

ANTIMICROBIAL DRUG RESISTANCE FROM FOOD SOURCES

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Abstract – Objective: Antimicrobial Resistance (AMR) happens when microbes, infections, organisms, and parasites change over the long run, becoming resistant to any drug, as well as making contaminations harder to treat and expanding the danger of the disease spreading, severity, and death. Because of medication obstruction and anti-infection agents, antimicrobial drugs become ineffectual, and diseases become progressively troublesome or difficult to treat. AMR keeps on representing a public health concern because of high mortality rate and expensive treatments. Food assumes a significant part in the transmission of commensal microorganisms yet in addition, food-borne microbes include zoonotic organic entities. The aim of this meta-analysis review is to report the predominance of antimicrobial resistance in food from animals and a few vegetables from India and to compare the data with countries like Switzerland and Taiwan.

Material and Methods: To evaluate AMR pervasiveness in retail food a literature review survey of information distributed in the range of 2013 to 2020 was done. The research articles were identified through Google scholar, PubMed, and ResearchGate. The Keywords AMR, INDIA, food source like seafood, goat meat, chicken meat, pork, raw eggs, milk, and vegetables were used for the search.

Results: Out of the 63 eligible studies, 10 articles (all articles from India) were included in this review. A total of 2,126 AMR tests were collected for various bacteria found in various food products. Nine distinct bacteria and resistance to about 13 different antimicrobial agents/drugs were identified. The sample sources, bacterial species, and their proportion are displayed in Tables 1. In these 9 distinct microorganisms, 1800 microorganism isolates of which 611 samples and 698 isolates were AMR positive. A middle AMR commonness of >50% was noticed for meat and fish with *Escherichia coli*, *Staphylococcus aureus*, *Enterococci*, *Salmonella*, *Enterobacter*, *Klebsiella*, *Streptococci*, *Vibrio spp.*, and *Shigella*.

Conclusions: AMR potential for Gram-negative foodborne bacteria was found in raw meat, milk, fish, and certain matured dairy products. To enable an expanded AMR hazard appraisal for customers, AMR genetics attributes are suggested to be better coordinated into regulated One Health AMR observation and alleviation systems.

Keywords: Antimicrobial Resistance (AMR), Antimicrobial drugs, Gram-negative bacteria, One health.

INTRODUCTION

AMR emerges when the microorganisms that cause infection survive exposure to a medication that regularly kills them or stops their development. This has prompted the rise of superbugs, for example, methicillin-resistant *Staphylococcus aureus* (MRSA) and extremely drug-resistant *Mycobacterium tuberculosis*, microorganisms that are troublesome or difficult to treat with existing prescriptions¹.



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Antibiotics are frequently used in the food animal production system to promote and advance their growth as well as to avoid infection and disease, which has resulted in the rise of microorganisms that are resistant to antibiotics. These antibiotics are often used for preventive and growth stimulation of meat animals as well as for the treatment of infected humans and animals. Numerous scholars² recommend that the lack of choice and improper use of antimicrobials might promote obstruction in different bacteria and make the treatment of bacterial infections more difficult.

There is a considerable worldwide variety of antibiotic resistance, thus it is an issue that concerns each country. It is anticipated that most of the future antibiotic obstruction deaths will be in Africa and Asia, with India, Nigeria, Indonesia, and Russia most at risk. Antimicrobial resistance is a very serious issue, challenging to handle, but there are ongoing efforts toward its control³. Efforts to increase antibiotic use should first identify the major contributing causes and, when practical, adopt treatments that are specifically targeted at resolving the noted concerns¹. Antimicrobial resistance influences the health of people, animals, and the climate; “One Health” alleviation draws near with the inclusion of relevant areas, which are required⁴. The Global Action Plan by the World Health Organization (WHO) shows various systems that nations could use to relieve the expanding hazard, including “further developing mindfulness and comprehension of AMR through powerful correspondence, schooling and preparing”³. Endeavors to battle AMR have been started by the Indian health authorities yet are currently at the initial stages⁵.

The data collected in this article was gathered from research articles that found AMR isolates in retail meat shops and from a few vegetable retail markets; because of this, it will be easy for us to identify the potential transmission of antimicrobial-resistant microbes between humans and animal.

MATERIALS AND METHODS

The Portrayal of Research Area

We collected data from the subtropical country India; huge parts of the population across every religion consume meat in some structure in this country. Despite the country registering less meat utilizations compared to other countries⁶, its southern territory of Telangana recorded 98.8 percent of its population as meat-eaters (meat and seafood), higher than in nations like the United States or Australia. Nevertheless, the quantity of meat ate in the state was far lower than in some nations. Asia is one of the largest meat producers. In India, poultry consumption increased meat production by almost 50%⁶. Four million metric tons of poultry meat was consumed in India in 2021, along with 81 million metric tons of milk consumed in the same year, standing as the most milk-consuming country in the world⁷.

Search Strategy

The search strategy of this work is based on the different food categories not certified by The Food Safety and Standards Authority of India (FSSAI). Some research articles were identified through Google scholar, PubMed, ResearchGate database. The keywords AMR, INDIA, food source like seafood, goat meat, chicken meat, pork, raw eggs, milk, and vegetables were used for the search. From all the research, 2,897 papers were identified. From those papers, 2,887 studies were eliminated due to duplicate records, irrelevant and incomplete data, or because they were not eligible for the review.

Study Selection Criteria

2,897 papers were initially screened for the data collection. Papers with food categories linked to the antimicrobial resistance have been collected from many parts of the country. This paper mainly concentrated on food categories like seafood, goat meat, chicken meat, pork, raw eggs,

milk, and vegetables. The literature papers, reviews, observational studies, and prospective examinations about AMR were included. We excluded studies that did not match the inclusion criteria because they were irrelevant to this research. The full text was required for further screening.

Antibiotic Selection

The WHO has designated few antibiotics that are considered to be the most beneficial as “Critically Important” in therapeutic applications⁸. These particular antibiotic classes have been tested for this data.

Data Extraction

Data used in this research included food category, its production, phenotypic and genotypic data related to antimicrobial resistance. The data extracted have been represented graphically in the Figures 1, 2, 3 and along with a tabular format in Table 1 and 2.

Data Analysis

A total of 10 papers were selected for data retrieval and inclusion or exclusion. The following measures were considered. Initially, we considered access to the entire text and abstract of the article followed by the paper that reported food pathogens along with AMR. Then, we analyzed the pathogens that are mentioned from those literature survey and the food sample source and also the method for conformational tests that assess AMR, which includes various molecular techniques, disc diffusion, and minimum inhibitory concentration (MIC). The quantitative analysis proceeded by calculating the total number of samples and differentiated them along with the food source to identify the pathogens from those food source samples followed by the percentage calculation.

RESULT

10 out of 63 reviews and research literature were included. The collected data from different research studies were performed in different parts of India. From the studied research papers

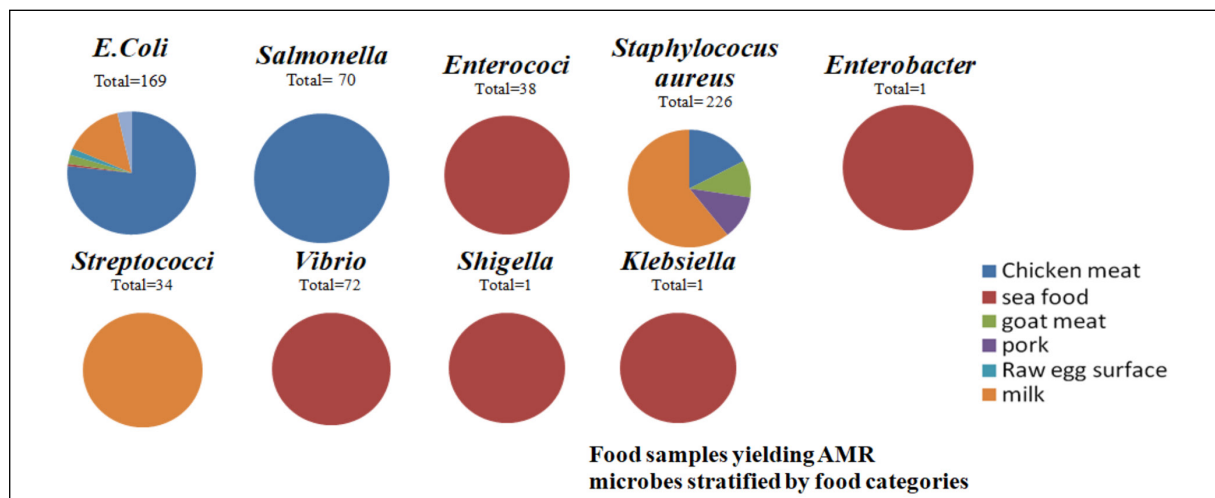


Figure 1. Distribution of the number of food tests identified microbes and defined by food classifications. The complete beneath every pie outline indicates the absolute of tests used to calculate the chart.

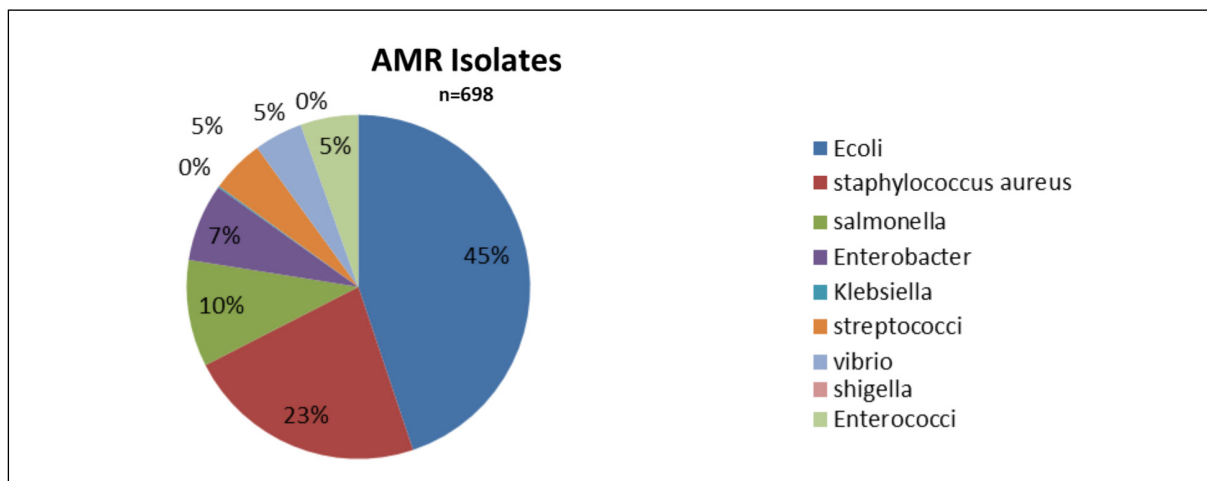


Figure 2. Percentage of individual AMR isolates.

2,126 samples were identified, which includes seven different food categories⁹⁻¹⁷ (Table 1). Most of the infected microbial species were found on the meat, which is 400 samples out of 1,722. 197 samples out of 320 infected microbial species were in the milk samples, followed by the vegetables with 6 out of 30 and on raw egg surface, which is 3 samples in total 54 samples. 32.83% of the microbes have been detected from a total of 2,126 samples. *Staphylococcus* were the most seen (n=225) followed by *Escherichia coli* (n=168) and then *enterococci* (n=38), *salmonella* (n=70), *Enterobacter* (n=1), *klebsiella* (n=2), *streptococci* (n=34), *Vibrio spp* (n=72) and *shigella* (n=1) (Figure 1).

Detected AMR with Respective Food Categories

Antimicrobial sensitivity tests were performed in all the research data by using antibiotic disks to identify the AMR isolates and following the guidelines of clinical and laboratory standards (CLSI)¹⁸. A total of 698 AMR isolates were detected from 611 microbial-detected samples (Figure 2). *E. coli* was detected with around 313 AMR isolates, then 158 isolates of *staphylococcus*, followed by *salmonella* with 70 AMR isolates, *Enterobacter* with 51 AMR isolates, *enterococci* with 38 isolates, *vibrio* with 32 isolates, 35 *streptococcus* isolates, and

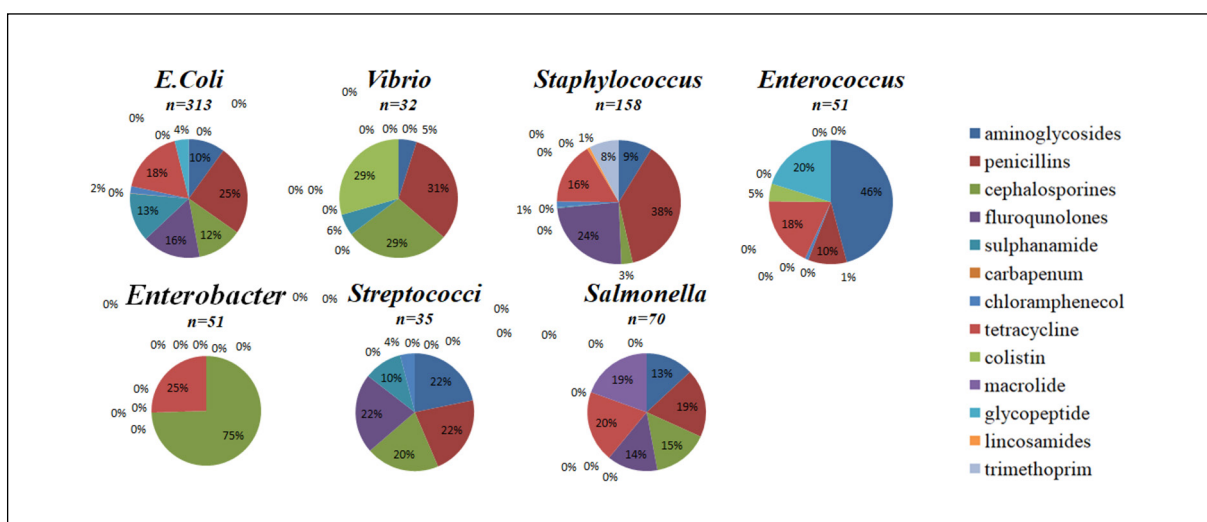


Figure 3. Distribution of the number of AMR isolates detected phenotypic AMR against 13 main AM classes.

TABLE 1. AN OVERVIEW OF THE FOOD PRODUCTS CATEGORIES ALONG WITH THE MICROBES THAT HAVE BEEN DETECTED.

Microbes	Chicken n = 1267	Fish n = 164	Goat n = 160	Pork n = 131	Raw Egg surface n = 54	Milk n = 320	Vegetables n = 30	Total n = 2126
1. <i>Escherichia coli</i>	129 (10.2%)	1 (1.64%)	4 (2.5%)	-	3 (5.5%)	25 (8%)	6 (20%)	168
2. <i>Staphylococcus aureus</i>	39 (3%)	-	23 (14.37%)	27 (20.6%)	-	136 (43%)	-	225
3. <i>Enterococcus</i>	-	38 (23.2%)	-	-	-	-	-	38
4. <i>Salmonella</i>	70 (5.5%)	-	-	-	-	-	-	70
5. <i>Enterobacter</i>	-	1 (1.64%)	-	-	-	-	-	1
6. <i>Klebsiella</i>	-	1 (1.64%)	-	-	-	1 (3.2)	-	2
7. <i>Streptococci</i>	-	-	-	-	-	34 (11%)	-	34
8. <i>Vibrio</i>	-	72 (44%)	-	-	-	-	-	72
9. <i>Shigella</i>	-	1 (1.64%)	-	-	-	-	-	1
Total infected	238 (18.8)	114 (74%)	27 (17%)	27 (20.6)	3 (5.5)	196 (61.7)	6 (20%)	611

TABLE 2. OVERVIEW OF THE COMPARATIVE STUDY OF AMR BETWEEN INDIA, TAIWAN, AND SWITZERLAND.

	India	Switzerland ¹²	Taiwan ²⁶⁻³⁴
No of the samples tested	n = 2126	n = 2404	n = 3809
No positive samples	611 (28.7%)	859 (35.7%)	1123 (29.48%)
No of AMR positive strains	698 (32.83%)	682 (28.36%)	643 (16.88%)

1 *Klebsiella* isolate were detected. These bacteria were evaluated to find the distribution of antimicrobial-resistant phenotypes. Most of the AMR in all groups showed resistance to penicillin and then against tetracycline, cephalosporin, and amino glycosides. The predominance of antibiotic-resistant microbes is observed in these four antibiotics while the rest show less prevalence.

Escherichia coli were identified in 6 studies and most of the AMR isolates were *Escherichia coli*, found in meat followed by milk. Compared prevalence of AMR is shown in Figure 3, where resistance to aminoglycosides, penicillin, cephalosporin, fluoroquinolones, sulphonamide, carbapenems, tetracycline, and glycopeptides classes of antibiotics are presented. Multidrug resistance was reported. AMR genes *stx₂*, *aer*, *afa*, *papC*, *cvaC*, *alr*, *bla_{TEM}*, and *bla_{CTM-M}* were reported.

Non-typhoidal *Salmonella* predominance was noticed. Three serotypes of *Salmonella* (*Salmonella Kentucky*, *Salmonella Virchow*, and *Salmonella Typhimurium*) were found to be multidrug-resistant. Tetracycline, erythromycin, nalidixic acid, ampicillin, and ciprofloxacin were shown as high-resistant (Figure 3). *Salmonella* genetic element, which encodes for AMR, was identified as the *tetA* gene, *bla_{TEM}*; multiple virulence genes such as *sipA*, *mgtC*, *sopE1*, *stn*, *sopB*, *fliC*, *spvC*, and *gipA* were additionally identified.

Vibrio spp were reported in 32 samples in shellfishes like clams, shrimps, and crabs with six different potential *vibrio* spp like *v. alginolyticus*, *v. cholera*, *v. harveyi*, *v. parahaemolyticus*, *v. mimicus*, and *v. vulnificus*. Most of them are highly susceptible to penicillin and show low susceptibility to tetracycline and chloramphenicol. No reports of AMR genes.

A total of 158 AMR isolates of *Staphylococcus* were detected. Most of them were identified in the milk samples with more than 70%. *Coagulase-negative staphylococci* were the most predominant ones followed by *staphylococcus aureus*. These are multidrug-resistant but more prominent than β lactam antibiotics. Meat phenotypic was found mainly resistant to antibiotic penicillin, followed by ciprofloxacin, tetracycline, and erythromycin – most of the isolates were multidrug-resistant. Only MRSA was identified in the chicken sample. The AMR gene shows resistance is *bla_Z*, *mecA*, *aacA-aphD*, *ermB*, *ermC*, *tetK*, *tetL*, and *tetM*.

Fifty-one *Enterococcus faecalis* were isolated. Various antibiotics show high resistance against kanamycin, vancomycin and gentamicin, tetracycline, and rifampicin. Multidrug- and vancomycin-resistant strains contain the *vanA* genotype. Virulence genes of AMR *gelE*, *agg*, *esp*, *cpd*, *efa*, *Afs*, and *cylA* were detected in *Enterococcus faecalis*.

All the isolates of *streptococci* displayed 100% resistance to methicillin and showed more resistance to streptomycin, ceftioxin, and penicillin-G. Intermediate resistance was seen between gentamicin and ceftriaxone, and chloramphenicol and oxacillin were the least resistant, respectively. AMR genes were not reported.

ESBL (*aac(6')-Ib-cr*) *Enterobacteriaceae* were detected. *Enterobacteriaceae* strains carried the *bla_{CTX-M}* gene, which is a common ESBL gene in clinics. *aac(6')-Ib-cr* gene, which confers resistance to aminoglycosides and low-level resistance to ciprofloxacin, was detected.

This research paper was made with limited data and the total samples collected were 2,126. A 34.4% of AMR-positive isolates were found in the analyzed food categories. A similar research paper¹⁹ in Switzerland shows similar data; they have collected total of 2,404 samples, which included food sources similar to that included in this paper, and out of 611

positive sample, 682 positive isolates of antimicrobial resistance strains were identified (28.36%). Different meta-analysis data has been collected from Taiwan which included the AMR in the retail food markets and the street food in Taiwan. This meta-analysis data shows 3,809 samples of which 1,123 positive isolates and 643 of them were positive AMR isolates²⁰⁻²⁸ (16.88%). Indian data has been compared with food source from Switzerland and Taiwan and we concluded that India has more exposure to antimicrobial resistance isolates as shown in Table 2.

DISCUSSION

Antimicrobial resistance is now a major issue on a global scale. A multi-sectoral strategy must be taken in consideration to solve the complicated issue of AMR. The One Health strategy brings together various sectors and decision-makers involved in the design and implementation of programs, policies, legislation, and research to improve public health outcomes for people, terrestrial and aquatic animal and plant health, food and feed production, and the environment²⁹. Numerous organizations have made several new efforts over the past ten years to address this issue. CDC has presented 4 core action plans to protect from antibiotic-resistant; the first is to prevent the infection in the first place so that we can stop it from spreading. The second thing is tackling by collecting the data on antibiotic-resistant infections, the reason for the infection, and the risk factor of that particular infection so that strategies are developed to stop the spread. The third one is to stop prescribing antibiotics if not strictly necessary. Appropriate and safe use of antibiotics should be considered. The last one is to develop new antibiotics as the bacteria evolve and they get naturally resistant to the new antibiotics with time⁹. Thus, we need to focus on these four core methods before planning any strategy against AMR. The outcomes of these antimicrobial prevention strategies and improvement to the national policies and programs can favorably collaborate with the pharmaceutical companies to ensure appropriate licensing, marketing and promotion of the existing antibiotics, as well as to encourage the development of the further drugs and vaccines¹⁰. To combat the AMR threat, a meticulous effort at all levels of healthcare is urgently required.

CONCLUSIONS

For current clinical care AMR shows significant challenges. This research expounds on the degree of human exposure to AMRB through food including the distinguishing proof of a few observations and information about AMRB in food. Significant degrees of AMRB exposure were noticed for crude meat, fish, and plant and AMR against many antibiotic classes. The possible danger of predisposition implied with AMR exposure assessments dependent on systematic literature survey information limits the capacity to give an immediate danger appraisal to the customer. In the Indian environment, AMR has been neglected, now presenting a constantly expanding danger of AMR. Different multidisciplinary approaches should be implemented.

Conflict of Interest

The authors declared no conflict of interest.

Ethics Approval

Not applicable.

Informed Consent

Not applicable.

Availability of Data and Materials

Not applicable.

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