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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 β-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, enviornment, animals and their products in develpoing 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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misuse, or incomplete dosing increases the chance of developing antibiotic resistance since it increases the mutation rate. Moreover, multidrug 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] regardlless the application of several measures to

Literature search

190 articles were identified in the databases

21 duplicate articles rejected

169 distinct articles identified for screening

Screening

61 articles excluded
- Identification, isolation and characterisation of pathogens (12)
- Proper screening techniques were not mentioned (18)
- Shelf life studies were performed (19)
- Reviews of MDR (12)

Inclusion

108 potentially relevant articles

52 articles excluded
- Molecular techniques like disk diffusion, MIC were not addressed (9)
- AMR was not analysed (19)
- Essential statistics missing (13)
- Outcomes not measured/reported (11)
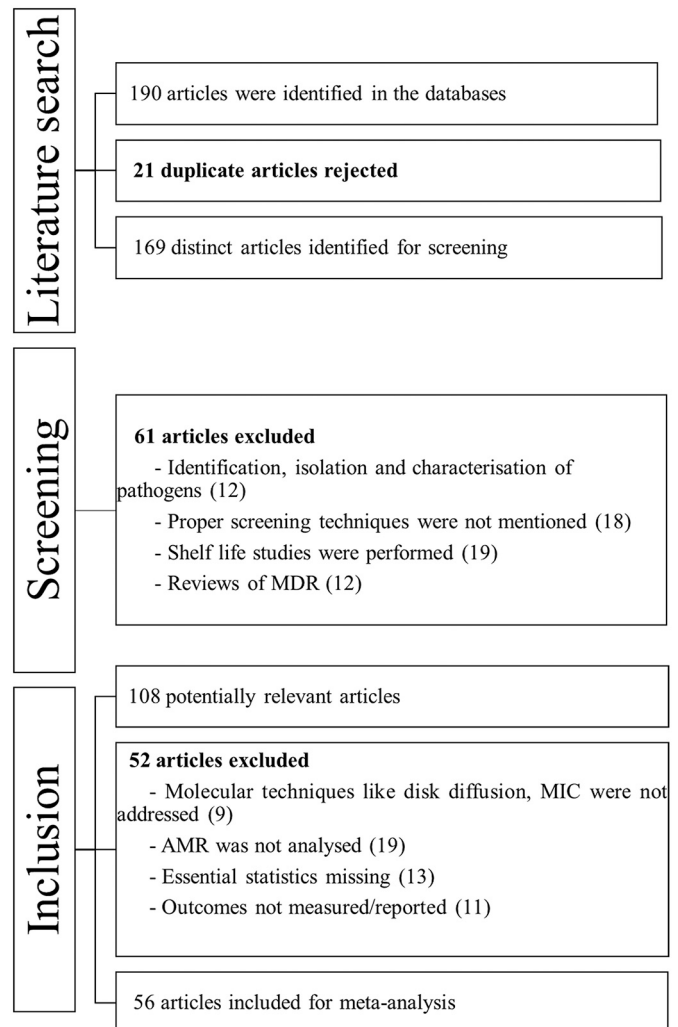
56 articles included for meta-analysis

Fig. 2. An approach for identifying, screening, and incorporating data from various food sources and their AMR in meta-analyses.
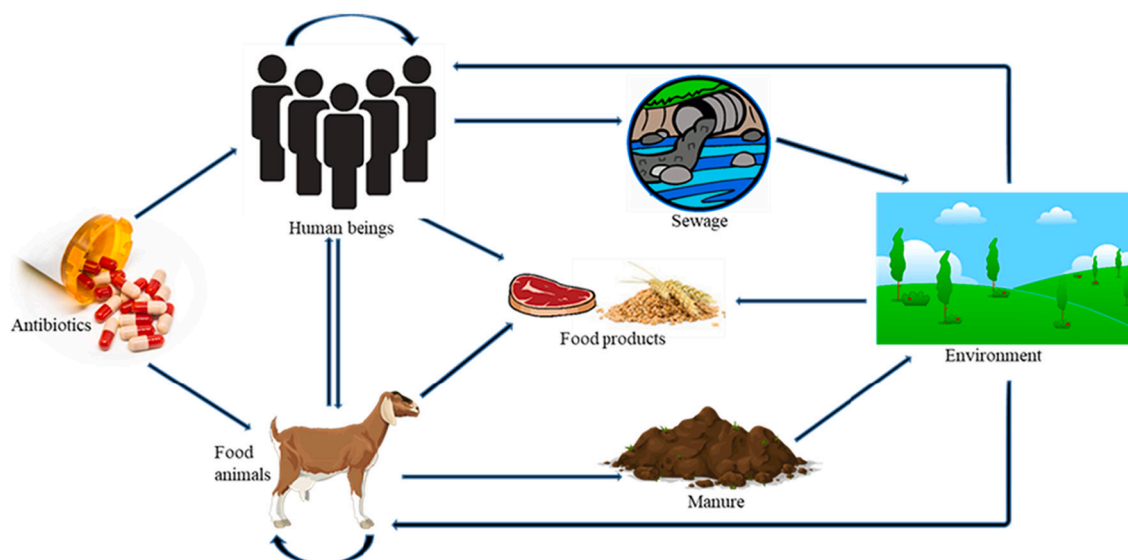
Fig. 1. Relationship between animal-human-environment in spreading of AMR by different sources.

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 (%)
Escherichia coli	531 (12.76)	85 (33.60)	21 (7.5)	–	181 (10.61)	–	–	101 (26.72)	919 (9.67)
Enterococcus spp.	440 (10.57)	–	–	–	296 (17.35)	–	–	–	736 (7.74)
Vibrio spp.	–	–	–	–	–	624 (48.86)	–	–	624 (6.56)
Staphylococcus spp.	–	–	–	–	92 (5.39)	50 (3.92)	–	–	142 (1.49)
Streptococcus spp.	–	–	–	–	29 (1.70)	–	–	–	29 (0.30)
Yersinia enterocolitica	–	–	–	55 (4.63)	–	–	–	–	55 (0.58)
Campylobacter spp.	262 (6.30)	40 (15.81)	–	–	25 (1.47)	311 (24.35)	–	–	638 (6.71)
Salmonella spp.	52 (1.25)	–	–	–	28 (1.64)	84 (6.58)	–	–	164 (1.73)
Enterobacter 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 = 11,753
	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 (%)
Escherichia coli	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)
Salmonella	532 (14.82)	111 (14.64)	–	–	–	250 (22.75)	24 (2.12)	–	–	–	–	–	917 (7.80)
Staphylococcus spp.	208 (5.80)	–	–	–	0 (0)	–	41 (3.62)	–	–	36 (15.92)	–	41 (33.61)	326 (2.77)
Bacillus spp.	–	–	–	–	–	81 (7.37)	31 (2.74)	53 (23.35)	–	–	–	–	165 (1.40)
Yersinia enterocolitica	–	–	–	–	–	3 (0.27)	–	–	–	–	–	–	3 (0.03)
Cronobacter	–	–	–	–	–	6 (0.55)	–	–	–	–	–	–	6 (0.05)
Enterococcus spp.	–	96 (12.66)	–	135 (3.63)	–	57 (5.19)	–	–	–	–	–	–	288 (2.45)
Listeria spp.	–	–	–	–	–	7 (0.64)	–	–	–	–	–	–	7 (0.06)
Campylobacter spp.	61 (1.70)	–	–	–	–	–	–	–	–	–	–	–	61 (0.52)
Klebsiella 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 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.
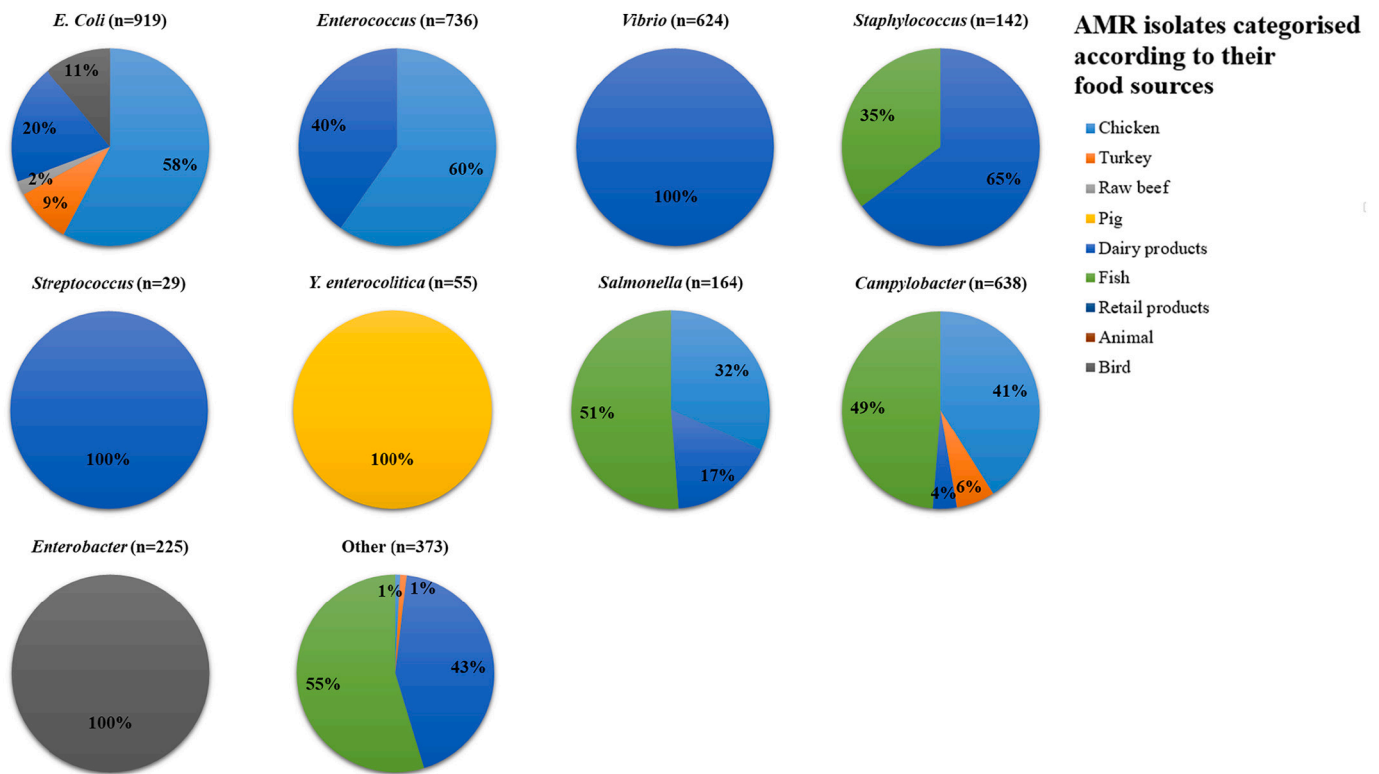
Table 3
Vigilance of antimicrobial resistance and monitoring system of Italy and Thailand.

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

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
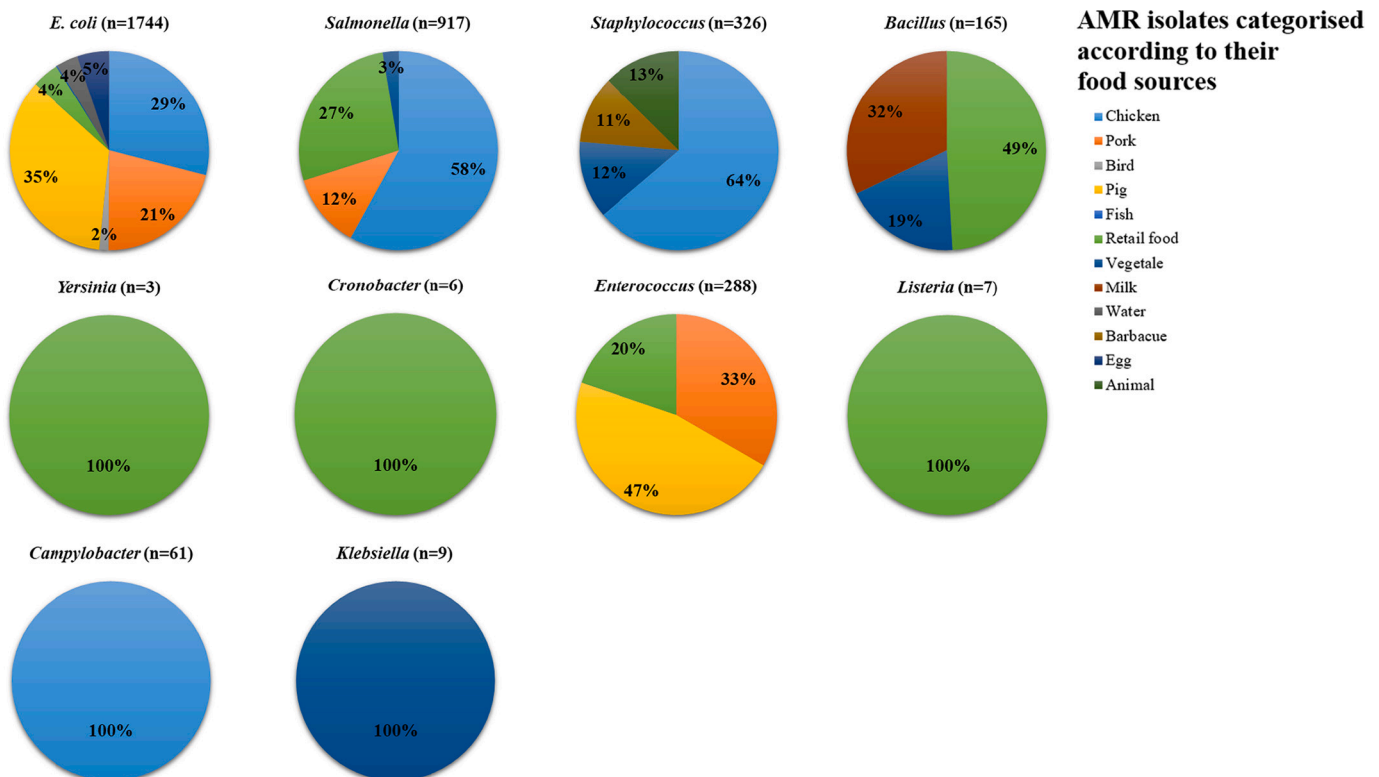

Fig. 4. AMR positive isolated microbes categorized in different food sources (n = 11,753) in Thailand, (n represent the number of isolates) from 2012 to 2021.

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 prevelent 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 β-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 β-lactams, cephalosporin, aminoglycosides, fluroquinolone, 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 β-lactam and tetracycline
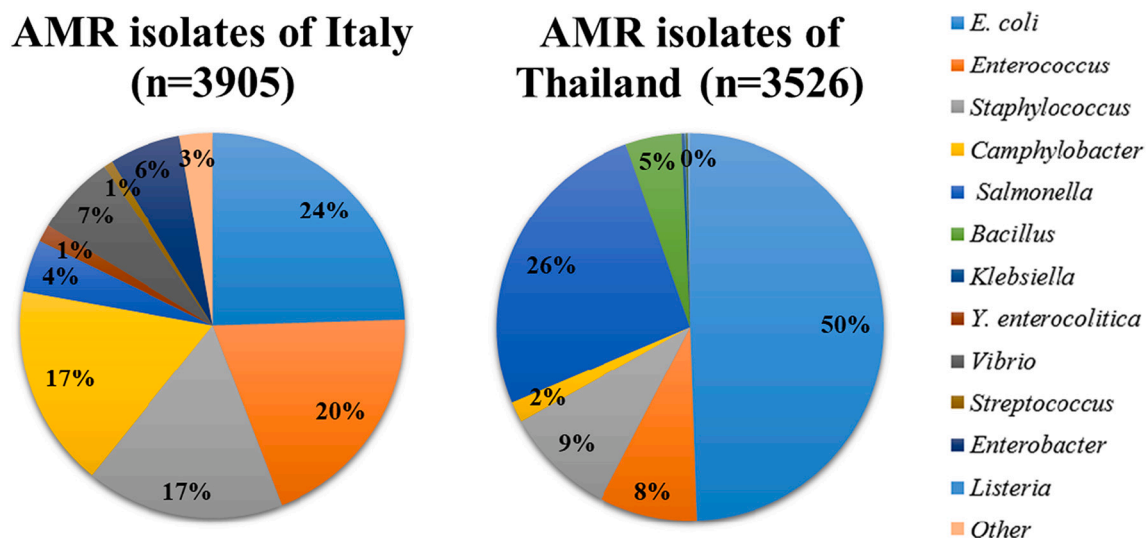

Fig. 5. Comparison between AMR isolates from different food sources in Italy (*n* = 3905) and Thailand (*n* = 3526) from 2012 to 2021.
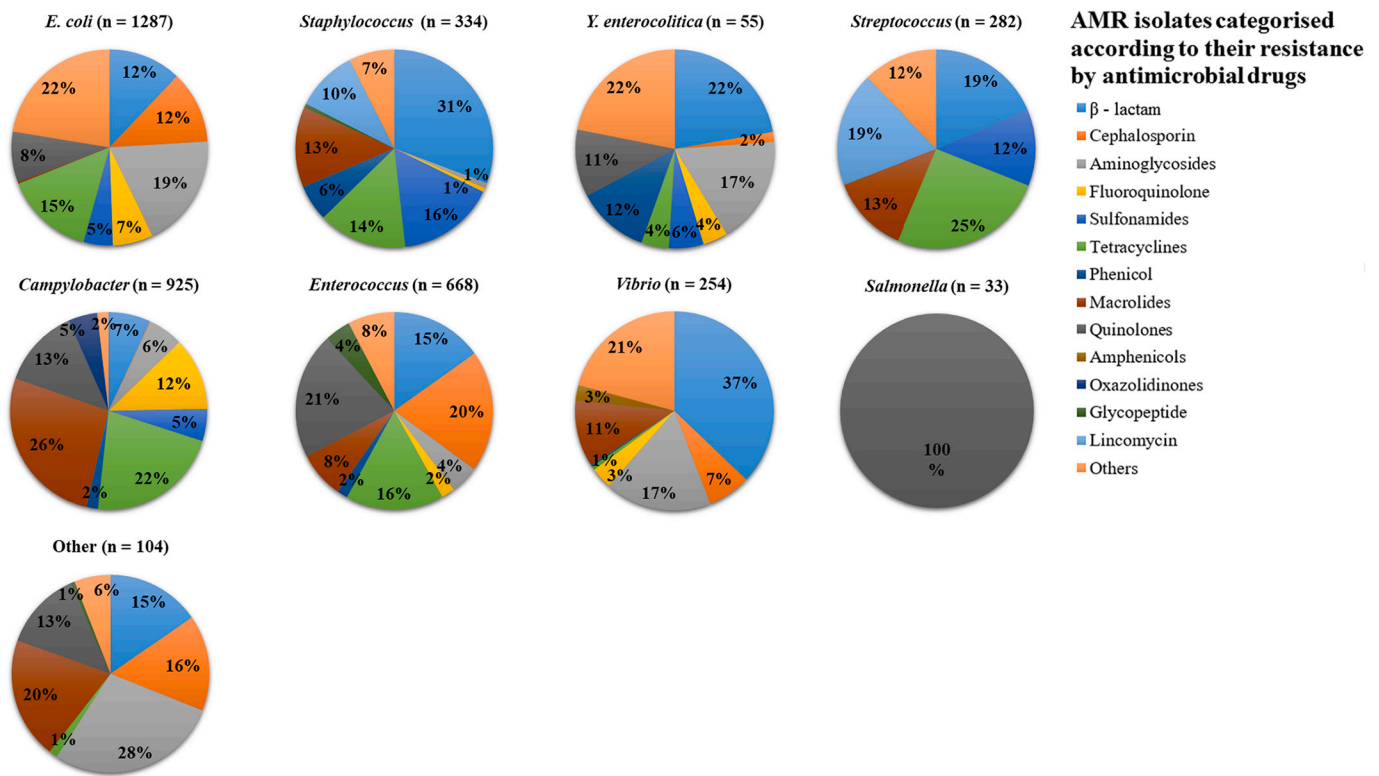
Fig. 6. Antimicrobials resistance prevalence for isolates (denoted by n) from foods of animal and non-animal origin (*N* = 3905) in Italy. Antimicrobial agents are represented by different colors in the pie charts.
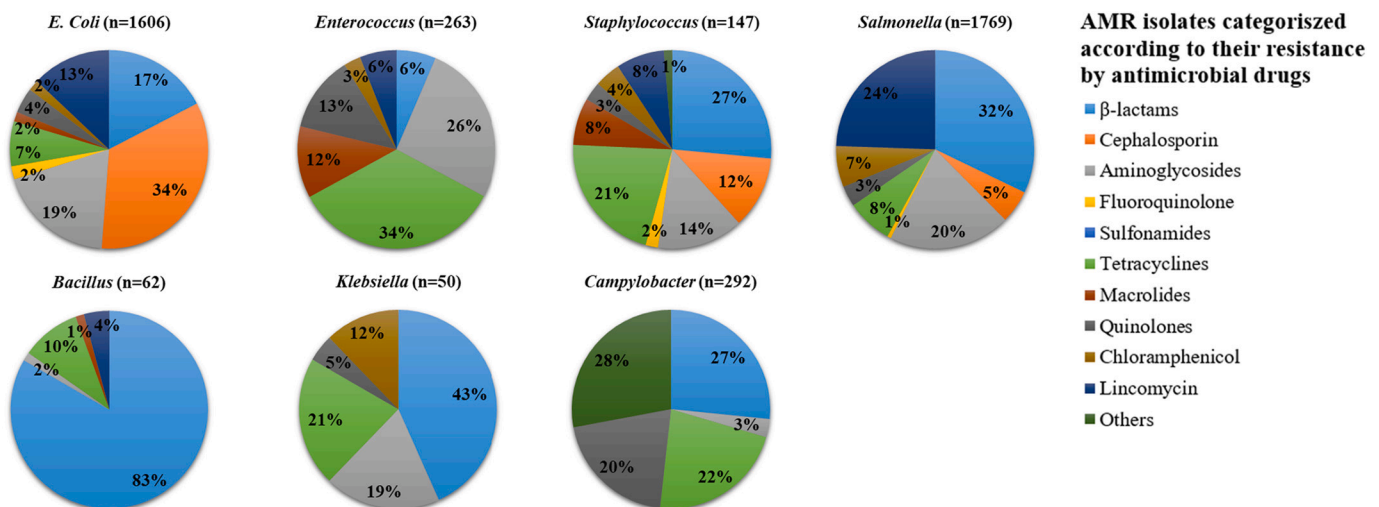

Fig. 7. Antimicrobials resistance prevalence for isolates (denoted by n) from foods of animal and non-animal origin (*N* = 3526) in Thailand. Antimicrobial agents are represented by different colors in the pie charts.

resistant. The resistance to aminoglycosides and quinolones had middle prevalence whereas cephalosporin, fluroquinolone, 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 β-lactam shows middle prevalence and quinolones, chloramphenicol, fluroquinolone, 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
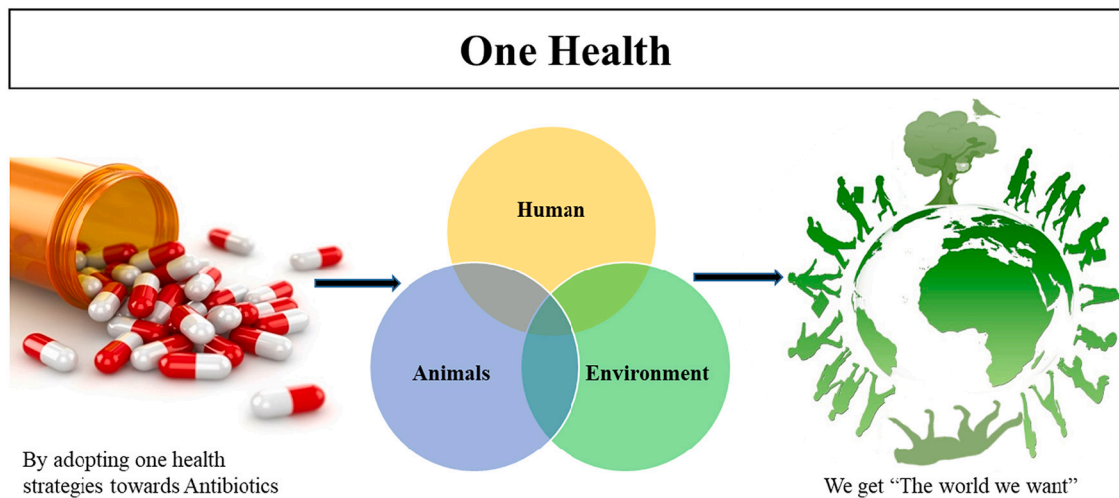
Fig. 8. One Health approach.

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.

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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.

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