



FEAMR: A Database for Surveillance of Food and Environment-Associated Antimicrobial Resistance

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Abstract

The rapid dissemination of antimicrobial resistance (AMR) has emerged as a serious health problem on an unprecedented global scale. AMR is predicted to kill more than 10 million people annually by 2050 leading to huge economic losses worldwide. Therefore, urgent action is required at the national as well as international levels to avert this looming crisis. Effective surveillance can play an important role in the containment of AMR spread by providing data to help determine AMR hotspots, predict an outbreak, maintain proper stewardship and propose immediate and future plans of action in this respect. Although many existing databases provide genetic and molecular information on AMR in microorganisms, there is no dedicated database of AMR from non-clinical samples. The FEAMR database is a one-of-its-kind database to provide manually collated and curated information on the prevalence of AMR in food and the environment. For designing the FEAMR webpage, Microsoft Visual Studio with HTML, CSS, ASP.NET, Bootstrap for the front-end and C# for the back-end were used. The FEAMR database is a free access resource (<https://feamrudbt-amrlab.mu.ac.in/>), accepting verified food- and environment-related AMR submissions from across the globe. To the best of our knowledge, it is probably the first database providing AMR-related surveillance data from non-clinical samples. It is designed from the ‘One Health Approach’ perspective to help in the containment of global AMR spread.

Graphical Abstract

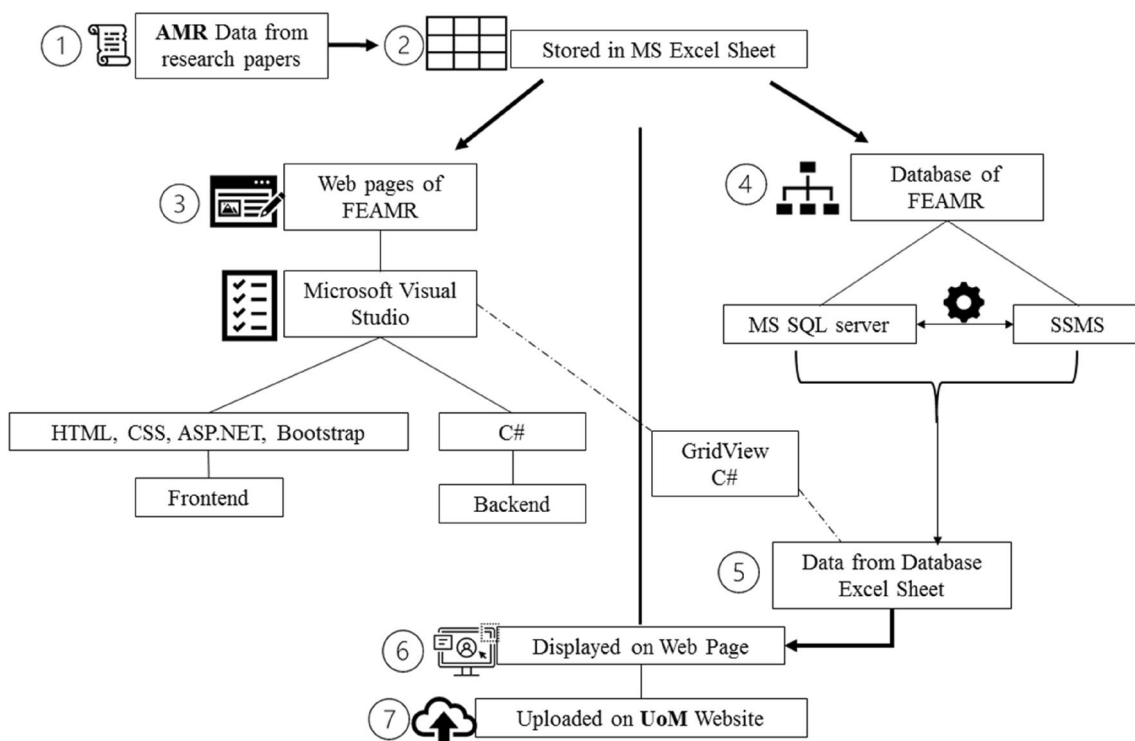
Flowsheet of steps for making FEAMR database 1. Research articles relating to **Antimicrobial Resistance (AMR)** were searched on the internet. 2. Data relating to AMR were retrieved from these articles and stored in an MS-Excel sheet. 3. The web pages of the FEAMR database (DB) were created using Microsoft Visual Studio (MVS) and its various tools. HTML, CSS, ASP.NET and Bootstrap were used for the front end and C# used for the back-end of the website. 4. The DB of FEAMR was created using MS SQL Server which was controlled by SQL Server Management Studio (SSMS). 5. The data from the MS-Excel sheet in step 2 was stored in the SQL server and displayed on the web page using GridView tool of MVS and C#.

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The database created was then uploaded on the **University of Mumbai (UoM)** website, where it can be accessed by all users having the link to the DB (<https://feamrudbt-amrlab.mu.ac.in/>).



Keywords Antimicrobial resistance · Surveillance · Database · Zoonotic · FEAMR · Antibiotics · Pandemic · One Health

1 Introduction

The unwarranted and unrestricted use of antibiotics has led to the emergence of antimicrobial resistance (AMR) as a serious health concern of global proportions [1]. The damaging effects of AMR have led to limited therapeutic options for the treatment of microbial infections, to an extent that even common infections may become life-threatening. Conventional treatment using antibiotics fails to successfully treat infections caused by antimicrobial-resistant microorganisms, leading to prolonged illness and increased mortality [2]. Treatment failures also lead to longer periods of infectivity, with increased numbers of infected people in the community, thereby leading to rapid community spread of infections [3]. Multiple recent reports of resistance observed to antibiotics used for the treatment of COVID-19-related infections further reiterate the problems associated with AMR, especially for the treatment of secondary infections. Thus, AMR may acquire pandemic proportions if not tackled immediately [4–6].

To address the challenge of the spread of AMR and to guide coordinated action against it, the WHO adopted Global Action Plan on Antimicrobial Resistance (GAP-AMR) in

2015 for an effective global response against AMR. One of the main priority areas of GAP-AMR is effective surveillance. Surveillance of AMR from non-clinical sources can help track the transmission of AMR through water bodies, food and environment and identify AMR hotspots arising through these sources. Accordingly, one of the main objectives to counter AMR is “to strengthen the knowledge and evidence base through surveillance and research” [3]. Subsequently, the Global Antimicrobial Resistance and Use Surveillance System (GLASS) was launched by WHO in 2015 to collect official data from participating countries about their national AMR status [7]. In line with GAP-AMR, the Government of India launched a National Action Plan on Antimicrobial Resistance (NAP-AMR) in 2017 [8]. According to NAP-AMR, India is likely to suffer heavily from the impact of AMR owing to a high population density and high burden of infections. Therefore, one of the six strategic priority areas of NAP-AMR is to strengthen knowledge and evidence through surveillance in human, animal/food and environment sectors to facilitate evidence-informed policy-making [8].

Various institutions are contributing locally, nationally, and globally to aid the surveillance of AMR. For instance,

NCBI maintains a National Database of Antibiotic Resistant Organisms (NDARO) to access AMR data and facilitate surveillance of pathogenic microorganisms in real-time [9]. The Centre for Disease Control and Prevention (CDC) established The National Antimicrobial Resistance Monitoring System for Enteric Bacteria (NARMS) in the United States way back in 1996 [10]. The European Antimicrobial Resistance Surveillance Network (EARS-Net) is a publicly funded system for surveillance of AMR across Europe [11]. The Indian Council of Medical Research (ICMR) initiated the Antimicrobial Resistance Surveillance and Research Network (AMRSN) to analyse AMR patterns in different pathogens across Indian hospitals in 2013 [12]. However, most of these databases focus on AMR microorganisms isolated from clinical samples.

However, in recent times there has been a lot of stress on a holistic outlook toward AMR sources & subsequent spread. As per the One Health concept, the health of human beings is connected to the health of animals, plants, and the environment they interact with [13]. Various data suggest a steady increase in animal-based food consumption worldwide [14–17]. Such high demand has led to intensive farming with heavy reliance on the use of antibiotics for prophylaxis, etc. This in turn has resulted in an increased load of AMR in animals, wastewaters, water bodies and soil and also the agricultural produce [18]. The resulting heavy load of AMR in the environment can indirectly lead to an increase in AMR in humans via the food chain [19, 20]. Moreover, studies indicate that more than two-thirds of existing and emerging infectious diseases are zoonotic (can be transmitted across species, between animals and humans) [21]. The ongoing COVID-19 pandemic and zoonotic viral outbreaks in recent years like the SARS, MERS, the Nipah virus, Ebola and Avian influenza have further highlighted the need to look at AMR in the context of the One Health approach. Although the burden of AMR in animals, plants, and the environment as a whole is ever increasing, there is no dedicated database for non-clinical AMR and such data are poorly documented.

Thus, surveillance of AMR through data collection, collation, analysis and information management in food animals, plants and the environment is necessary and will help the national and global action plans toward containment of AMR. The present database has been created to help achieve these goals.

A report by the World Health Organization (WHO) on the Integrated Surveillance of Antimicrobial Resistance in Foodborne Bacteria recommends the development of an isolate-level database (DB) containing microbiological and epidemiological data of samples for the creation of a core of an integrated surveillance system on AMR. The report suggests data in the DB should be secure, easy

to enter and retrieve, and comparable with similar DBs at national and international levels [22].

In the present study, we have developed the Food and Environment associated Anti-Microbial Resistance (FEAMR) DB to provide comprehensive information on AMR in different food and environmental samples globally. The FEAMR DB has been created recognizing the important role that food and environment play towards the overall health of individuals. The DB was developed using Microsoft Visual Studio and Microsoft SQL Server. To the best of our knowledge, the FEAMR DB is the first-of-its-kind DB designed for surveillance of AMR in food, environment and other non-clinical samples globally.

2 Materials and Methods

2.1 Data Collection

The search engines like Google Scholar, PubMed, Web of Science, etc. were used for searching literature related to AMR in food and environment spanning roughly the past 3 decades. The searches were restricted to reporting incidences of AMR globally in meat, fish, sprouts and dairy and dairy products only. Only open-source articles available in the public domain and published in the English language were selected. The search strategy focused on original research and review articles that reported AMR profiles of microorganisms isolated from specific samples as mentioned above. Antimicrobial Susceptibility Testing (AST) and Minimum Inhibitory Concentration (MIC) data from these articles were considered. Information regarding Location, Sample used, Microorganisms isolated and Antibiotics tested against were entered into an appropriate format in a Microsoft Excel sheet. The last column of the Excel sheet also contains the references from where the data were collated.

Data validation of entries was done multiple times by the team before it was finalized for final visualization in the Excel Sheet.

Accession IDs were allotted to each isolate from each sample. The ID was alphanumeric with one letter and five digits, with the first letter indicating the food type (M—meat, F—fish, S—sprouts, D—dairy and dairy products). The selection of antibiotics was done based on clinical relevance for treating human and veterinary infections and grouped into 12 major types, namely—penicillins, tetracyclines, cephalosporins, quinolones, lincomycins, macrolides, sulfonamides, glycopeptides, aminoglycosides, carbapenems, polymyxins and others.

2.2 Tools Used

2.2.1 Microsoft Visual Studio

Microsoft Visual Studio was used to create the web pages of the FEAMR DB. It is an open-source software application from Microsoft that works as an integrated development environment (IDE). IDEs provide facilities to programmers for the development of software.

2.2.2 Languages

Visual Studio supports various programming languages used for software development. HTML, CSS, ASP.NET and Bootstrap were used for the front-end and C# was used for the back-end of FEAMR DB.

HyperText Markup Language (HTML) is the language that helps documents to be displayed on a web page in a browser. It is the backbone of the webpage development process. Cascading Style Sheets (CSS) is a style sheet language that helps decide the presentation of text on the web page. ASP.NET is a framework developed by Microsoft to help produce dynamic web pages and websites. It is used for fixing the positions of the resources on the webpage and making them work. Bootstrap is a CSS-based front-end framework that contains templates for interface components (such as navigation and typography). It divides the screen into columns and that allows to fix the website on any screen with simple codes and get rid of the additional scrollbar which gets added to the website when the website size is not matching with the screen. Lastly, C# (C-Sharp) is a programming language developed by Microsoft. It is object-oriented and has been used for back-end functions in this study.

2.2.3 SQL Server Management Studio (SSMS)

SSMS is an advanced development environment developed by Microsoft. It is a unique software application that allows controlling the Microsoft SQL Server using a graphical user interface instead of input by command-line interface.

2.2.4 GridView

It is a tool on visual Studio to display data in a tabulated form on the webpage.

2.3 Creation of Database

Microsoft SQL Server was used to create the DB. The data was imported and stored in the server using SSMS. Additions or changes in the excel data imported into the server were done by performing SQL commands or using a graphical user interface.

This data was stored in the back-end which was to be displayed on the webpage later on. This was done using the GridView tool of Visual Studio. SQL commands were executed in C# to connect the GridView to the DB, that is, to connect the front end and back end. For fetching the data backend was connected with the front end using connecting string.

For the search option, a simple dropdown list was used which fetched the data from the DB related to the requested search. Three search options, namely—Food type, Location and Microorganism have been provided for better flexibility while using the FEAMR DB (Fig. 1).

3 Results and Discussion

3.1 Overview of FEAMR DB

The FEAMR DB has been created to provide food and environment-related AMR data from across the globe to aid AMR surveillance at the local, national and international levels. It provides data specifically from non-clinical samples. The FEAMR DB has been created recognizing the important role that food and environment play towards the overall health of individuals.

It has been made using open-source software by research and postgraduate students. It has a user-friendly interface and has been created in an easy-to-understand language.

3.2 Contents of FEAMR DB

The FEAMR DB contains the following web pages -

- (a) Home—The first page of FEAMR DB contains information about the DB (Fig. 2).
- (b) About—This page contains information about AMR and its global importance. It also contains information about the Terms of Use of components of the DB (Fig. 3).
- (c) Contact—The contact page is for users who wish to contact the FEAMR team for submitting data to the DB or for giving any suggestions or feedback.
- (d) Search Tool—The FEAMR DB has a search tool in the database for understanding AMR prevalence category-wise. Users can search for AMR data under three categories—Sample, Location and Microorganism (Fig. 4a, b).

Fig. 1 Use-Case diagram explaining the flow of user interactions with the FEAMR database

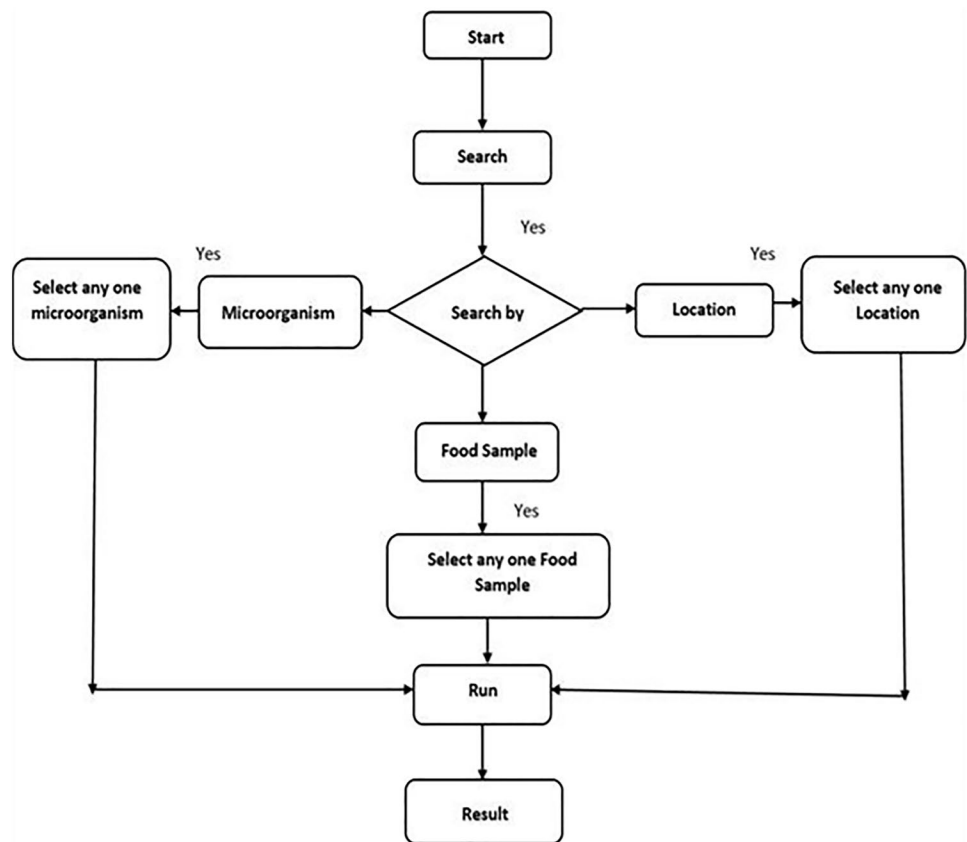
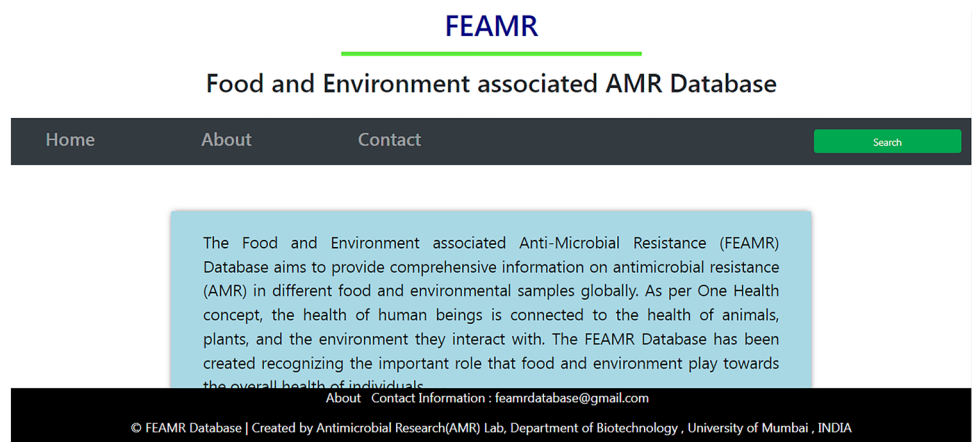


Fig. 2 Home Page of FEAMR DB



3.3 Database Entry and User Interface

The FEAMR DB contains data on AMR in different samples across the globe. The base of the DB is an excel sheet that is displayed based on the search options chosen. The DB also gives identification ID to microorganisms showing AMR from food samples; such as S00001 for sprouts, D00021 for Dairy and Dairy products, M00040 for meat and beef and F00023 for fish.

The FEAMR DB classifies data based on the categories: Sample, Location and Microorganism. On the Search page,

when the user selects one of the three categories, another dropdown list on the web page gets activated which contains respective entries from which the user can select one and click “Search”.

The result displays the location, sample and microorganisms which were a part of the study. Data on the antibiotic classes to which the isolated microorganisms are resistant are included in 12 columns of antibiotic classes, namely—penicillins, tetracyclines, cephalosporins, quinolones, lincosamides, macrolides, sulfonamides, glycopeptides, aminoglycosides, carbapenems, polymyxins and others. The reference

Fig. 3 About Page of FEAMR DB

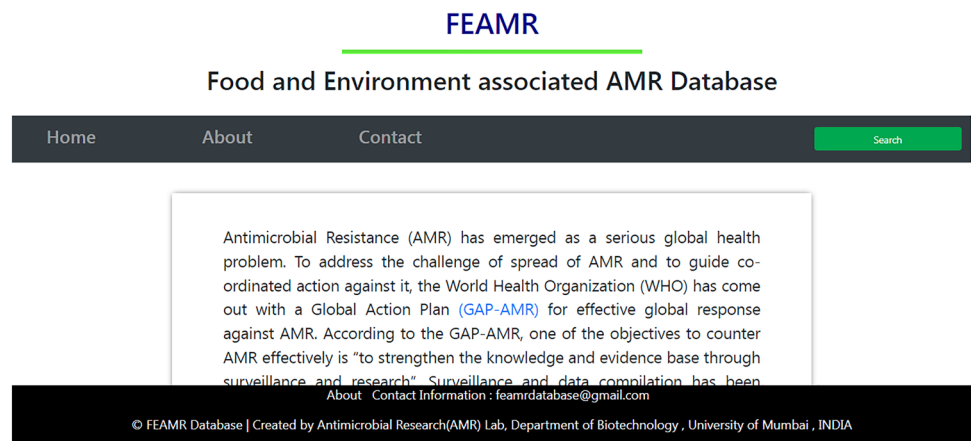
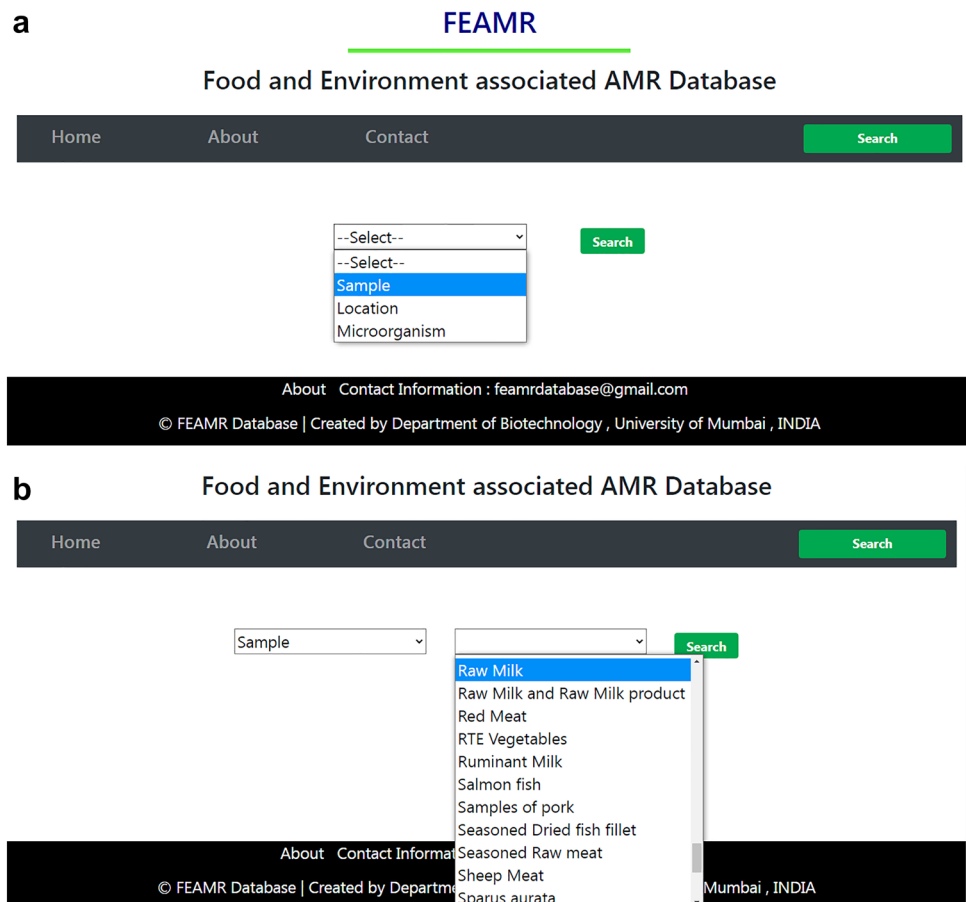


Fig. 4 a Search Page of FEAMR DB displaying the three categories available for searching AMR data. **b** Search Page of FEAMR DB: Each category has entries, each of which can be selected for precise AMR information



article of the said study is mentioned in the last column. The result is a table containing AMR data specific to that sample/location/microorganism selected by the user. A sample search result is shown in Fig. 5.

3.4 Surveillance Studies

The DB is a compilation of data from published research articles and the information available in the public domain.

A total of 339 entries are presently available on the FEAMR DB, out of which 41 are sprout samples, 72 are dairy and dairy product samples, 139 are poultry/meat/ beef samples and 87 are fish samples, covering 189 entries from Asia, 71 entries from Africa, 39 entries from Europe, 32 entries from North America and 08 entries from South America. The DB also gives information about the prevalence of AMR in different microorganisms: 271 out of 339 entries belong to Gram-negative microorganisms, out of which, approximately

Home
About
Contact
Search

Sample

Raw Milk

Search

FEAMR Code	Location	Sample	Microorganism	Penicillins	Tetracyclines	Cephalosporins	Quinolones	Lincomycins	Macrolides	Su
D00007	Anand City, Gujarat, India	Raw Milk	Escherichia coli	Ampicillin, Amikacin	Oxytetracycline, Doxycycline	Cefotaxime	Ciprofloxacin, Levofloxacin, Nalidixic Acid			T
D00027	New Haven, United States of	Raw Milk	Aerobes	Penicillin, Ampicillin	Tetracycline					

About Contact Information : feamrdatabase@gmail.com

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Fig. 5 Result for Raw Milk Sample as obtained from FEAMR DB. The first column displays the FEAMR accession code, followed by the location, sample, microorganism, 12 antibiotic classes and reference columns

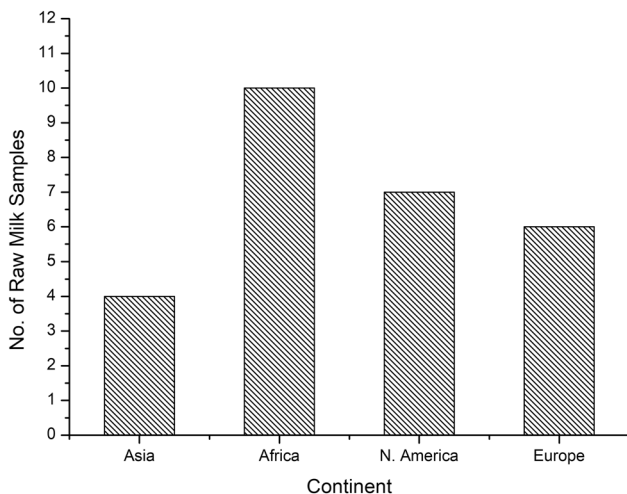


Fig. 6 Prevalence of antibiotic-resistant *E. coli* in raw milk across different continents based on FEAMR data. The highest prevalence can be observed in Africa (10 samples), followed by, North America (07 samples), Europe (06 samples) and Asia (04 samples)

90 isolates belong to *Escherichia coli*. Among Gram-positive microorganisms, *Staphylococcus aureus* appears most frequently (18 out of 67 entries). It should be noted that the DB in its present form is not exhaustive. The results will get modified as more data is submitted, verified and then added to the DB. The FEAMR DB is open to accepting food and environmental AMR-related data submissions. Submissions can be done by filling out the contact form on the FEAMR website. Figure 6 shows the prevalence of *E. coli* in raw

milk samples across different continents as per entries in FEAMR DB to date. The highest prevalence can be observed in Africa (10 samples), followed by North America (07 samples), Europe (06 samples) and Asia (04 samples).

It is evident from the FEAMR DB design that it can be used to get comprehensive data about AMR in microorganisms against all major classes of antibiotics, from various types of non-clinical samples across the globe.

4 Conclusion

Antimicrobial Resistance has become a public health challenge on an unprecedented global scale. Surveillance of AMR, with a focus on non-clinical samples, is crucial to monitor the progress of AMR from the One Health perspective. With zoonotic diseases on the rise, many times leading to pandemics, it is all the more important to have a dedicated food and environment-related AMR DB. The FEAMR database aims to fill this gap by providing exhaustive data concerning AMR associated with food and the environment globally. This may help in monitoring the spread of AMR from non-clinical sources and facilitate the global coordinated fight against AMR. It may also facilitate the discovery and development of new antibiotics. The data may be used to design algorithms to predict AMR hotspots and track the progression of AMR spread in food and the environment. The database may be linked to other databases such as CARD, NDARO, MegaRes, and NCBI Nucleotide to connect the surveillance of AMR with molecular aspects

of resistant microorganisms, thus providing comprehensive information to the users.

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Availability of Data and Materials The datasets used and/or analysed during the current study can be made available from the corresponding author on reasonable request.

Declarations

Conflict of Interest The authors declare that they have no competing interests.

Ethics Approval and Consent to Participate Not applicable.

Consent for publication Not applicable.

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