F. Esposito, R. Lopes, L.K. Otutumi, D.D. Gonçalves, M. Dropa, M.H. Matté, D.F. Monte, M. Landgraf, G.R. Francisco, M.F. Bueno, D. de Oliveira Garcia, T. Knöbl, A. M. Moreno, N. Lincopan, Silent dissemination of colistin-resistant *Escherichia coli* in South America could contribute to the global spread of the mcr-1 gene, *Euro Surveill.* 21 (2016), <https://doi.org/10.2807/1560-7917.ES.2016.21.17.30214>.
- [12] B.C. Iweriebior, C.J. Iwu, L.C. Obi, U.U. Nwodo, A.I. Okoh, Multiple antibiotic resistances among Shiga toxin producing *Escherichia coli* O157 in feces of dairy cattle farms in eastern cape of South Africa clinical microbiology and vaccines, *BMC Microbiol.* 15 (2015) 1–9, <https://doi.org/10.1186/S12866-015-0553-Y/FIGURES/4>.
- [13] R. Elgroud, F. Zerdoumi, M. Benazzouz, C. Bouzitouna-Bentchouala, S.A. Granier, S. Frémy, A. Brisabois, B. Dufour, Y. Millemann, Characteristics of *Salmonella* contamination of broilers and slaughterhouses in the region of Constantine (Algeria), *Zoonoses Public Health* 56 (2009) 84–93, <https://doi.org/10.1111/J.1863-2378.2008.01164.X>.
- [14] B. Aslam, M. Khurshid, M.I. Arshad, S. Muzammil, M. Rasool, N. Yasmeen, T. Shah, T.H. Chaudhry, M.H. Rasool, A. Shahid, X. Xueshan, Z. Baloch, Antibiotic Resistance: one health one world outlook, *Front. Cell. Infect. Microbiol.* 11 (2021) 1–20, <https://doi.org/10.3389/fcimb.2021.771510>.
- [15] P.M.C. Huijbers, H. Blaak, M.C.M. De Jong, E.A.M. Graat, C.M.J. E. Vandembroucke-Grauls, A.M. De Roda Husman, Role of the environment in the transmission of antimicrobial resistance to humans: a review, *Environ. Sci. Technol.* 49 (2015) 11993–12004, [https://doi.org/10.1021/ACS.EST.5B02566/SUPPL\\_FILE/ES5B02566\\_SI\\_001.PDF](https://doi.org/10.1021/ACS.EST.5B02566/SUPPL_FILE/ES5B02566_SI_001.PDF).
- [16] E. Marti, E. Variatza, J.L. Balczar, The role of aquatic ecosystems as reservoirs of antibiotic resistance, *Trends Microbiol.* 22 (2014) 36–41, <https://doi.org/10.1016/j.tim.2013.11.001>.
- [17] J.L. Martinez, General principles of antibiotic resistance in bacteria, *Drug Discov. Today Technol.* 11 (2014) 33–39, <https://doi.org/10.1016/J.DDTEC.2014.02.001>.
- [18] A.J. Mathers, G. Peirano, J.D.D. Pitout, The role of epidemic resistance plasmids and international high- risk clones in the spread of multidrug-resistant Enterobacteriaceae, *Clin. Microbiol. Rev.* 28 (2015) 565–591, <https://doi.org/10.1128/CMR.00116-14>.
- [19] A.H. Holmes, L.S.P. Moore, A. Sundsfjord, M. Steinbakk, S. Regmi, A. Karkey, P. J. Guerin, L.J.V. Piddock, Understanding the mechanisms and drivers of antimicrobial resistance, *Lancet.* 387 (2016) 176–187, [https://doi.org/10.1016/S0140-6736\(15\)00473-0](https://doi.org/10.1016/S0140-6736(15)00473-0).
- [20] E. Christaki, M. Marcou, A. Tofarides, Antimicrobial Resistance in Bacteria: mechanisms, evolution, and persistence, *J. Mol. Evol.* 88 (2020) 26–40, <https://doi.org/10.1007/S00239-019-09914-3>.
- [21] S. Khamsarn, Y. Nampoosak, S. Busamaro, T. Tangkoskul, C. Seenama, P. Rattanaumpawan, A. Boonyasiri, V. Thamlikitkul, Epidemiology of antibiotic use and antimicrobial resistance in selected communities in Thailand, *J. Med. Assoc. Thai.* 99 (2016) 270–275.
- [22] G. Gronvall, C. Boddie, R. Knutsson, M. Colby, One health security: an important component of the global health security agenda, *Biosecurity and Bioterrorism.* 12 (2014) 221–224, <https://doi.org/10.1089/bsp.2014.0044>.
- [23] L. Munkholm, O. Rubin, The Global Governance of Antimicrobial Resistance : a Cross-Country Study of Alignment between the Global Action Plan and National Action Plans 3, 2020, pp. 1–11.
- [24] J. Zinsstag, Convergence of ecohealth and one health, *Ecohealth.* 9 (2012) 371–373, <https://doi.org/10.1007/s10393-013-0812-z>.
- [25] Implementation Plan, 2023.
- [26] H.H. Balkhy, World Health Organization : Update on AMR Developing a Fit for Purpose Response a Major Threat to Global Health Drug-Resistant Infections Are Affecting the Lives of Thousands Worldwide Current and Future Impact of AMR, 2021.
- [27] The OIE, Strategy on Antimicrobial Resistance and the Prudent Use of Antimicrobials, 2016.
- [28] One Health Strategy Against Antibiotic Resistance, 2017.
- [29] A. Prigitano, L. Romanò, F. Auxilia, S. Castaldi, A.M. Tortorano, Antibiotic resistance: Italian awareness survey 2016, *J. Infect. Public Health.* 11 (2018) 30–34, <https://doi.org/10.1016/J.JIPH.2017.02.010>.
- [30] D. Faour-Klingbeil, E.C.D. Todd, Prevention and control of foodborne diseases in middle-east north African countries: review of National Control Systems, *Int. J. Environ. Res. Public Health* 17 (2020), <https://doi.org/10.3390/IJERPH17010070>.
- [31] P. Sornchuer, R. Tiengtong, Prevalence, virulence genes, and antimicrobial resistance of *Bacillus cereus* isolated from foodstuffs in Pathum Thani Province, Thailand, *Pharm. Sci. Asia.* 48 (2021) 194–203, <https://doi.org/10.29090/psa.2021.02.19.119>.
- [32] C. Ananchaipattana, Y. Hosotani, S. Kawasaki, S. Pongsawat, B. Mdlatiful, S. Isobe, Y. Inatsu, Prevalence of foodborne pathogens in retail foods in Thailand, *Foodborne Pathog. Dis.* 9 (2012) 835–840, <https://doi.org/10.1089/fpd.2012.1169>.
- [33] T. Bintsis, Foodborne pathogens, *AIMS Microbiol.* 3 (2017) 529, <https://doi.org/10.3934/MICROBIOL.2017.3.529>.
- [34] B. Sripaurya, R. Ngasaman, S. Benjakul, K. Vongkamjan, Virulence genes and antibiotic resistance of *Salmonella* recovered from a wet market in Thailand, *J. Food Saf.* 39 (2019) 1–8, <https://doi.org/10.1111/jfs.12601>.
- [35] C. Ananchaipattana, Y. Hosotani, S. Kawasaki, M.L. Bari, K.A. Yamaguchi, Y. Inatsu, Serotyping, RAPD grouping and antibiotic susceptibility testing of *Salmonella enterica* isolated from retail foods in Thailand, *Food Sci. Technol. Res.* 20 (2014) 905–913, <https://doi.org/10.3136/FSTR.20.905>.
- [36] Y. Mehdi, M.P. Létourneau-Montminy, M. Lou Gaucher, Y. Chorfi, G. Suresh, T. Rouissi, S.K. Brar, C. Côté, A.A. Ramirez, S. Goubout, Use of antibiotics in broiler production: global impacts and alternatives, *Anim. Nutr.* 4 (2018) 170, <https://doi.org/10.1016/J.ANINU.2018.03.002>.
- [37] B.A. Gameda, A. Assefa, M.B. Jaleta, K. Amenu, B. Wieland, Antimicrobial resistance in Ethiopia: a systematic review and meta-analysis of prevalence in foods, food handlers, animals, and the environment, *One Heal.* 13 (2021), <https://doi.org/10.1016/J.ONEHLT.2021.100286>.
- [38] Report, M.: Mission Report ECDC Country Visit to Italy to Discuss Antimicrobial Resistance Issues, 2017.
- [39] A. Cangani, F. Fortinguerra, A. Di Filippo, A. Pierantozzi, R. Da Cas, F. Villa, F. Trotta, M.L. Moro, C. Gagliotti, Monitoring the community use of antibiotics in Italy within the National Action Plan on antimicrobial resistance, *Br. J. Clin. Pharmacol.* 87 (2021) 1033–1042, <https://doi.org/10.1111/bcp.14461>.
- [40] H.D. Agenda, Health Development Agenda, 2020.
- [41] A. Qijia, M. Verma, L. Yang, H. Legido-quigley, The lancet regional health - Western Pacific an analysis of national action plans on antimicrobial resistance in Southeast Asia using a governance framework approach, *Lancet Reg. Heal. - West. Pacific.* 7 (2021), 100084, <https://doi.org/10.1016/j.lanwpc.2020.100084>.
- [42] L. Cavocchio, G. Dotto, M. Giacomelli, D. Giovanardi, G. Grilli, M.P. Franciosini, A. Trocino, A. Piccirillo, Class 1 and class 2 integrons in avian pathogenic *Escherichia coli* from poultry in Italy, *Poult. Sci.* 94 (2015) 1202–1208, <https://doi.org/10.3382/ps/pev095>.
- [43] C. Scarano, C. Spanu, G. Ziino, F. Pedonese, A. Dalmasso, V. Spanu, S. Virdis, E.P. L. De Santis, Antibiotic resistance of *Vibrio* species isolated from Sparus aurata reared in Italian mariculture, *New Microbiol.* 37 (2014) 329–337.
- [44] E. Di Giannatale, G. Di Serafino, K. Zilli, A. Alessiani, L. Sacchini, G. Garofolo, G. Aprea, F. Marotta, Characterization of antimicrobial resistance patterns and detection of virulence genes in *Campylobacter* isolates in Italy, *Sensors (Switzerland).* 14 (2014) 3308–3322, <https://doi.org/10.3390/s140203308>.
- [45] S.M. Puah, K.H. Chua, J.A. Mary Anne Tan, Virulence factors and antibiotic susceptibility of *Staphylococcus aureus* isolates in ready-to-eat foods: detection of *S. aureus* contamination and a high prevalence of virulence genes, *Int. J. Environ. Res. Public Health* 13 (2016), <https://doi.org/10.3390/ijerph13020199>.
- [46] C. Bacci, A. Vismarra, S. Dander, E. Barilli, P. Superchi, Occurrence and antimicrobial profile of bacterial pathogens in former foodstuff meat products used for pet diets, *J. Food Prot.* 82 (2019) 316–324, <https://doi.org/10.4315/0362-028X.JFP-18-352>.
- [47] F. Bertelloni, C. Salvadori, A. Moni, D. Cerri, P. Mani, V.V. Ebani, Antimicrobial resistance in *Enterococcus* spp. isolated from laying hens of backyard poultry flocks, *Ann. Agric. Environ. Med.* 22 (2015) 665–669, <https://doi.org/10.5604/12321966.1185771>.
- [48] F. Marotta, L. Di Marcantonio, A. Janowicz, F. Pedonese, G. Di Donato, A. Aredean, R. Nuvoloni, E. Di Giannatale, G. Garofolo, Genotyping and antibiotic resistance traits in *Campylobacter jejuni* and *coli* from pigs and wild boars in Italy, *Front. Cell. Infect. Microbiol.* 10 (2020) 1–11, <https://doi.org/10.3389/fcimb.2020.592512>.
- [49] T. Zottola, S. Montagnaro, C. Magnapera, S. Sasso, L. De Martino, A. Bragagnolo, L. D'Amici, R. Condoleo, G. Pisanelli, G. Iovane, U. Pagnini, Prevalence and antimicrobial susceptibility of *Salmonella* in European wild boar (*Sus scrofa*); Latium region - Italy, *Comp. Immunol. Microbiol. Infect. Dis.* 36 (2013) 161–168, <https://doi.org/10.1016/j.cimid.2012.11.004>.
- [50] M. Foti, A. Siclari, A. Mascetti, V. Fischella, Study of the spread of antimicrobial-resistant Enterobacteriaceae from wild mammals in the National Park of Aspromonte (Calabria, Italy), *Environ. Toxicol. Pharmacol.* 63 (2018) 69–73, <https://doi.org/10.1016/j.etap.2018.08.016>.
- [51] C. Scarano, F. Piras, S. Virdis, G. Ziino, R. Nuvoloni, A. Dalmasso, E.P.L. De Santis, C. Spanu, Antibiotic resistance of *Aeromonas* spp. strains isolated from Sparus aurata reared in Italian mariculture farms, *Int. J. Food Microbiol.* 284 (2018) 91–97, <https://doi.org/10.1016/j.ijfoodmicro.2018.07.033>.
- [52] M.A. Moreno, S. García-Soto, M. Hernández, C. Bárcena, D. Rodríguez-Lázaro, M. Ugarte-Ruiz, L. Domínguez, Day-old chicks are a source of antimicrobial resistant bacteria for laying hen farms, *Vet. Microbiol.* 230 (2019) 221–227, <https://doi.org/10.1016/j.vetmic.2019.02.007>.
- [53] M. Giufre, C. Graziani, M. Accogli, I. Luzzi, L. Busani, M. Cerquetti, *Escherichia coli* of human and avian origin: detection of clonal groups associated with fluoroquinolone and multidrug resistance in Italy, *J. Antimicrob. Chemother.* 67 (2012) 860–867, <https://doi.org/10.1093/jac/dkr565>.
- [54] Resistance, A., Factors, V.: Crossm 84, 2018, pp. 1–10.
- [55] E. Di Donato, F. Marotta, R. Nuvoloni, K. Zilli, D. Neri, D. Di Sabatino, P. Calistri, E. Di Giannatale, Prevalence, population diversity and antimicrobial resistance of *Campylobacter coli* isolated in Italian swine at slaughterhouse, *Microorganisms.* 8 (2020) 1–12, <https://doi.org/10.3390/microorganisms8020222>.

- [56] R. Ranjbar, F. Safarpour Dehkordi, M.H. Sakhaei Shahreza, E. Rahimi, Prevalence, identification of virulence factors, O-serogroups and antibiotic resistance properties of Shiga-toxin producing *Escherichia coli* strains isolated from raw milk and traditional dairy products, *Antimicrob. Resist. Infect. Control* 7 (2018) 1–11, <https://doi.org/10.1186/s13756-018-0345-x>.
- [57] C. Centi, D. Britti, A.M.L. Santoro, R. Musarella, L. Ciambone, F. Casalinuovo, N. Costanzo, Phenotypic antimicrobial resistance profile of isolates causing clinical mastitis in dairy animals, *Ital. J. Food Saf.* 6 (2017) 84–87, <https://doi.org/10.4081/ijfs.2017.6612>.
- [58] A. Ghodousi, C. Bonura, A.M. Di Noto, C. Mammina, Extended-spectrum  $\beta$ -lactamase, AmpC-producing, and fluoroquinolone-resistant *Escherichia coli* in retail broiler chicken meat, Italy, *Foodborne Pathog. Dis.* 12 (2015) 619–625, <https://doi.org/10.1089/fpd.2015.1936>.
- [59] G. Nobili, I. Franconieri, G. La Bella, M.G. Basanisi, G. La Salandra, Prevalence of Verocytotoxinogenic *Escherichia coli* strains isolated from raw beef in southern Italy, *Int. J. Food Microbiol.* 257 (2017) 201–205, <https://doi.org/10.1016/j.ijfoodmicro.2017.06.022>.
- [60] E. Di Giannatale, P. Calistri, G. Di Donato, L. Decastelli, E. Goffredo, D. Adriano, M.E. Mancini, A. Galleggiante, D. Neri, S. Antoci, C. Marfoglia, F. Marotta, R. Nuvoloni, G. Migliorati, Thermotolerant *Campylobacter* spp. in chicken and bovine meat in Italy: Prevalence, level of contamination and molecular characterization of isolates, *PLoS One* 14 (2019) 1–15, <https://doi.org/10.1371/journal.pone.0225957>.
- [61] G. Pesavento, C. Calónico, B. Ducci, A. Magnanini, Lo Nostro, A.: prevalence and antibiotic resistance of *Enterococcus* spp. isolated from retail cheese, ready-to-eat salads, ham, and raw meat, *Food Microbiol.* 41 (2014) 1–7, <https://doi.org/10.1016/j.fm.2014.01.008>.
- [62] S. Bonardi, I. Bruini, M. D'Incau, I. Van Damme, E. Carniel, S. Brémont, P. Cavallini, S. Tagliabue, F. Brindani, Detection, seroprevalence and antimicrobial resistance of *Yersinia enterocolitica* and *Yersinia pseudotuberculosis* in pig tonsils in Northern Italy, *Int. J. Food Microbiol.* 235 (2016) 125–132, <https://doi.org/10.1016/j.ijfoodmicro.2016.07.033>.
- [63] C.G.A. Nobile, R. Costantino, A. Bianco, C. Pileggi, M. Pavia, Prevalence and pattern of antibiotic resistance of *Campylobacter* spp. in poultry meat in Southern Italy, *Food Control* 32 (2013) 715–718, <https://doi.org/10.1016/j.foodcont.2013.02.011>.
- [64] M. Golob, M. Pate, D. Kušar, U. Dermota, J. Avberšek, B. Papić, I. Zdovc, M. Bondi, Antimicrobial resistance and virulence genes in *Enterococcus faecium* and *Enterococcus faecalis* from humans and retail red meat, *Biomed. Res. Int.* 2019 (2019) 14–16, <https://doi.org/10.1155/2019/2815279>.
- [65] J.Y. Kim, J.L. Lee, Correlation of total bacterial and *Vibrio* spp. populations between fish and water in the aquaculture system, *Front. Mar. Sci.* 4 (2017) 1–10, <https://doi.org/10.3389/fmars.2017.00147>.
- [66] K. Schärer, S. Savioz, N. Cernela, G. Saegesser, R. Stephan, Occurrence of *Vibrio* spp. in fish and shellfish collected from the Swiss market, *J. Food Prot.* 74 (2011) 1345–1347, <https://doi.org/10.4315/0362-028X.JFP-11-001>.
- [67] M. Tamba, R. Rocca, A. Prosperi, G. Pupillo, P. Bassi, G. Galletti, E. Martini, A. Santi, G. Casadei, N. Arrigoni, Evaluation of control program against *Streptococcus agalactiae* infection in dairy herds during 2019–2021 in Emilia-Romagna region Northern Italy, *Front. Vet. Sci.* 9 (2022) 827, <https://doi.org/10.3389/fvets.2022.904527/BIBTEX>.
- [68] E. Carra, S. Russo, A. Micheli, C. Garbarino, M. Ricchi, F. Bergamini, P. Bassi, A. Prosperi, S. Piva, M. Cricca, R. Schiavo, G. Merialdi, A. Serrano, N. Arrigoni, Evidence of common isolates of *Streptococcus agalactiae* in bovines and humans in Emilia Romagna region (Northern Italy), *Front. Microbiol.* 12 (2021) 1–10, <https://doi.org/10.3389/fmicb.2021.673126>.
- [69] F. Safarpour Dehkordi, A.A. Basti, H. Gandomi, A. Misaghi, E. Rahimi, Pathogenic *Staphylococcus aureus* in hospital food samples; prevalence and antimicrobial resistance properties, *J. Food Saf.* 38 (2018) 1–6, <https://doi.org/10.1111/jfs.12501>.
- [70] C. Ananchaipattana, Y. Hosotani, S. Kawasaki, S. Pongsawat, B. Mdlatiful, S. Isobe, Y. Inatsu, Prevalence of foodborne pathogens in retail foods in Thailand, *Foodborne Pathog. Dis.* 9 (2012) 835–840, <https://doi.org/10.1089/fpd.2012.1169>.
- [71] K. Assawatheptawee, U. Tansawai, A. Kiddee, P. Thongngon, P. Punyadi, T. Romgaew, P. Kongthai, T. Sumpadit, P.R. Niumsup, Occurrence of extended-spectrum and AmpC-type  $\beta$ -lactamase genes in *Escherichia coli* isolated from water environments in Northern Thailand, *Microbes Environ.* 32 (2017) 293–296, <https://doi.org/10.1264/jsm.2017.050>.
- [72] C. Chokboonmongkol, P. Patchanee, G. Gözl, K. Zessin, T. Alter, Prevalence, Quantitative Load, and Antimicrobial Resistance of *Campylobacter* spp. from Broiler Cecae and Broiler Skin Samples in Thailand, 2009, pp. 462–467.
- [73] U. Tansawai, D. Sanguansermri, A. Na-udom, T.R. Walsh, P.R. Niumsup, Occurrence of extended spectrum  $\beta$ -lactamase and AmpC genes among multidrug-resistant *Escherichia coli* and emergence of ST131 from poultry meat in Thailand, *Food Control* 84 (2018) 159–164, <https://doi.org/10.1016/j.foodcont.2017.07.028>.
- [74] N. Niyomdecha, N. Mungkornkaew, W. Samosornsuk, Serotypes and antimicrobial resistance of *Salmonella Enterica* isolated from pork, chicken meat and lettuce, Bangkok and Central Thailand, *Southeast Asian J. Trop. Med. Public Health.* 47 (2016) 31–39.
- [75] H. Khudor, Molecular detection of enterotoxin (Cyt K) gene and antimicrobial susceptibility of *Bacillus cereus* isolates from milk and milk products, *J. Basrah. Vet. Res.* 11 (2012) 164–173, <https://doi.org/10.33762/bvetr.2012.54771>.
- [76] N. Sinwat, S. Angkittitrakul, R. Chuanchuen, Characterization of antimicrobial resistance in *Salmonella enterica* isolated from pork, chicken meat, and humans in northeastern Thailand, *Foodborne Pathog. Dis.* 12 (2015) 759–765, <https://doi.org/10.1089/fpd.2015.1946>.
- [77] D. Kanungpean, S. Takai, T. Kakuda, Contamination and antimicrobial susceptibility testing of *Staphylococcus aureus* isolated from pork in fresh markets, Nongchok District, Thailand, *Vet. Med. Int.* 2021 (2021) 10–12, <https://doi.org/10.1155/2021/6646846>.
- [78] P. Patchanee, K. Tansirichareonkul, T. Buawiratler, A. Wiratsudakul, K. Angchokchatchawal, P. Yamsakul, T. Yano, P. Boonhot, S. Rojanasatien, P. Tadee, *Salmonella* in pork retail outlets and dissemination of its pulsotypes through pig production chain in Chiang Mai and surrounding areas, Thailand, *Prev. Vet. Med.* 130 (2016) 99–105, <https://doi.org/10.1016/j.pvetmed.2016.06.013>.
- [79] T. Prasertsee, N. Chokesajjawatee, P. Santiyant, P. Chuammitri, M. Deudom, P. Tadee, P. Patchanee, Quantification and rep-PCR characterization of *Salmonella* spp. in retail meats and hospital patients in Northern Thailand, *Zoonoses Public Health* 66 (2019) 301–309, <https://doi.org/10.1111/zph.12565>.
- [80] F.S. Dehkordi, H. Gandomi, A.A. Basti, A. Misaghi, E. Rahimi, Phenotypic and Genotypic Characterization of Antibiotic Resistance of Methicillin-Resistant *Staphylococcus aureus* Isolated from Hospital Food 1–11, 2017, <https://doi.org/10.1186/s13756-017-0257-1>.
- [81] N.R. Na Phuket, S. Siripornadulsil, W. Siripornadulsil, Prevalence of antibiotic-resistant *Salmonella* in vegetables and fermented foods and their control by lactic acid bacteria, *J. Pure Appl. Microbiol.* 13 (2019) 1929–1939, <https://doi.org/10.22207/JPAM.13.4.05>.
- [82] W.P. Thu, N. Sinwat, A.A. Bitrus, S. Angkittitrakul, R. Prathan, R. Chuanchuen, Research unit in microbial food safety and antimicrobial resistance, *SC. Integr. Med. Res.* (2019), <https://doi.org/10.1016/j.jgar.2019.05.032>.
- [83] K. Chotinantakul, N. Chansiw, S. Okada, Antimicrobial resistance of *Enterococcus* spp. isolated from Thai fermented pork in Chiang Rai Province, Thailand, *J. Glob. Antimicrob. Resist.* 12 (2018) 143–148, <https://doi.org/10.1016/j.jgar.2017.09.021>.
- [84] C. Romyasamit, P. Sornsene, S. Chimplee, S. Yuwalaksanakun, D. Wongprot, P. Saengsuwan, Prevalence and characterization of extended-spectrum  $\beta$ -lactamase-producing *Escherichia coli* and *klebsiella pneumoniae* isolated from raw vegetables retailed in southern Thailand, *PeerJ.* 9 (2021), <https://doi.org/10.7717/peerj.11787>.
- [85] U. Tansawai, T.R. Walsh, P.R. Niumsup, Extended spectrum  $\beta$ -lactamase-producing *Escherichia coli* among backyard poultry farms, farmers, and environments in Thailand, *Poult. Sci.* 98 (2019) 2622–2631, <https://doi.org/10.3382/ps/pez009>.
- [86] B. Noppou, S.W. Sampao, P. Sornplang, A. Sopa, P. Sukon, K. Kanistanon, Multi-drug resistance characteristics of *e. coli* isolated from water sources in chicken farms, Khon Kaen, Thailand, *Southeast Asian J. Trop. Med. Public Health.* 49 (2018) 1034–1042.
- [87] T. Kong-Ngoen, S. Santajit, W. Tunyong, P. Pumirat, N. Sookrung, W. Chaicumpa, N. Indrawattana, Antimicrobial Resistance and virulence of non-Typhoidal *Salmonella* from retail foods marketed in Bangkok, Thailand, *Foods.* 11 (2022), <https://doi.org/10.3390/foods11050661>.
- [88] A. Siriphap, C. Suwancharoen, W. Laenoi, P. Kraivuttinun, O. Suthienkul, W. Prapasawat, First study on virulence genes, antimicrobial resistance, and integrons in *Escherichia coli* isolated from cage, free-range, and organic commercial eggs in Phayao Province, Thailand, *Vet. World.* 15 (2022) 2293–2301, <https://doi.org/10.14202/vetworld.2022.2293-2301>.
- [89] N. Tangitwattanachai, D. Sakhong, Antimicrobial resistance *Salmonella* isolated from beef in upper northeastern Thailand, *Int. J. Geomate* 17 (2019) 236–241, <https://doi.org/10.21660/2019.61.4849>.
- [90] N. Sinwat, S. Angkittitrakul, K.F. Coulson, F.M.I.R. Pilapil, D. Meunsene, R. Chuanchuen, High prevalence and molecular characteristics of multidrug-resistant *Salmonella* in pigs, pork and humans in Thailand and Laos provinces, *J. Med. Microbiol.* 65 (2016) 1182–1193, <https://doi.org/10.1099/jmm.0.000339>.
- [91] T. Thomrongsuwannakij, P.J. Blackall, N. Chansirpornchai, A study on *Campylobacter jejuni* and *Campylobacter coli* through commercial broiler production chains in Thailand, *Avian Dis.* 61 (2017) 186–197.
- [92] K.K. Lay, S. Jeamsripong, K.P. Sunn, S. Angkittitrakul, R. Prathan, S. Srisanga, R. Chuanchuen, Colistin resistance and esbl production in *salmonella* and *escherichia coli* from pigs and pork in the thailand, cambodia, lao pdr, and myanmar border area, *Antibiotics.* 10 (2021), <https://doi.org/10.3390/antibiotics10060657>.
- [93] C. Seenama, V. Thamlikitkul, P. Rathawongjirakul, Multilocus sequence typing and blaESBL characterization of extended-spectrum beta-lactamase-producing *escherichia coli* isolated from healthy humans and swine in northern Thailand, *Infect. Drug Resist.* 12 (2019) 2201–2214, <https://doi.org/10.2147/IDR.S209545>.
- [94] C. Pungpian, S. Lee, S. Trongjit, N. Sinwat, S. Angkittitrakul, R. Prathan, S. Srisanga, R. Chuanchuen, Colistin resistance and plasmid-mediated mcr genes in *Escherichia coli* and *Salmonella* isolated from pigs, pig carcass and pork in Thailand, Lao PDR and Cambodia border provinces, *J. Vet. Sci.* 22 (2021) 1–15, <https://doi.org/10.4142/JVS.2021.22.E68>.
- [95] S. Trongjit, S. Angkittitrakul, R.E. Tuttle, J. Pongsere, P. Padungtod, R. Chuanchuen, Prevalence and antimicrobial resistance in *Salmonella enterica* isolated from broiler chickens, pigs and meat products in Thailand–Cambodia border provinces, *Microbiol. Immunol.* 61 (2017) 23–33, <https://doi.org/10.1111/1348-0421.12462>.
- [96] D. Phongaran, S. Khang-Air, S. Angkittitrakul, Molecular epidemiology and antimicrobial resistance of *Salmonella* isolates from broilers and pigs in Thailand,

- Vet. World. 12 (2019) 1311–1318, <https://doi.org/10.14202/vetworld.2019.1311-1318>.
- [97] P. Fungwithaya, K. Boonchuay, R. Narinthorn, N. Sontigun, C. Sansamur, Y. Petcharat, T. Thomrongsuwannakij, T. Wongtawan, First study on diversity and antimicrobial-resistant profile of staphylococci in sports animals of southern Thailand, *Vet. World*. 15 (2022) 765–774, <https://doi.org/10.14202/vetworld.2022.765-774>.
- [98] J.P. Greenhalgh, D. Amund, Examining the presence of *Cronobacter* spp. in ready-to-eat edible insects, *Food Saf* 7 (2019) 74–78, <https://doi.org/10.14252/foodsafetyfscj.d-19-00004>.
- [99] N. Miranda, P. Banerjee, S. Simpson, K. Kerdahi, I.M. Sulaiman, Molecular surveillance of *cronobacter* spp. isolated from a wide variety of foods from 44 different countries by sequence typing of 16S rRNA, rpoB and O-antigen genes, *Foods* 6 (2017) 36, <https://doi.org/10.3390/FOODS6050036>.
- [100] K. Vongkamjan, S. Benjakul, Vu Kim, H.T., Vuddhakul, V., Longitudinal monitoring of *Listeria monocytogenes* and *Listeria* phages in seafood processing environments in Thailand, *Food Microbiol.* 66 (2017) 11–19, <https://doi.org/10.1016/j.fm.2017.03.014>.
- [101] K. Vongkamjan, J. Fuangpaiboon, M.P. Turner, V. Vuddhakul, Various ready-to-eat products from retail stores linked to occurrence of diverse *Listeria* monocytogenes and *Listeria* spp. Isolates. *J. Food Prot.* 79 (2016) 239–245, <https://doi.org/10.4315/0362-028X.JFP-15-361>.
- [102] E. Di Giannatale, G. Garofolo, A. Alessiani, G. Di Donato, L. Candeloro, W. Vencia, L. Decastelli, F. Marotta, Tracing back clinical *Campylobacter jejuni* in the northwest of Italy and assessing their potential source, *Front. Microbiol.* 7 (2016) 1–9, <https://doi.org/10.3389/fmicb.2016.00887>.
- [103] S. Prachantasena, P. Charununtakorn, S. Muangnoicharoen, L. Hankla, N. Techawal, P. Chaveerach, P. Tuitemwong, N. Chokesajjawatee, N. Williams, T. Humphrey, T. Luangtongkum, Climatic factors and prevalence of *Campylobacter* in commercial broiler flocks in Thailand, *Poult. Sci.* 96 (2017) 980–985, <https://doi.org/10.3382/ps/pew364>.
- [104] K. Koutsoumanis, A. Allende, A. Álvarez-Ordóñez, D. Bolton, S. Bover-Cid, M. Chemaly, R. Davies, A. De Cesare, L. Herman, F. Hilbert, R. Lindqvist, M. Nauta, G. Ru, M. Simmons, P. Skandamis, E. Suffredini, H. Argüello, T. Berendonk, L.M. Cavaco, W. Gaze, H. Schmitt, E. Topp, B. Guerra, E. Liébana, P. Stella, L. Peixe, Role played by the environment in the emergence and spread of antimicrobial resistance (AMR) through the food chain, *EFSA J.* 19 (2021), <https://doi.org/10.2903/J.EFSA.2021.6651>.
- [105] C. Verraes, S. Van Boxtael, E. Van Meervenne, E. Van Coillie, P. Butaye, B. Catry, M.-A. De Schaetzen, X. Van Huffel, H. Imberechts, K. Dierick, G. Daube, C. Saegerman, J. De Block, J. Dewulf, L. Herman, Antimicrobial Resistance in the food chain: a review, *Int. J. Environ. Res. Public Health* 10 (2013) 10, <https://doi.org/10.3390/ijerph10072643>.
- [106] C.J.H. Von Wintersdorff, J. Penders, J.M. Van Niekerk, Dissemination of Antimicrobial Resistance in Microbial Ecosystems through Horizontal Gene Transfer 7, 2016, pp. 1–10, <https://doi.org/10.3389/fmicb.2016.00173>.