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Article

Systematic Surveillance and Meta-Analysis of Antimicrobial Resistance

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Abstract: Human exposure to antimicrobial resistance (AMR) through food is now very imperfectly understood, creating a significant gap in the design of interventions. The interchange of AMR genes and the transfer of AMR bacteria from animals to humans through the food chain necessitate comprehensive methods to risk reduction. With a focus on AMR in bacterial species isolated from food products, foods (of both animal and non-animal origin), and ambient samples, the current meta-analysis gathered up-to-date information on the epidemiology of AMR in animal-source food chain. As a result, the combined prevalence of AMR across the various food sources was calculated. From the 18,784 food samples obtained as a result of selected publications, 7,676 (40.9%) samples were contaminated, including 4343 (56.6%) and 3363 (43.4%) samples from Taiwan and India, respectively. Meat (chicken, pork, and beef), fish and milk all have moderate to medium potential for AMR exposure to both Gram-positive and Gram-negative foodborne pathogens such *S. aureus*, *Clostridium*, *E. coli*, *Salmonella*, etc. Antibiotic resistance to β-lactam, fluoroquinolone, carbapenem etc, is present in the majority of food samples. The results of this study emphasize the persistent danger of antimicrobial residue in animal-derived foods in Taiwan, India, and other nations with comparable customs.

Keywords: antimicrobial resistance (AMR); antibiotics; surveillance; India; Taiwan

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1. Introduction

Highlights:

- A meta-analysis was conducted in order to assess the spread of AMR in different food sources.
- Both India and Taiwan shows high contamination in meat (chicken, pork and beef) against *E. coli*.
- The combined prevalence of AMR for bacterium-antibiotic combinations in different food samples was reported against β-lactam and fluoroquinolones.
- In the majority of the food samples from both nations, multidrug resistance was found.

Antimicrobial drugs are used on both humans and animals and are crucial for maintaining public health all over the world, but now it has become a serious global health issue, impacting every country to some extent. It is an unavoidable result of the improper use of antibiotics in people and animals. AMR has been identified as a global hazard to public health due to its links to higher rates

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of morbidity, mortality, and financial costs.(Dadgostar 2019; Shrestha et al. 2018) By 2050, it is predicted that AMR will cause 10 million deaths annually, reduce the global GDP by 3% to 4%, and cost $100 trillion US dollars.(Antimicrobial Resistance (AMR) n.d.; New report calls for urgent action to avert antimicrobial resistance crisis n.d.) Therefore, AMR is among the top priorities in achieving the 2030 UN Sustainable Development Goals (SDGs)(Grace 2015; Tang et al. 2017) Additionally, WHO has developed several of approaches to counter the rise of antibiotic resistance, including enhancing sanitation and hygiene to lower overall infection rates and optimizing the use of antibiotics (and avoiding their abuse) in both humans and animals.(Global antimicrobial resistance surveillance system (GLASS) report: early implementation 2020 n.d.)

Though the factors influencing the occurrence of AMR are difficult and complicated, it is undeniable that AMR is linked to the irrational or incorrect use of antimicrobial agents (specifically antibiotics) in humans, livestock, agriculture, and aquaculture combined with the self-mutating capacity of the organisms.(Aidara-Kane et al. 2018) Antibiotic resistance can develop in animals due to bacteria that have been treated with antibiotics. These bacteria that may carry resistance genes can subsequently be passed from animals to humans. This inter-species transfer of bacteria from animals to humans can occur due to direct contact, food, or common environmental sources such as contaminated water, etc. (Ghimpețeanu et al. 2022; Malijan et al. 2022) There are shreds of evidences of several connections between humans, animals, and the larger environment that permit not just the movement of bacteria but also that of mobile genetic elements (MGEs) of microorganisms, furthering the spread of AMR.(Woolhouse et al. 2015) (Figure 1).

Livestock raised for food is given antibiotics for a various reasons, including non-therapeutic uses, disease management within a herd or flock, and the treatment of infectious diseases.(H. C. Lee et al. 2018; S. Sivaraman and Parady 2018) This leads to a wide range of potential antibiotic limitation strategies. The least restrictive strategies would limit the use of antibiotics to only certain non-therapeutic purposes, such as using antibiotics for the fast growth of broilers, layers, cattle, etc. For example, in *E. coli* and *S. aureus* recovered from the community and unknown origin blood and urine specimens, the rates of resistance to methicillin β-lactam antibiotic and cephalosporin (3rd generation antibiotic) were reported by several countries, territories, and areas, respectively (Global Antimicrobial Resistance and Use Surveillance System (GLASS) Report 2020; A. S. Lee et al. 2018)

Antibiotics are frequently used as a preventative measure in food-producing animals (such as cattle, poultry, and pigs); it is estimated that such use will increase by about 67% globally by 2030.(Van Boeckel et al. 2015) As a result, humans consuming food products originating from agricultural farms, livestock and aquaculture may develop resistance against these specific anti-microbial's due to AMR residues being introduced in them.(Cheng et al. 2019; Hudson et al. 2017) India has one of the highest rates of multidrug-resistant diseases and has the highest burden of drug-resistant microorganisms. According to the Scoping Report on Antimicrobial Resistance in India, from 2000 to 2030, it is expected that poultry consumption will increase by 577%, whereas the use of antibiotics in animal feed will increase by 82%. Some of the most heavily used antibiotics to meet up this load are penicillin, tetracycline and quinolones.(S. Sivaraman and Parady 2018)

In India, chicken is highly consumed and one of the most common contaminated food sources. Poultry and livestock can be infected by water or food contaminated with human or animal feces, or through human carrier workers. One possible entry point for numerous microorganisms could be inappropriate sanitary procedures used during the handling and processing of meat and meat products. Raw meat and unfermented milk, are especially prone to bacterial contamination.(Lorenzo et al. 2018) In comparison to India chicken is a highly consumed food as well in Taiwan which is also thought to have a substantial negative impact on the formation of a number of health problems. To understand the current scenario of AMR we collect data not only from animal-based products but also other RTE food categories with high consumption in Taiwan, including fresh-cut fruits/vegetables, ice desserts, rice products and low-water activity foods. Various investigations in human patients, food animals, foods, and the environment revealed the risk of losing valuable treatments. However, because the studies are not thorough and difficult to compare, it can be difficult to provide a complete picture of the problem. A compilation of current information is required to

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adequately analyze the situation and direct our limited resources toward minimizing knowledge gaps.

To investigate the situation of antimicrobial residues in different food sources, we have performed a meta-analysis of two representative countries, India (A developing nation) and Taiwan (A developed nation). The present study aimed at retrieving and analyzing the existing information on AMR, focusing on bacteria species in the animal and non-animal-source food chain by including foods (animal origin and non-animal origin), aquaculture and agriculture.

2. Materials and methods

2.1. Data extraction and search strategy

Systematic searches were conducted through a number of electronic databases, including Google Scholar, Science Direct, and PubMed, to find relevant published works that were published between January 2013 and December 2022. The process of Data retrieval and inclusion procedures closely followed to Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) standards. The databases listed above were searched for all pertinent articles using pertinent medical subject heading (MeSH) terms and keywords. The MeSH phrases and keywords were: “AMR/antibiotic from food sources in India/Taiwan”, “AMR/antibiotic prevalence from food sources in India/Taiwan”, “E. coli from food sources in India/Taiwan”, “Salmonella and India/Taiwan”, “Staphylococcus and India/Taiwan”, “Listeria and India/Taiwan”, “AMR/antibiotic prevalence in animals/livestock and India/Taiwan”, “E. coli in animals and India/Taiwan”, “Salmonella in animals/livestock and India/Taiwan”, “Staphylococcus in animals/livestock and India/Taiwan”, AMR/anti-biotic in foods and India/Taiwan”, “AMR/antibiotic prevalence in foods and India/Taiwan”, “E. coli in foods and India/Taiwan”, “Salmonella in foods and India/Taiwan”, “Staphylococcus in foods and India/Taiwan”, “Listeria in foods and India/Taiwan”, “E. coli from water and India/Taiwan”, “Salmonella water and India/Taiwan”, etc. The search queries were applied using the Boolean operators "AND", "OR", “NOT” and “AND NOT”.

2.2. Inclusion and exclusion criteria

The literature search defined by the aforementioned strategy yielded 53 articles, and we used pre-defined inclusion and exclusion criteria to identify eligible articles. The inclusion criteria were as follows: 1) abstracts and full text only available in English 2) the source of samples for bacteria isolation investigations, which should include food handlers, live food animals, foods (animal origin or non-animal source foods), 3) longitudinal/cross-sectional studies that report the proportion of bacterial pathogens and AMR in food sources, 4) an acceptable representative sample size with a clear report on the proportion of resistant and vulnerable organisms, 5) reliable methods for detecting bacterial species (phenotypic identification using culture and biochemical tests, molecular detection methods) and 6) similarly reliable methods for assessing AMR using disc diffusion, minimum inhibitory concentration (MIC) inhibition, or molecular techniques in accordance with international manuals and AMR cut-off standards. Furthermore, research lumped AMR results into big categories such as "Gram-negative organisms," and lacked the essential comprehensive and explicit information such as types of samples from which the bacteria were isolated, as well as studies done outside of India/Taiwan or studies not following the above-mentioned inclusion criteria were eliminated.

2.3. Extraction of data

The necessary information from the publications was retrieved and validated for consistency and data quality. Data extraction templates were created in Excel (Microsoft® office excel 2013) and pre-tested before the entire extraction by extracting random papers and making any required revisions. The variables extracted were the year of publication (2013-2022), sample sources (foods, food producing animals, and non-animal source food), sample size (number of study units/samples), number of positive food samples (to calculate prevalence) and species of microorganism investigated, microbiological and AMR detection methods (disc diffusion, MIC and molecular techniques) for

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which antimicrobials were tested, name and number of susceptible and resistant pathogens. Papers were managed using Mendeley (version 1.19.8, Elsevier, London, UK)

2.4. Food categories

Food samples from twelve different categories were evaluated which includes: Fish, Pork, Chicken, Egg, Turkey, Beef, Sea food, Ready to eat food (RTE), Fruits and vegetables, Milk, Mutton and Others (Frog, Goat, Duck, Geese, Raw meat, Duck, Emu, Slaughter house environment swabs/sewage, Chopping boards and knives).

3. Result

3.1. Data acquisition

The preliminary search yielded 687 articles published between January 2013 and December 2022. After excluding articles that did not meet the inclusion criteria, 53 reports (34 from India and 19 from Taiwan) were identified as eligible for data extraction and qualitative analysis, as shown in Figure 2. Prevalence estimates from these studies were calculated from 18,784 samples that meet the meta-analysis inclusion criteria on AMR from different food sources (food-producing animals and non-animal source food, agriculture, and aquaculture). Out of 18,784 samples, 9,456 food samples were from India, and 9,328 samples were from Taiwan. The included articles had tested for resistance to 14 different bacteria involved in 12 different food contamination.

3.2. Meta-analysis

Out of the total 18,784 samples acquired for meta-analysis from different studies, 7,676 positive samples were found (4,313 were from India and 3,363 were from Taiwan) were obtained from various bacteria found in various food items. A total of 18 different antimicrobial agents/drugs and 16 different bacteria had resistance. The sample sources, species of bacteria, and their proportions are represented in Tables 1 and 2.

3.2.1. Prevalence of pathogenic bacteria in India

From 34 research articles,(Access et al. 2015; Adesiji, Deekshit, and Karunasagar 2014; Dutta et al. 2016; Hussain et al. 2017; Jeyasanta and Patterson 2016; Kar et al. 2015; Kaushik et al. 2018; Kerala 2017; Koovapra et al. 2016; Kumar et al. 2021; Kumari and Sarkar 2014; Mahanti et al. 2013; Mailk et al. 2013; Maloo et al. 2017; Mistry et al. 2016; Nirupama et al. 2018; Preethirani et al. 2015; Rasheed et al. 2014b; Rashid et al. 2013; Sadashiv and Kaliwal 2014; Saksena, Malik, and Gaind 2020; Samanta et al. 2014; Samples, Rathore, and Abulreesh 2018; Savariraj et al. 2018; Shah et al. 2019; Sharma et al. 2019; Singh 2016; G. K. Sivaraman et al. 2020; Sudha et al. 2014; Suresh et al. 2018; Verma et al. 2018; Visnuvinayagam et al. 2015; Zehra et al. 2019) 9,456 food samples were acquired, out of which 4,313 (45.6%) samples were contaminated with pathogenic bacteria's. The maximum contamination was found in Beef (881; 62.8%) and Milk (1036; 60.7%) followed by Chicken (944; (30.6%). The prevalence of contamination in other food products was in Fruit and vegetables, Fish, RTE, Pork, and Sea food which accounts for (404, 57.7%; 323, 81%; 151, 54.5%; 362, 34.7%; and 45, 33.8%). The minimum amount of pathogenic bacteria was found in others (83, 25.4%); egg (48, 25.4%); and mutton (36, 18%).

The maximum pathogenic bacteria found in India from different food sources were in *E. coli* (1760, 18.6%) and *Staphylococcus aureus* (969, 10.2%); followed by *Klebsiella* (370, 3.9%), *Bacillus* (365, 3.9%), *Campylobacter* (209; 2.2%), *Salmonella* (205, 2.2%), *Vibrio* spp. (159,1.7%) while the lesser number of pathogenic microbes were of *Acinetobacter* spp. (97,1.0%); Other (*Citrobacter* spp., *Proteus* spp., *Providencia* spp., *Aeromonas* spp., *Enterococcus* spp.) (43, 0.4%); *Enterobacter* spp., (38, 0.4%) *Streptococcus*, (35, 0.4%); *Pseudomonas* spp. (15, 0.2%) (Table 1 and 2).

3.2.2. Prevalence of Pathogenic bacteria in Taiwan

From 19 research articles,(Chang et al. 2022; Chen et al. 2017; Chu et al. 2017; Fan et al. 2016; Hsieh, Yen, and Chuang 2019; Hsueh et al. 2020; S. I. Lee et al. 2020; W. C. Lee and Yeh 2017; Lin et al. 2017a; Lo et al. 2017; Nguyen et al. 2017; Publication 2017; Su et al. 2016; J. Wang, Hussain, and Huang 2021; Y. T. Wang et al. 2019; C. J. Wu et al. 2019; Y. C. Wu et al. 2017; Yeh et al. 2018) 9328 food samples were found out of which 3,363 (36%) samples were contaminated with pathogenic bacteria. The maximum contamination was found in Fish (388; 71.2%) and Pork (896; 50.8%) followed by Chicken (651; (48.5%). The prevalence of contamination in other food products was in others (Frog, Goat, Duck, and Geese), (118, 66.7%); RTE, (535, 38%); Sea food, (150, 36.7%); Beef, (96, 29.6%); Milk, (242, 22.2%) Turkey (285, 13.5%) and Fruit and vegetables (5, 4.2%) The only dietary item completely devoid of harmful microorganisms was eggs (0, 0.0%).

The maximum pathogenic bacteria found in Taiwan from different food sources were *E. coli* (1467, 15.7%) and *Staphylococcus aureus* (596, 6.4%); followed by *Salmonella* (444, 4.8%), *Aeromonas* spp. (382, 4.1%), *Streptococcus* spp. (262, 2.8%), *Clostridium* (142, 1.5%) while the lesser number of pathogenic microbes was of *Acinetobacter* spp. (22, 0.2%); *Bacillus* (21, 0.2%), *Enterobacteriaceae* spp., (15, 0.2%) *Pseudomonas* spp. (15, 0.1%). (Table 1 and 2)

When we compare the antimicrobial-resistant bacteria (AMRB) prevalence in both countries, 9676 AMR isolates were yielded (4313 and 3363 were from India and Taiwan, respectively) (Figure 3). The majority of AMR isolate samples in India were from *E. coli* (41% in India and 43% in Taiwan), which shows prevalence in the maximum of the food samples in both countries. Followed by *Staphylococcus aureus* that originated from meat products (beef, pork, and chicken), vegetables, fish, and others, yielding 22% of the samples in India and 18% in Taiwan. This was followed by *Klebsiella* (9%), *Bacillus* (8%), and *Campylobacter* (5%), *Vibrio* (4%), *Acinetobacter* (2%), in India, whereas in Taiwan, the AMR isolates were followed by *Salmonella* (13%), *Aeromonas* (11%), *Streptococcus* (8%), *and Clostridium* (4%) (Figure 3).

3.3. Comparison of AMR prevalence in India and Taiwan

To further understand the spread of AMR, we looked at the key species of foodborne pathogens and indicator bacteria from India and Taiwan separately (Figures 4 and 5). In India, most of the pathogenic bacteria show resistance against β-lactam and cephalosporin, whereas in Taiwan, the most resistance was seen against quinolone and fluoroquinolones (Figures 4 and 5), followed by amino glycoside. β-lactam shows more resistance in Gram-positive bacteria, while quinolones were more likely in Gram-negative bacteria.

3.3.1. Gram positive bacteria

3.3.1.1. Staphylococcus

Among other species, *S. aureus* was the most prominent, with two strains isolated: Methicillin-resistant *Staphylococcus aureus* (MRSA) and methicillin-susceptible *Staphylococcus aureus* (MSSA). Bacteria were regularly found in milk and other animal products such as pork, chicken, beef, RTE, and others. The country with the most tainted food samples was India. AMR was most common for the following drugs: β-lactam, aminoglycosides, and tetracycline, whereas, folic-acid inhibitors, and fluoroquinolones were less common.

3.3.1.2. Streptococcus

Streptococcus agalactiae, *Streptococcus dysgalactiae* and *Streptococcus uberis* were the genus found in Streptococcus. The most prevalent contaminated foods were milk and fish. In Taiwan, 8% of the isolates was streptococcus. AMR was observed against β-lactam, cephalosporin, and aminoglycoside, whereas less resistance was shown against macrolide and sulfonamide.

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3.3.1.3. Listeria spp.

Listeria is an important bacterial infection that occurs in animals and humans and arises mainly from the ingesting contaminated food. From the data, about 1% of the total positive samples were contaminated with *listeria*. It is commonly found in beef and sea food. High resistance was seen against aminoglycoside, monocarboxylic and quinolone, and less resistance was seen against β-lactam, tetracycline, and chloramphenicol.

3.3.1.4. Bacillus

Bacillus is responsible for the spoilage of most of the dairy products and have been associated with foodborne outbreaks. *B. cereus*, *Bacillus weihenstephanensis*, and *Bacillus cytotoxicus* are closely related species. About 8 % of the positive samples of *Bacillus* were seen in India. AMR was observed against β-lactam, cephalosporin, and macrolide. Less resistance was shown against tetracycline and fluoroquinolones drugs.

3.3.1.5. Clostridium

C. perfringens infection is one of the most common foodborne diseases in humans, along with *Salmonella* and *Campylobacter* infections. It has been claimed that chicken meat is responsible *for* about 30% of *C. perfringens* human infections.(la Mora et al. 2020) From the data, around 4% of the positive samples were from Taiwan. AMR was observed against β-lactam, macrolide, lincosamide and tetracycline. Less prevalence was seen against fluoroquinolones and phenicol.

3.3.2. Gram negative bacteria

3.3.2.1. Escherichia coli

Pathogenic *E. coli* is the leading cause of infection both in humans and animals. About 41% in India and 44% in Taiwan of the total positive samples were contaminated with *E. coli*. The most prevalent contaminated food was pork, chicken, beef, fish, egg, mutton and milk. Across the entire data set of *E. coli* isolates were found resistant against quinolone, fluoroquinolones, and β-lactam, whereas just a small proportion of total *E. coli* were identified to be resistant to tetracycline, and folic acid inhibitors.

3.3.2.2. Salmonella

Salmonella is one of the most significant zoonotic bacterial foodborne pathogens of humans that cause diarrhea, focal suppurative infections and bacteraemia. Pork, turkey, chicken, beef, sea food, fruit and vegetables, and mutton have maximum *salmonella* contamination. The most prevalent antibiotic to which the various *Salmonella* serovars were resistant to β-lactam, tetracycline, and aminoglycoside. Lower resistance was observed for quinolone, polymyxin, and cephalosporin.

3.3.2.3. Campylobacter

Campylobacter spp. has been attributed globally as one of the four key causes of diarrheal diseases.(Campylobacter n.d.) From the data, about 2.2% of the total positive sample shows the bacterial prevalence of campylobacter in India. Presence of Campylobacter spp. isolates in chicken meat samples were seen maximum. The isolates showed higher resistance against tetracycline, sulfonamides, and cephalosporin, whereas a small proportion of the sample was resistant against monocarboxylic, and macrolide.

3.3.2.4. Acinetobacter

In recent decades, *Acinetobacter* spp. has become a significant global source of nosocomial infections. From the data, the most prevalent contaminated food sources were fruits and vegetable and REF in India and Taiwan, respectively. The isolates shows higher resistance against

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carbapenems, cephalosporin, and β-lactam. In contrast, just small proportion was seen resistant against tetracycline, polymyxin and folic acid inhibitors.

3.3.2.5. Enterobacter

Enterobacter spp. is a food-borne pathogen that has been related to infantile meningitis, septicemia, and necrotizing colitis after consuming contaminated powdered infant meals. From the data, the most prevalent contaminated food sources were fruits and vegetable and REF. The isolates show higher resistance against β-lactam, polymyxin, and cephalosporin,. Lower resistance was observed against folic acid inhibitors, fluoroquinolones, and tetracycline.

3.3.2.6. Klebsiella

In humans, *Klebsiella pneumoniae* is a significant food-borne pathogen that can lead to septicemia, liver abscesses, and diarrhea. (Davis and Price 2016; Liao, Huang, and Hsueh 2022) From data, the prevalence was seen in fish, fruits and vegetables and RTE, about 9% of the total positive sample was found in India. Most of the resistance was seen against aminoglycoside, β-lactam, and cephalosporin, while lesser resistance was seen against tetracycline, lincosamide and sulfonamide.

3.3.2.7. Vibrio spp.

Vibrio species have been identified as human entero-pathogens and as the etiological agents of gastroenteritis, septicemia, and wound infection that is transmitted via shellfish. (Baker-Austin et al. 2018) From our data, the prevalence of *vibrio* spp. was seen in sea food particularly in shellfish. About 4% of the total positive sample was seen in India. The most prevalent antibiotic to which the various *vibrio* spp. were resistant to cephalosporin, β-lactam and quinolone, the less resistance was seen against tetracycline, fluoroquinolones and aminoglycoside.

3.3.2.8. Aeromonas

Aeromonas spp. is opportunistic bacteria that cause a wide range of human disorders, including gastroenteritis, urinary tract infections, etc., which is transmitted via food-borne pathogens.(Piotrowska and Popowska 2014) From the data, about 11% of the total positive was seen in Taiwan. The most contaminated food was fish and sea food. The highest resistance was seen against cephalosporin, tetracycline, and carbapenems.

3.3.2.9. S. maltophillia

Stenotrophomonas maltophilia is an important opportunistic pathogen that has been reported to be associated with a wide variety of infections; it is ubiquitously present in aqueous environments and REF.(Li et al. 2019) From the data, about 1% of the total positive samples were contaminated. It shows high resistance against chloramphenicol, cephalosporin, folic acid inhibitor and less resistance was seen against β-lactam, and fluoroquinolones.

3.3.2.10. Pseudomonas

Transmission of *Pseudomonas aeruginosa* along the food chain could cause gastrointestinal infections. From the data, about 1% of the samples were contaminated in both against, particularly against fruit and vegetables and RTE. The isolates show higher resistance against cephalosporin, β-lactam, and folic acid inhibitor.

4. Discussion

The threat posed by AMR to both human and animal health is significant, and it has garnered attention from all around the world in an effort to stop its spread before it is too late. Due to a lack of surveillance networks, laboratory capacity, and adequate diagnostics, AMR is typically not consistently monitored in many nations.(Iskandar et al. 2021) This is worsened by overuse, misuse and improper use of antibiotics by animal handlers, farmers, etc.

The goal of this systematic data analysis was to quantify AMR exposure in various foods from butcher shops and retail food markets in India and Taiwan. The study's goal is to give a literature-based analysis of AMR bacteria occurrence and food vulnerability. The AMR exposure assessment serves as the foundation for developing an AMR action plan that incorporates risk analysis into systemic surveillance systems at the consumer and retail levels. This meta-analysis is essential in providing answers that can influence antibiotic usage strategies in livestock.

The meta-analysis study suggests that most of the food samples were contaminated with *E.coli* and *Staphylococcus* in both India and Taiwan. A high contamination rate was seen in chicken and beef in India, which is highly consumed, whereas in Taiwan, the resistance was seen against fish and pork. This indicates that proper hygiene practices are not being followed consistently. The data provided revealed that contamination occurred in the food most often consumed in each country. The isolated bacteria were mostly resistant to β-lactam, fluoroquinolone and quinolone. Resistance to carbapenem, tetracycline, and cephalosprin was moderate, whereas resistance to macrolides, phenicol, folic acid inhibitors, fusidane, lincosamide, glycylcycline, and monobactam was low. Raw foods consumption makes it more serious to consumers because resistant germs can thrive in untreated food.

In India beef, milk, pork and chicken are the most contaminated food as their consumption is high due to low prices. Raw foods contaminated with pathogens (meat, eggs, milk) and diseased animals are major sources of human diseases.(Rincón-Gamboa, Poutou-Piñales, and Carrascal-Camacho 2021) Furthermore, antimicrobial drugs are employed in animals not only for diagnosis and prevention of bacterial illness, but also for growth promotion also a major cause.(Chattopadhyay 2014) In addition, different animal-adapted serotypes are far more likely to cause invasive illness in humans. Similarly, vegetables may be contaminated by inadequately treated water and fertilizers, or they may be harmed by the use of bio-control agents during cultivation. (Rasheed et al. 2014a)

However in Taiwan, food such as pork, chicken and meat is mostly contaminated by pathogens. In addition intake of raw milk, uncooked meat, the frozen fish ready for human consumption, some are employed as fermentation starters in meat, or other food processing, shows principal carriers of AMR.(Hoel, Vadstein, and Jakobsen 2017) According to one estimate, over 150,000 different varieties of food and drink are served on the streets and in night markets around the country.(Lin et al. 2017b) The culture of street food has always been linked to food poisoning and other digestive disorders and is associated with the food chain.(Alimi 2016; Huynh-Van et al. 2022) This suggests that the food supply chain could be a significant route for resistant genes to spread. As a result, examining the genetic arrangement of AMR genes is crucial for determining AMR risk and should be done more thoroughly.

It is essential to understand how the AMR is developing worldwide, and the current severity of the problem if it is unchecked. Similar to disease surveillance, AMR surveillance and meta-analysis offers data to guide intervention options. For instance, AMR surveillance can assist in evaluating of the effects of interventions on antibiotic usage guidelines or infection control. Additionally, effective surveillance systems can give decision-makers information on the emergence and prevalence of AMR.(Johnson 2015) Various countries including India and Taiwan have implemented policies like introduction monitoring systems and the One Health approach(Hernando-Amado et al. 2019) of resistance in food animals considering the public health risks of possible transfer of resistant bacteria or genes from animals or the environment to humans.(Carlos Franco et al. 2022; Gunjan et al. 2023).

Therefore, devising successful measures to target a reduction in the formation and spread of AMR requires an understanding of the epidemiology of AMR. As a result, organized multi-sectorial, collaborative AMR surveillance is critical for decision-making at the national, regional, and worldwide levels. It aids in tracking the burden of AMR and resistance trends in order for countries to develop cost-effective, evidence-based AMR response strategies. It will be beneficial in analyzing foodborne pathogens from multiple sources and reducing the knowledge gap.

5. Conclusion

The systematic meta-analysis depicted the overall antimicrobial drug resistance problem across different food samples with higher estimates of clinically important resistance from the pork in Taiwan and chicken in India. It also emphasized the importance of understanding the probable linkage, transmission mechanisms, and flow pattern of resistant bacteria in the human-animal-environmental interface in order to reduce the potential risk to public health. As a result, measures to lessen the burden of antimicrobial resistance should be based on a thorough knowledge of the essence of a coordinated One Health strategy.

AMR is becoming a serious health issue in the country as some widely used antimicrobials are not effective in the treating bacterial infections in animals and humans. Fluoroquinolone and β-lactam shows the highest drug resistance. Therefore, drug susceptibility for treating bacterial infections should be practiced as much as possible. To overcome or eliminate the risk of Antimicrobial resistance bacteria in the food chain, two important stages must be monitored: antimicrobial usage in foods and AMRB arising from livestock and agricultural practices. On-time revision and implementation of standard treatment guidelines, shall be prioritized in livestock as strategy to tackle AMR in the respective countries. The proposed methods should be policy-based, universally applied, and fully supported by legislative measures. A single nation cannot solve the AMR issues affecting the world's food supply, but a worldwide collaborative effort can solve it.

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