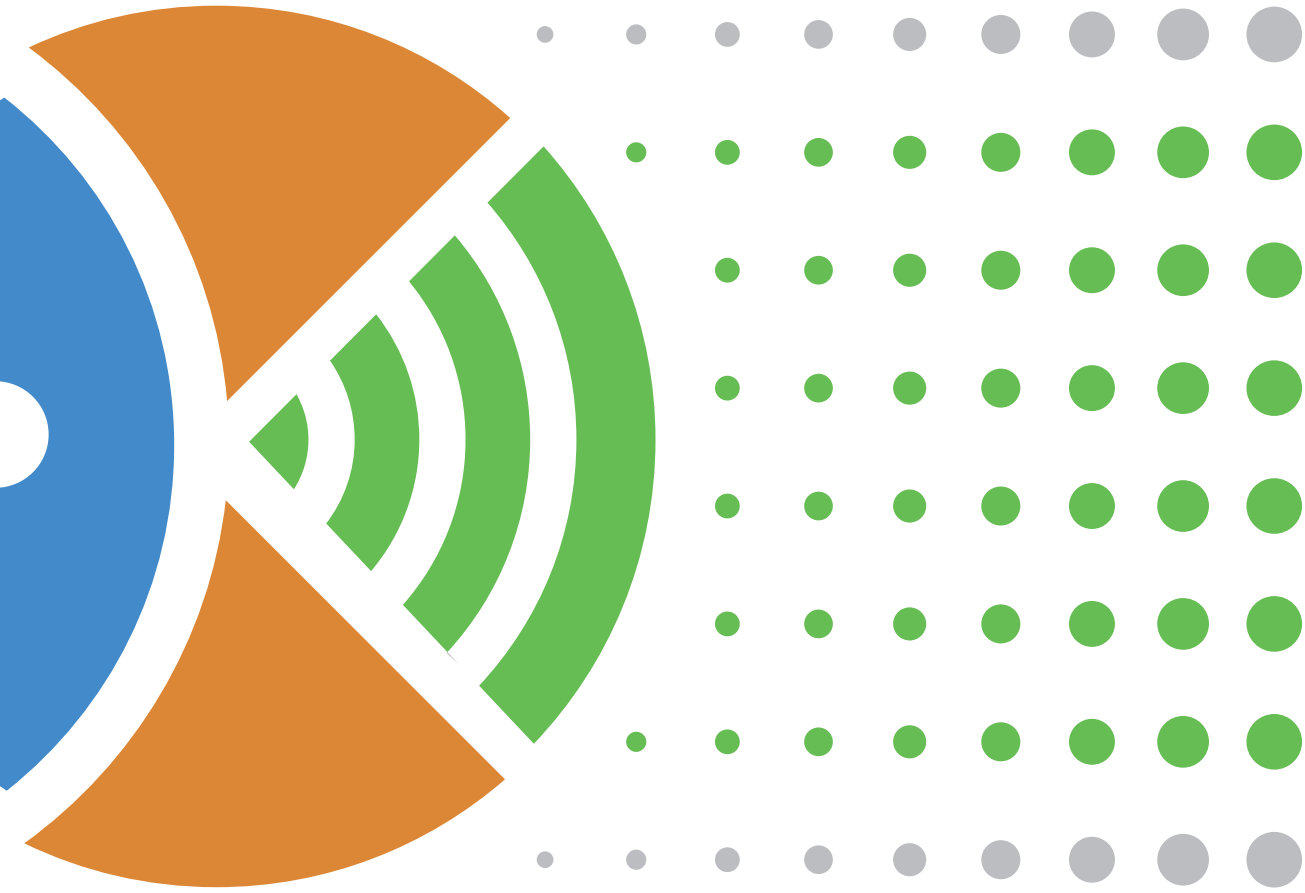
Food and Agriculture Organization of the United Nations

THE INTERNATIONAL FAO ANTIMICROBIAL RESISTANCE MONITORING (InFARM) SYSTEM

Manual for implementation

2024



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Foreword

In today's world, the challenges facing global food security and safety are more pronounced than ever. To meet this challenge, it is imperative that we increase the sustainability and resilience of our global agrifood systems, in line with the Sustainable Development Goals (SDGs). FAO's Strategic Framework 2022–2031 serves as our guide on this transformative journey encapsulating the ideals of better production, better nutrition, better environment, and better life for all.

Antimicrobials are vital tools in the prevention, control, and treatment of diseases in humans, aquatic and terrestrial animals, and crops. Their efficacy is crucial for maintaining productive and sustainable agrifood systems, upon which countless livelihoods depend worldwide. However, the escalating threat of antimicrobial resistance (AMR) jeopardizes the effectiveness of these critical medicines.

AMR looms as a "silent" pandemic, presenting one of the foremost global challenges. Its unchecked emergence and spread threatens recent advances in human and animal health, environmental integrity, food security, and economic prosperity, particularly impacting regions in the global south. Unmitigated AMR could substantially disrupt livestock production, with a possible 11 percent loss by 2050 in low-income countries.

FAO is proud to lead global efforts to address the threat of AMR in agrifood sectors. Collaborating with esteemed partners such as the United Nations Environment Programme (UNEP), the World Health Organization (WHO), the World Organisation for Animal Health (WOAH, formerly OIE), and a network of research and academic institutions, we adopt a multisectoral One Health approach to address this multifaceted challenge.

The International FAO Antimicrobial Resistance Monitoring (InFARM) system is an FAO flagship initiative, supporting countries to establish and reinforce operational national surveillance systems in line with international standards. InFARM empowers countries to generate reliable evidence to measure the extent of AMR in animals and food, at local, regional, and global scales, filling critical gaps in AMR data within agrifood systems.

This manual serves as a guide for country officials, providing a step-by-step approach to support the implementation of the InFARM system at a national level. It provides specific steps and recommendations to guide national focal points in mobilizing country participation through the collection and sharing of available AMR data, along with information on the status of implementation of monitoring and surveillance activities.

Through the InFARM system, FAO invites its Members to establish and strengthen operational national AMR surveillance systems to strengthen AMR data generation, sharing, and utilization. FAO is committed to providing evidence for decisive action against AMR to ensure resilient agrifood systems and safeguard the associated livelihoods and economies.

Thanawat Tiensin
Director and Chief Veterinarian, Animal Production and Health Division.
Food and Agriculture Organization of the United Nations

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Abbreviations

AMR	antimicrobial resistance
AMU	antimicrobial use
ANIMUSE	ANImal antiMicrobial USE Global Database (WOAH)
AST	antimicrobial susceptibility testing
CBP	clinical breakpoint
CLSI	Clinical and Laboratory Standards Institute
ECOFF	epidemiological cut-off value according to EUCAST
ECV	epidemiological cut-off value according to CLSI
EUCAST	European Union Committee for antimicrobial susceptibility testing
FAO	Food and Agriculture Organization of the United Nations
ATLASS	FAO's Assessment Tool for Laboratories and AMR Surveillance Systems
GISSA	Global Integrated System for Surveillance of AMR and AMU (Quadripartite)
GLASS	Global Antimicrobial Resistance and Use Surveillance System (WHO)
GLG	Global Leaders Group on AMR
InFARM	International FAO Antimicrobial Resistance Monitoring system
LIMS	Laboratory Information Management System
NAP	National Action Plan on AMR
NCC	National Coordinating Centre
GISSA	Global Integrated System for Surveillance of AMR and AMU
UNEP	United Nations Environment Programme
WHO	World Health Organization
WOAH	World Organisation for Animal Health (founded as OIE)

1. Introduction

1.1 BACKGROUND

Antimicrobial resistance (AMR) occurs when bacteria, viruses, fungi, and parasites no longer respond to antimicrobial medicines. The global spread of AMR is rapidly emerging as a major threat to human and animal health, as well as to plant health and the environment. In 2019 alone, 4.95 million deaths were estimated to be associated with bacterial AMR.[1] The same year, the World Health Organization (WHO) declared AMR to be a top-ten global public health threat facing humanity, with misuse and overuse of antimicrobials as the main drivers in the development of antimicrobial-resistant pathogens.[2]

The recent COVID-19 pandemic has underlined the fragility of health systems across the world, forcing governments and global organizations to shift paradigms to tackle global health challenges such as AMR. Given the intermingled web of transmission pathways of antimicrobial-resistant microorganisms across four major sectors – humans, animals, plants, and the environment – addressing AMR requires concerted action through an integrated One Health approach.[3] Integrated monitoring and surveillance of AMR and antimicrobial use (AMU) are critical across all sectors to ensure an effective One Health response. However, sectors not only face significant individual challenges in implementing and sustaining their efforts over time in their area of influence, but they also encounter collective issues related to data sharing and harmonization across all sectors. Additionally, all sectors confront major challenges including a scarcity of harmonized and high-quality data, unstable financing, poor laboratory infrastructure, and weak governance.

Currently, AMR data are mostly available for the human health sector and to a lesser extent for the animal sector associated with the agrifood chain, with a bias towards high-income countries. Furthermore, there is a paucity of data in the plant sector and the environment.[4] Most countries (~90 percent) have developed a multisectoral National Action Plan (NAP) to tackle AMR, including priority activities for AMR and AMU monitoring and surveillance, but in 2021 only ten percent of these plans had sustained funding for their implementation.

Antimicrobial resistance does not have geographical or sectoral borders, and governance structures to facilitate coordinated and multisectoral One Health collaboration are sometimes weak within and between countries. Additionally, even with national surveillance programmes in place, many countries do not utilize the data generated for risk analysis and decision-making processes, due to a lack of appropriate data capturing and management systems, questionable data quality, poorly defined responsibilities for data sharing, or insufficient expertise for analysis and interpretation of AMR data.[5]

AMR surveillance efforts across all sectors, and at all levels (global, regional, and national) need to be coordinated to strengthen technical capacities and infrastructure to generate and share good-quality harmonized AMR data that can be analysed and translated into action. FAO, together with the World Organisation for Animal Health (WOAH), the United Nations Environment Programme (UNEP) and the World Health Organization (WHO) (the Quadripartite), play a key role in supporting multisectoral One Health responses to AMR,

including integrated surveillance of AMR.[6] In 2021, during the 166th Session of the FAO Council, the FAO Action Plan on Antimicrobial Resistance 2021–2025 was adopted.[7] This Action Plan committed FAO to establishing a comprehensive global epidemiological information system to support countries on the systematic collection, collation, management, analysis, visualization, and use of AMR data in animals and food, contributing to the global integrated surveillance efforts made by the Quadripartite. In pursuit of this commitment, FAO embarked on the development and global rollout of the International FAO Antimicrobial Resistance Monitoring (InFARM) system.

InFARM builds on prior collective experience and knowledge gained by FAO and the Quadripartite organizations through the implementation of activities on surveillance capacity building.[8] These include the deployment of the FAO Assessment Tool for Laboratories and AMR Surveillance Systems (ATLASS)[9] and the extensive support on the development of national surveillance activities and programmes through the provision of guidelines and materials.

1.2 THE INTERNATIONAL FAO ANTIMICROBIAL RESISTANCE MONITORING (InFARM) SYSTEM

InFARM is a global information system consisting of an IT platform and related FAO activities that assist countries in collecting, collating, analysing, visualizing, and effectively utilizing their AMR monitoring and surveillance data primarily from livestock, fisheries, and aquaculture, along with their associated food products.[i]

The InFARM system is initially designed to host and present AMR data generated through phenotypic antimicrobial susceptibility testing (AST) from:

- priority bacterial species of public health significance, including zoonotic and foodborne pathogens and commensal indicator bacteria from animals and food sources; and
- bacterial pathogens causing impacts in animal health and productivity.

The implementation of InFARM adheres to international standards and recommendations set forth by the Codex Alimentarius Commission[10] and WOAH.[11]

InFARM is expected to play a pivotal role in assisting countries that are willing to share their AMR data in animals and food for global surveillance. It will act as the bridge for integrating these data with information from the WHO Global Antimicrobial Resistance and Use Surveillance System (GLASS)[12] and the WOAH ANImal antiMicrobial USE Global Database (ANIMUSE)[13] into the Quadripartite Global Integrated System for Surveillance of Antimicrobial Resistance and Antimicrobial Usage (GISSA).

In addition to its initial focus, FAO is currently expanding the scope of evidence-generation activities to other areas under the remit of the Organization, such as AMR monitoring in food production environments, monitoring of the use of antimicrobials in plant production and monitoring of antimicrobial residues in foods and the food production environment. The InFARM system will be adapted in the future to host and disseminate data generated from these expanding areas as per national, regional, and global needs.

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[i] The primary focus of the InFARM system is to gather AMR data primarily from livestock, fisheries, and aquaculture, along with their associated food products (i.e. agrifood sectors). However, the system and its IT platform also has the capability to incorporate AMR data from food production environments, and other animals, such as companion, recreational and wild animals, under a One Health lens and as part of the expanding efforts on AMR monitoring and surveillance.

1.3 InFARM GOAL AND OBJECTIVES

The goal of InFARM is to assist countries in developing and strengthening operational national surveillance systems that can efficiently contribute to generating reliable and timely AMR evidence in animals and food at national, regional, and global levels.

InFARM aims to achieve this overarching goal by pursuing specific objectives, at national, regional, and global level which include:

- encouraging countries to generate high-quality AMR data and contribute to global AMR evidence, regardless of the level of development and implementation of their national systems for AMR surveillance in animals and food sectors;
- enhancing existing capacities to meet global harmonized standards for AMR surveillance established by the Codex Alimentarius and WOAH;
- analysing and disseminating information to stakeholders including interactive data visualizations on AMR prevalence and trends in animals and food in a regular manner;
- detecting the emergence of new AMR traits at different geographical levels and monitor dissemination and trends;
- informing targets for the design, implementation, and monitoring of the effectiveness of evidence-based interventions against AMR in agrifood systems;
- aggregating data to estimate the extent and burden of AMR in animals and food sectors using selected indicators; and
- facilitating the integration of AMR surveillance information into risk analysis, decision-making, and monitoring and evaluation processes.

1.4 INFARM ROAD MAP

The InFARM system will be deployed by FAO in a progressive manner. FAO will administer and operate the application of a roadmap with three consecutive phases for implementation.

Early implementation phase (2023–2024)

In the early implementation phase, FAO is making the IT platform of the InFARM system available to countries through a first annual open call for baseline information on implementation of surveillance and AMR data and is facilitating the voluntary participation of countries in the system through the provision of tools, training, and guidance materials. The latter includes this manual.

BOX 1

This manual aims to provide:

- an introduction to the InFARM system and its roadmap for implementation;
- recommendations and technical specifications for countries to participate in the initial phases of the implementation of InFARM;
- a framework to support and harmonize the process of obtaining information on national surveillance activities and gathering AMR data from the different monitoring and surveillance programmes in animals and food sectors; and
- a description of data-sharing options, outlining reporting at different levels of confidentiality, and highlighting the benefits of an active engagement with the system.

This manual should be read in conjunction with:

- International standards on AMR:
  - Codex Alimentarius Guidelines on integrated monitoring and surveillance of foodborne AMR.[10]
  - WOAH standards:[11] Terrestrial Animal Health Code, Chapter 6.8., Harmonization of national antimicrobial resistance monitoring and surveillance programmes; Aquatic Animal Health Code, Chapter 6.4., Development and harmonization of national antimicrobial resistance monitoring and surveillance programmes for aquatic animals; Terrestrial Manual of Diagnostic Tests and Vaccines for Terrestrial Animals, Chapter 2.1.1., Laboratory methodologies for bacterial antimicrobial susceptibility testing.
- FAO Guidelines on monitoring and surveillance of antimicrobial resistance in bacteria from healthy food animals intended for consumption (Volume 1).[14]
- FAO guidelines on monitoring and surveillance of antimicrobial resistance in bacterial pathogens from aquaculture (Volume 3).[15]
- FAO and WOAH Guidelines on Monitoring of antimicrobial use at farm level (Volume 5).[16]
- Additional related FAO guidelines in preparation for the monitoring and surveillance of antimicrobial resistance, use and residues in food and agriculture: Monitoring of antimicrobial resistance surveillance in animal pathogens recovered from clinically or sub-clinically diseased livestock and poultry (Volume 2) (forthcoming); Monitoring of antimicrobial resistance in animal settings/environment (Volume 4) (forthcoming); Monitoring of antimicrobial residues in foods of animal origin (Volume 6) (forthcoming)
- Other additional existing guidelines and protocols developed at regional or country levels.

Additional activities in this phase of early implementation include:

- supporting InFARM national focal points through mentoring and training on AMR data collection, collation, management, analysis, visualization, and use;
- establishing interoperability of AMR data management solutions such as WHONET and BacLink software,[ii] AMR-related tools,[iii] or other locally-adapted Laboratory Information Management Systems (LIMS)[iv] with InFARM technical specifications. This integration aims to facilitate the standardized management and sharing of AMR data within the InFARM system;
- developing an IT solution to facilitate deployment and expansion of the FAO Assessment Tool for Laboratories and AMR Surveillance Systems (ATLASS). The information collected through FAO-ATLASS assessments will be essential to identify the level of reliability of the AMR data hosted in the InFARM system;[9]
- expanding the evidence-generation activities to additional areas under the remit of FAO such as monitoring of the use of antimicrobials as pesticides in plant production and protection; and
- continuous consultation with participating countries to obtain feedback on strengths and gaps identified during early implementation.

Expansion phase (2025–2026)

In this phase, FAO will launch the second and third open calls for countries to submit information on implementation of surveillance and AMR data, establishing a continuous annual cycle of data submission from participating countries. At the same time, InFARM system activities will be expanded to address barriers and gaps identified in the early implementation phase. Some potential gaps expected in the early implementation include limited knowledge of countries on the system and mechanisms to participate, and a scarcity of AMR data from specific surveillance programmes (e.g. AMR in diseased animals, or AMR in healthy aquatic animals and their environment). By addressing these gaps, it is expected to stimulate wider participation and coverage of the AMR information generated across all AMR surveillance programmes in animals and food. Furthermore, during this second phase of expansion, InFARM will actively strive for integration with other data platforms, underlining its dedication to harmonization and the interconnectedness of valuable data resources.

Additional activities in this phase of expansion include:

- developing detailed InFARM protocols for surveillance of AMR in specific food and agriculture domains enabling globally harmonized generation of epidemiological information and AMR data;
- incorporating into the InFARM system the mechanisms identified in the previous phase for a regular collection of data on antimicrobials used in plants;

[ii] WHONET has modules for laboratory configuration, data entry, data analysis, public health reporting, and data encryption among others. WHONET also includes a data import software called BacLink for the capture and standardization of data from existing desktop applications, laboratory instruments, and laboratory information systems to avoid the need for double-entry of data. More information: https://whonet.org/

[iii] https://dhis2.org/

[iv] https://www.izs.it/IZS/Cooperation/IZSAM_and_Africa/SILAB_for_Africa_Project

- regularly updating the interoperability between InFARM system and data management software; and
- integrating the InFARM system with the IT solution for digitalized deployment of the FAO-ATLASS tool.

Consolidation phase (2027–2030)

During this phase, FAO will further consolidate InFARM activities enabling annual reporting of global AMR prevalence and trends from an increasing number of countries willing to share their information publicly, and across all AMR surveillance programmes in animals and food. It is expected that in this phase, a growing number of countries will establish AMR surveillance systems covering animal health and public health purposes, and throughout all stages of the food chain, from primary production to food consumption. Global and regional consultations will be conducted to share InFARM data and key findings, and to obtain feedback, discuss lessons learned during previous phases, and set the way forward to continue supporting countries to strengthen their AMR surveillance capacities.

Additional activities in this phase of consolidation include:

- exploring mechanisms to incorporate AMR data generated through next-generation sequencing technologies;
- supporting integrated analyses of AMR and AMU data in animals and food, with human and environment sectors; and
- evaluating potential evolutions of the system in terms of mechanisms for collection, collation, analysis, visualization, and use of the data.

2. Recommendations for gathering AMR data in animals and food under the InFARM framework

Countries should design tailored AMR monitoring and surveillance programmes based on their national priorities, needs, capacities, and availability of resources to ensure relevance and sustainability. Additionally, countries should follow international guidelines and recommendations for harmonization of surveillance to ensure that the information produced is relevant for objectives set at national, regional, and global levels.

There are different approaches for the design and implementation of AMR monitoring and surveillance in animals and food depending on whether the prevailing purpose is to inform policies and interventions in public health, or to inform clinical decisions in veterinary medicine.

This section provides a framework and general recommendations for countries to collect, gather and organize systematically (i.e. to collate) the different types of AMR data generated in animals and food, fostering harmonization at national and international levels, and facilitating the preparation and submission of AMR data files into the InFARM system. The recommendations provided are compatible with international standards and guidelines from WOAH and Codex.[10, 11]

2.1 PURPOSE AND TARGET POPULATION OF MONITORING AND SURVEILLANCE PROGRAMMES

The purpose and target population for AMR monitoring and surveillance should be tailored to national priorities, and programmes should be designed and implemented to allow continuous improvement and expansion as resources permit.

There are two prevailing purposes for most of the monitoring and surveillance programmes: one is focused on protecting public health, while the other is focused on protecting animal health. Among these purpose-oriented groups, there are at least five different domains or programmes. The InFARM system, along with its IT platform, accepts data files that compile AMR data generated for both purposes throughout five monitoring and surveillance programmes:

- **three programmes** with the prevailing purpose of informing policies and interventions in **public health**, which include monitoring and surveillance in the following domains:
  - **healthy terrestrial animals** (potentially expanded to cover their production environment);
  - **healthy aquatic animals** (potentially expanded to cover their production environment); and
  - **food at processing and/or point of sale**.

These programmes identify and monitor the zoonotic and foodborne transmission of AMR from animals to humans and throughout the food chain. These are typically active surveillance programmes that employ systematic and scheduled sample collection methods, enabling control over statistical representativeness.

- **two programmes** with the prevailing purpose of informing clinical decisions and antimicrobial treatment effectiveness for protecting **animal health**, which include monitoring and surveillance in the following domains:
  - **diseased terrestrial animals**; and
  - **diseased aquatic animals**.

These programmes identify and monitor AMR profiles and trends in bacterial pathogens isolated from sick animals suffering from a bacterial infection. These are normally passive surveillance programmes relying on existing sources of isolates and/or data from veterinary diagnostic laboratories, such as routine clinical samples sent for bacteriology and AST. The nature of these programmes involves several sources of selection bias, making it more challenging to attain statistical representativeness.

2.2 SAMPLE SOURCES AND MICROORGANISMS

The sources of sampling, type of specimen and microorganisms largely depend on the surveillance purpose and programme. Therefore, the selection of specimen-bacteria combinations by animal species and surveillance programmes should be founded on international recommendations and standards.

As elaborated previously, the InFARM system can encompass up to five monitoring and surveillance programmes. For programmes with a prevailing **public health purpose**, samples should reflect the main food-producing animal species in the country and/or their national consumption patterns/levels, and the likely prevalence of foodborne AMR present at the relevant stages of the food chain where there is evidence of AMR dissemination or transmission (e.g. farm, slaughterhouse, point of sale). The following specimens and sources should be considered as priority for programmes with prevailing public health purpose:

- Faecal material from fresh faeces, boot swabs, and caecal content from animals entering the food chain, collected at farms (ideally in their last stage of production) or slaughterhouses should be considered for the **surveillance programme in healthy terrestrial animals**. Live finfish, crustaceans, and molluscs collected at the farm level should be considered for the **surveillance programme in healthy aquatic animals**. Additionally, samples from the immediate environment of food-producing animals[v] could also be considered for these surveillance programmes as an area of expansion.

[v] E.g. Soil, water, animal wastewater, sewage, manure, slurry, organic fertilizers, litter and bedding, and dust.

- Food specimens obtained from animal derived products such as meat (e.g. carcasses, fresh meat cuts), milk, eggs, post-harvest specimens from finfish, crustaceans, and molluscs, as well as from vegetables and fruits, or processed foods, should be considered for the AMR **surveillance programme in food at processing and/or point of sale**. These samples can be sourced from various points along the production and distribution chain, including slaughterhouses, processing plants, packaging facilities, wholesalers, and retailers. The selection of collection sites should be tailored to align with the country's production systems and consumer purchasing habits, potentially involving sampling at open markets and/or chain stores (supermarkets and butcher shops). Moreover, the methodology employed for specimen collection should be designed to minimize or eliminate disruption to regular production workflows or points of sale at the designated sampling locations.

The selection of microorganisms for these programmes should be based on their relevance to food safety and public health. Priority bacterial species/genus should include:

- foodborne pathogens such as *Salmonella* spp., *Campylobacter* spp., *Aeromonas* spp. or other foodborne pathogens, depending on national or regional epidemiology and estimated risks; and
- indicator bacteria such as *Escherichia coli* and Enterococci (e.g. *Enterococcus faecium* and *Enterococcus faecalis*), which can contaminate food and harbour transferable resistance genes.

For programmes with a prevailing **animal health purpose**, the main source of samples are usually veterinary diagnostic laboratories receiving clinical specimens (e.g. faeces, milk, urine, nasal/pharyngeal swabs, tissues/organs, blood) from suspected infections in diseased animals for the recovery of bacterial pathogens. For these programmes, samples collected should reflect predominant diseases in major animal species in the country for which antimicrobials are used, and the likelihood of potential impacts on productivity caused by antimicrobial treatment failure. These programmes are highly variable in terms of design, methodologies, target bacteria and interpretative criteria depending on the region or country.[17] Additionally, they strongly rely on a routine submission of clinical samples to veterinary diagnostic laboratories, which is not commonly practised in many parts of the world because of scarcity of financial or human resources, and the lack of regulatory frameworks for evidence-based use of antimicrobials. Despite these challenges, such submissions yield valuable information that can significantly enhance antimicrobial stewardship and awareness.

2.3 SCALE OF ACTIVITIES AND LEVEL OF REPRESENTATIVENESS OF THE AMR DATA

AMR data should be grouped into different categories according to the scale of monitoring and surveillance activities, and their level of statistical representativeness. The InFARM system and its IT platform accept AMR data files broadly categorized as:

- **Limited pilot monitoring and surveillance activities**: This category refers to point prevalence surveys, small-scale projects, or research studies with a limited geographical scope (e.g. provincial, state or district levels). These pilot activities can be using non-probability sampling methods based on convenience, judgement, or availability of samples, or more rigorous probability sampling methods allowing statistical inferences at local or subnational levels.[vi] These activities are aimed at gaining a preliminary understanding of AMR, assessing the potential impact of AMR in a specific area, validating designs and methodologies, and engaging key stakeholders before scaling up to national surveillance. Therefore, the AMR data in files classified under this category do not represent the national situation.
- **Pilot monitoring and surveillance activities**: This refers to point prevalence surveys, or larger-scale studies not performed regularly but with a national scope that can be used for testing surveillance protocols and/or operationalizing wider surveillance programmes. These pilot activities should use rigorous probability sampling methods allowing statistical inferences on AMR prevalence at national level.[6] These activities aim to strengthen national capacities and gather baseline information to guide future nationwide implementation of systematic and regular surveillance. The AMR data in files classified under this category statistically represent the national situation at a specific year or point in time.
- **National surveillance**: This refers to a systematic, regular, and ongoing process of collecting, analysing, and monitoring AMR data using rigorous probability sampling methods that allow statistical inferences at national level.[6] National surveillance is usually implemented under the umbrella of country frameworks, strategies, plans or procedures that can be integrated across different surveillance programmes or sectors, or can be in place for specific surveillance programmes in animals and food (see section 2.1). The goal of structured and systematic surveillance is to track and periodically assess the patterns and trends of AMR in priority food production sectors and at different stages of the food chain. The AMR data in files classified under this category statistically represent the national situation longitudinally.

[vi] Probability sampling methods involve selecting samples from a population in a way that each member of the population has a known and non-zero chance of being included in the sample. This ensures that the sample is representative of the population and allows for statistical inference. Common probability sampling methods include simple random sampling, systematic sampling, stratified sampling, and cluster sampling. Non-probability sampling methods do not rely on random selection and do not ensure that every member of the population has an equal chance of being included in the sample. While these methods are often less rigorous statistically, they can be useful in situations where probability sampling is impractical or impossible. Common non-probability sampling methods include convenience sampling, judgemental or purposive sampling snowball sampling and quota sampling.

2.4 MONITORING AND SURVEILLANCE PERIODS AND REPORTING CYCLES

The duration of monitoring and surveillance activities depends on the type of programmes, scale of activities, and level of representativeness outlined in sections 2.1 to 2.3. For instance, national surveillance in programmes for public health purposes may entail longer data production cycles compared to more limited pilot activities, such as point prevalence surveys, which typically have shorter durations.

The InFARM system and its IT platform define and accept AMR data generated from all samples collected within the same calendar year, spanning from January to December. Annually, the InFARM IT platform will be open for a defined period to receive AMR data files generated from testing samples collected over the previous year(s).

2.5 THE InFARM FRAMEWORK FOR AMR MONITORING AND SURVEILLANCE IN ANIMALS AND FOOD

The InFARM system and its IT platform operate under a framework to accommodate the varying levels of development and implementation of AMR monitoring and surveillance activities across countries, and to gather AMR data from a comprehensive range of microorganisms and associated specimens covering all the surveillance programmes in animals and food. This **InFARM framework** aims at supporting and harmonizing the process of obtaining information on national surveillance activities and collating AMR data in animals and food (Figure 1). AMR data submitted to InFARM should be collated based on monitoring and surveillance programmes, associated sampling sources and microorganisms, statistical representativeness, scale at which surveillance activities are implemented, and reporting cycles, as elaborated in sections 2.1 to 2.4 and as outlined within the InFARM framework. A more extended explanation on preparation of AMR data files is provided in section 3.2 of this manual and in Annex 1.

2.6 ADDITIONAL RECOMMENDATIONS

Panel of antimicrobials for susceptibility testing

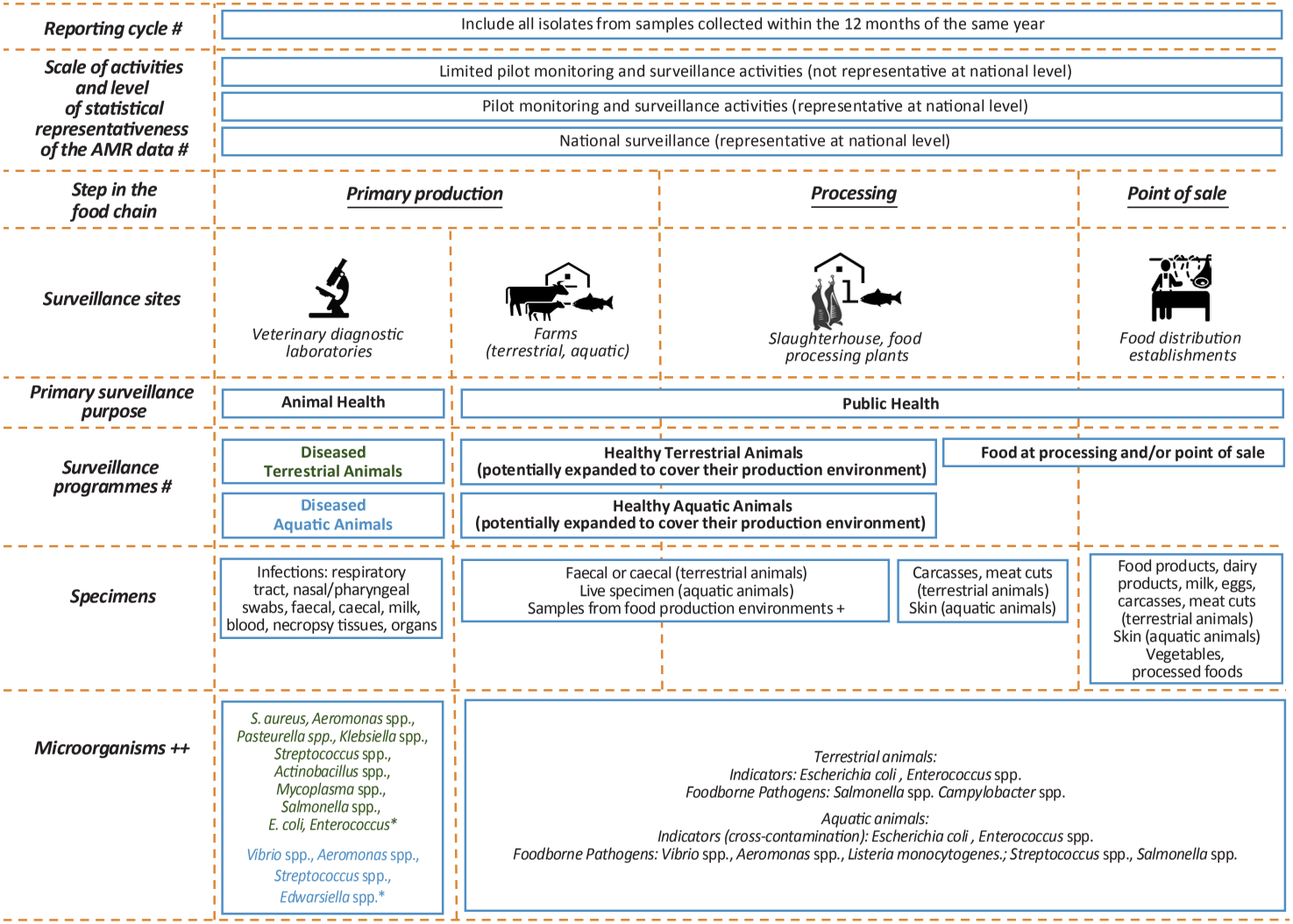
To select an appropriate panel of antimicrobials for phenotypic AST, it is recommended to follow international standards, while also customizing the selection to suit the specific needs of a country and the region. Detailed recommendations on suitable antibiotic panels can be found elsewhere.[14,15] Countries or regions may create their own antimicrobial panel with the same antimicrobial class representatives to ensure continuity and comparability of data. Regular reviews and updates of the antimicrobials panel might be necessary, considering observed trends in resistance and the emergence of new resistance patterns or mechanisms.

Generally, when the focus is on treating sick animals (i.e. animal health purpose), it is sensible to use antimicrobial panels tailored for animal-specific applications. However, when the objective is to compare data with AMR in human health for public health purposes (i.e. surveillance programmes for healthy animals and food sources), it is advisable to utilize panels relevant for human health, with potentially relevant veterinary-specific additions.

Efforts should be made to have panels including antimicrobials that represent:

- classes and uses in the relevant animal production sectors and pertinent for the country;
- higher priority ranking for human health and/or for animal health;[18,19] and
- increased selection or co-selection of resistance.

FIGURE 1
The InFARM framework for AMR monitoring and surveillance in animals and food



Attributes for gathering AMR data for submission into the InFARM system.
\+ E.g. Soil, water, animal wastewater, sewage, manure, slurry, organic fertilizers, litter and bedding, and dust.
++ The microorganism list depicted in the figure is not exhaustive.
* These are examples of bacterial pathogens in terrestrial (green) and aquatic (blue) animals that could be isolated from clinical samples in sick animals for the purpose of informing clinical decisions in animal health.
Source: Authors' own elaboration.

Additionally, disk contents (potencies) and/or minimum inhibitory concentration (MIC) ranges for AST should comply with the European Committee on Antimicrobial Susceptibility Testing (EUCAST)[20] (including the Veterinary Committee on Antimicrobial Susceptibility Testing [VetCAST])[21] or standards from the Clinical and Laboratory Standards Institute (CLSI).[22]

Interpretation of antibiotic susceptibility testing results

AMR data to be submitted into InFARM should be produced through standardized methods from internationally-recognized organizations, such as those of the recent versions of the CLSI and EUCAST AST methodology.[20,21,22] Interpretation of the AST results (MICs or disk diffusion inhibition zone diameters) should follow tables from EUCAST (including VetCAST) or from CLSI standards when available. This interpretation should categorize the isolates based on clinical breakpoints (CBPs) or epidemiological cut-off values (ECOFFs/ECVs). Countries are encouraged to consult these guidance documents regularly for any changes or updates to current CBPs/ECOFFs/ECVs.

Clinical breakpoints categorize isolates into resistant, intermediate,[vii] or susceptible, and are used for advising therapy, therefore they may differ between animal species or anatomical system affected. ECOFFs/ECVs categorize the isolates into wild type or non-wild type, without clinical context, and can be used for early detection of emerging acquired resistance, temporal analysis of trends, and comparability between isolates from different origins.

The choice between reporting CBPs and ECOFFs/ECVs values should depend on the surveillance methods implemented, purpose, and programme. Table 1 displays the recommended applications of AST interpretive criteria for each AMR surveillance programme under the InFARM framework.

In cases where internationally harmonized interpretive criteria have not been established, such as for the surveillance programmes on diseased or healthy aquatic animals, countries may develop interim epidemiological cut-off values based on their own laboratory data.[15] In such instances, InFARM will still accept the data if they are well-documented and consistently used for interpretation and reporting of AST results.

[vii] The "intermediate" category referred to in this manual and in CLSI standards is described as "susceptible, increased exposure" by EUCAST.

TABLE 1

Application of interpretive criteria, clinical breakpoint (CBP) or epidemiological cut-off values (ECOFF/ECV) for the different AMR surveillance programmes under the InFARM framework

Surveillance purpose	InFARM surveillance programmes	Interpretive criteria[#]		
		Human CBP	Animal CBP	ECOFF/ECV
Public health	Healthy terrestrial animals (potentially expanded to cover their production environment)	✓[+]	–	✓
	Healthy aquatic animals (potentially expanded to cover their production environment)	✓[+]	–	✓
	Food at processing and/or point of sale	✓[+]	–	✓
Animal health	Diseased terrestrial animals	✓	✓[*]	✓
	Diseased aquatic animals	✓	✓[*]	✓

[#] Given that interpretive criteria are subject to frequent updates, it is strongly advised that countries routinely monitor these changes.

[+] Human CBPs are particularly well-suited for surveillance programmes with public health purpose, for comparing with human health data and exploring the potential impact of AMR detected in animals and food.

[*] If CBPs for animal are available, they should be the preferred option for interpretation of AST results in diseased terrestrial or aquatic animal programmes.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3. Participation in InFARM

An invitation to participate in InFARM will be available online and will also reach countries through multiple channels on an annual basis including the network of Chief Veterinary Officers (CVOs), the International Food Safety Authorities Network (INFOSAN), the network of national Codex focal points, and other networks such as the FAO Members' gateway. This comprehensive approach to make InFARM accessible to all FAO Members aims to ensure that all national authorities responsible for AMR surveillance in animals and food are well-informed and equipped to engage effectively in the InFARM system.

3.1 REQUIREMENTS FOR PARTICIPATION

AMR surveillance in the animals and food sectors is at various stages of development and implementation across the world, therefore countries would be able to enrol in InFARM even if they are at the initial stages of establishing their surveillance programmes and if their ability to generate AMR data is limited. With the support of InFARM, countries are encouraged to progressively expand the scope of AMR surveillance activities towards the establishment of regular systematic surveillance at national level. As this expansion takes place, consideration should be given to covering all five programmes for AMR monitoring and surveillance defined under the InFARM framework.

The following sections define the general requirements for participation in InFARM. These requirements offer flexibility for countries to participate in the system according to their resources, infrastructures, capacity, and priorities for AMR surveillance.

Identify components of network(s) for monitoring and surveillance of AMR in animals and food

Countries are requested to identify the existing components (at any stage of development) that contribute to a national network(s) for surveillance in animals and food. Typically, this is determined during the national AMR surveillance planning stage where responsibilities of the network members are defined. For the purposes of AMR surveillance operationalization and technical oversight, there are typically three fundamental components that collectively form an ***AMR surveillance network***[23] (Figure 2):

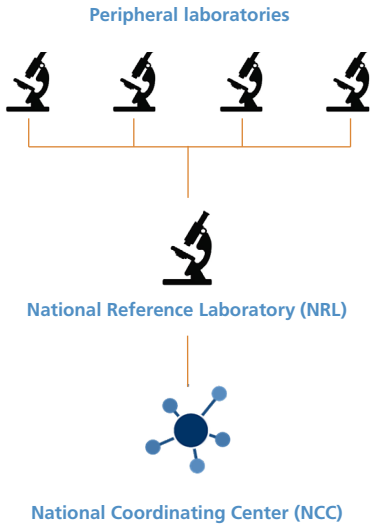
- **Peripheral laboratories**. A network of peripheral veterinary diagnostic and/or service laboratories primarily dedicated to processing samples received from different surveillance sites (farms, slaughterhouses, food wholesalers or retailers, and veterinary diagnostic laboratories) that contribute bacterial isolates for AMR monitoring and surveillance. These laboratories might be responsible for the primary isolation and sending the isolates to a reference laboratory for conducting AST, while in other cases they might perform AST themselves, depending on their capacities. Different networks of peripheral laboratories might exist under the remit or in collaboration with different ministerial bodies that provide oversight, for example, to the veterinary diagnostic laboratory network or food safety laboratory networks,

reflecting the different programmes for surveillance or mandates concerning animals and food in the country.

- **National Reference Laboratory (NRL)**. The NRL provides experience and expertise to the peripheral laboratories, supporting them in the harmonization of methods for bacterial isolation and characterization/identification, as well as in the detection and characterization of AMR, including the production and transmission of AST results and associated surveillance demographics about the sample or isolates. Some of its specific functions include the provision of external quality assurance and/or proficiency testing schemes to evaluate the quality of laboratory results and identify corrective actions. The NRL should advise on the inclusion of peripheral laboratories in the AMR surveillance network if they meet minimum quality assurance standards. Several NRLs might exist under diverse ministerial bodies, reflecting the different programmes for surveillance of AMR in animals and food.
- **National Coordinating Centre (NCC)**. A centralized structure overseeing the planning and implementation of AMR surveillance in animals and food is essential for alignment with national objectives. The NCC is typically multidisciplinary in nature to collectively address specific functions including but not limited to the development and/or revision of national AMR surveillance strategies, the coordination of AMR data collection, collation, analysis, and reporting processes, the dissemination of AMR results and have a key role in engaging diverse stakeholder groups. This structure could sit on national AMR steering committees, or in a multisectoral One Health coordinating group responsible for the implementation of the NAP on AMR, or it might be established at the ministerial level in epidemiology departments.

The structure, dynamics, and level of development of the AMR surveillance network(s) might vary from country to country depending on the level of integration of the different AMR surveillance programmes, and alignment of AMR surveillance activities with existing relevant programmes in animals and food (e.g. food safety, inspection, animal health). The three components of an AMR surveillance network described above might be customized for specific monitoring and surveillance programmes or could function to cover the entire food chain across all surveillance programmes. Some countries might have only some components of the network in place (e.g. only a NRL with absence of peripheral laboratories) for specific programmes, while others might have fully operational networks with all components.

FIGURE 2
Components of an AMR monitoring and surveillance network in animals and food



Source: Authors' own elaboration.

Identify national InFARM focal points

Countries are requested to identify and designate InFARM national focal points (InFARM-FPs) through officially established NCCs, or through other national bodies overseeing the planning and implementation of AMR surveillance in animals and food. In some cases, the focal points may be designated by the country's CVO or relevant authority with the animal health and production mandate in the country. Ultimately, the oversight of InFARM-FPs falls under the responsibility of national committees or bodies tasked with carrying out the implementation of the NAP on AMR.

InFARM-FPs may cover various tasks within all, several, or specific AMR surveillance programmes under the InFARM framework, based on the national surveillance network structure. Therefore, countries might require one or more InFARM-FPs to represent their needs and surveillance objectives. The coordination between these focal points is expected to be organized in a manner that is best suited to the country's circumstances.

BOX 2

InFARM Focal Points (InFARM-FPs) Profile

The InFARM-FPs should be national experts with knowledge and experience in microbiology and/or epidemiology, and data management of AST results originated from samples collected in animals and food. It is important for the InFARM-FPs to possess sufficient knowledge of national AMR surveillance and to have the authority to access national AMR data.

Specific roles and responsibilities that could be distributed among various national InFARM-FPs include:

- submitting and updating required documentation for countries' enrolment;*
- receiving and managing country user account credentials to access InFARM IT platform;*
- completing the AMR monitoring and surveillance components and implementation questionnaire(s);*
- collating national AMR data and producing AMR data files in compliance with the InFARM framework and technical specifications for submission into the IT platform. This includes ensuring the quality and reliability of the data;
- accessing interactive data visualizations for dissemination and action at national levels; and
- submitting AMR data files and validation of interactive data visualizations for migration into the global interface.

* These are minimum responsibilities of focal points when AMR data is not shared into the InFARM IT platform

Gradually establish national systems for monitoring and surveillance of AMR in animals and food

A fundamental requirement for countries participating in the InFARM system is their commitment to progressively enhance their capacities for national AMR surveillance in animals and food, thereby contributing to the global understanding of AMR. Countries should aim at increasing the scale of monitoring and surveillance activities and the level of representativeness of AMR data, progressively expanding their objectives and target population, while integrating all programmes throughout the food chain following the InFARM framework (Figure 1). By enrolling into InFARM, countries also commit to submit reliable information and high-quality AMR data[viii] in compliance with the technical recommendations in section 3.2. Therefore, designated laboratories within the surveillance networks generating AMR data to be submitted into InFARM, should adhere to minimum testing competence and quality assurance standards to ensure data reliability.

[viii] High-quality AMR data are generated by laboratories within the surveillance network employing reliable equipment and standardized methods for bacterial isolation and AST, as well as for interpretation and reporting of AST results. These processes undergo regular quality control to ensure precision and reliability.

Countries are encouraged to request support and follow FAO guidance for designing and implementing programmes for AMR monitoring and surveillance in animals and food. Through the implementation of the FAO Action Plan on AMR,[7] the Organization provides regular support to strengthen country capacities for AMR surveillance. One of FAO's flagship initiatives in this regard is the deployment of the FAO Assessment Tool for Laboratories and AMR Surveillance Systems (ATLASS).[9] This tool is designed to assess and define targets to improve national AMR surveillance systems in the food and agriculture sectors. The information obtained is used to feed into the calculation of progressive improvement pathway (PIP) stages, aimed at measuring different components and areas of country capacities for AMR surveillance systems on a scale from 1 to 5. ATLASS assessments provide a mechanism to identify the level of reliability of the AMR data received into InFARM.

3.2 RECOMMENDATIONS AND OPTIONS FOR SHARING INFORMATION AND AMR DATA WITHIN THE INFARM SYSTEM

The InFARM system offers a wide range of flexible options for countries to participate by:

- only sharing information on the level of development and implementation of AMR monitoring and surveillance through questionnaires (Annex 3); or
- by sharing both information about the development and implementation of AMR monitoring and surveillance through questionnaires (Annex 3), and national officially validated AMR data through different modalities and at different levels of confidentiality (Annex 1).

Submission of the enrolment and surveillance components and implementation questionnaires

As a first step for participation in InFARM, countries must complete an enrolment questionnaire document (Annex 2). Through this questionnaire, countries identify InFARM-FPs responsible for reporting information on the implementation of AMR surveillance and AMR data to InFARM. It also allows them to express the needs and commitment for progressively strengthening monitoring and surveillance capacities, and their agreement with the IT platform's Terms of Use. Upon validation, FAO grants access to the InFARM IT platform and focal points upload the enrolment questionnaire for verification and activation of their accounts.

The next step is for focal points to access the private interface of the InFARM IT platform to complete an online questionnaire on surveillance components and implementation (Annex 3). Focal points should provide responses based on their represented AMR monitoring and surveillance programmes. The aim of this questionnaire is to collect information on the components of AMR monitoring and surveillance networks and the level of implementation of activities.

Preparation and submission of AMR data

The InFARM IT platform is designed to host AMR data in priority bacterial species of interest for public health, animal health and indicator bacteria from animals and food under a flexible framework (Figure 1) covering activities at varying scales, purposes, and AMR surveillance programmes.

InFARM-FPs, in close coordination with the country's NCC or responsible authorities, are responsible for mapping, identifying, collating, and validating the AMR data under the AMR surveillance programme(s) they represent according to the InFARM framework (Figure 1). This means that an individual AMR data file for submission into the InFARM IT platform should be produced by collating AMR data generated:

i) from samples collected over the same calendar year;
ii) at the same scale of implementation of activities and statistical representativeness; and
iii) under the same surveillance programme.

These three attributes uniquely identify the AMR data files and enable stratification of the data for meaningful examination and analysis. For instance, all AMR data from samples collected over the year 2022 through regular systematic surveillance of healthy terrestrial animals, should be gathered to form an individual AMR data file (see Annex 1.1 for a more detailed explanation).

Additionally, AMR data files need to be prepared following a defined data model with essential variables and corresponding codes for harmonizing the organization and structure of the data received into the InFARM IT platform (see Annex 1.2).

Finally, AMR data files should undergo a comprehensive review and validation process to ensure adherence to the InFARM framework and technical data model specifications. Before uploading AMR data files into the InFARM IT platform, focal points should conduct visual inspections to ensure compliance with key technical checkpoints, as further detailed in Annex 1.3.

AMR data files that adhere to InFARM framework and technical specifications can be generated manually or automatically using data management software such as WHONET and BacLink, as well as Laboratory Information Management Systems (LIMS) locally adapted to align with the InFARM data model specifications.

An automated validation process is also incorporated through the submission of AMR data files into the IT platform. Initially, AMR data successfully uploaded into the platform will receive the status "*Draft*" allowing for continuous amendments. Once the InFARM focal point requests the online validation of the data submission, the status of the data is set as "*In Progress*". Following final validation by the InFARM coordination team at FAO, the data status will be promoted to "*Validated*" allowing the automatic production of interactive data visualizations in the private interface.

In case of any need for technical assistance or questions regarding the preparation of data files, focal points should contact the InFARM team at FAO-AMR-InFARM@fao.org.

Options for reporting AMR data files

The InFARM data model offers two modalities for reporting AMR data:

- **Option A**: Involves reporting AST results and associated metadata at the isolate level, with each row of the AMR data file corresponding to a distinct bacterial isolate.
- **Option B**: Entails reporting aggregated AST results, where each row in the AMR data file represents the count of isolates categorized as resistant, intermediate, susceptible, wild type, or non-wild type, and associated metadata for a specific bacterial genus/species/serotype.

Both reporting options are valid to share AMR data into the InFARM IT platform, however, countries are encouraged to report through option A when possible. Raw quantitative AST results (i.e. inhibition zone diameters including the disk content or MIC values) reported through option A are necessary when a retrospective analysis is needed due to changes in CBPs or ECOFF values. Quantitative results, as reported in option A, also allow early recognition of emerging AMR or reduced susceptibility through the analysis of AST results distributions, and reporting at isolate level enables the analysis of multidrug resistance patterns.

More details on AMR data preparation for each reporting option are provided in Annex 1.

Levels of confidentiality of AMR data files

The InFARM IT platform offers the countries the possibility of sharing individual AMR data files at three levels of confidentiality:

- **Level I. Private:** the AMR data file shared into the InFARM IT platform and associated interactive data visualizations will only be visible to the country InFARM focal point(s). Data shared at this level will not be included in regional, subregional, and global analyses.[ix] This level of confidentiality offers the highest privacy but also limits the possibility of understanding and interpreting the data as compared with other countries, subregions, regions or at global level.
- **Level II. Public with aggregation by region and subregion:** the AMR data file shared into the InFARM IT platform and associated interactive data visualizations will be visible to the country InFARM focal point(s). Data shared at this level will be included in the production of publicly available interactive data visualizations aggregating information at subregional, regional, and global levels, while keeping the identity of the country anonymized. This level of confidentiality offers the possibility of understanding and interpreting the data as compared to other subregions, regions or at global level.
- **Level III. Public showing country identity:** the AMR data file shared into the InFARM IT platform and associated interactive data visualizations will be visible to the country InFARM focal point(s). Data shared at this level will include the production of publicly available interactive data visualizations at country level (i.e. displaying country identity) and aggregating information at regional, subregional, and global levels. This level of confidentiality offers the possibility of understanding and interpreting the data as compared to other countries, subregions, regions or at global level.

All AMR data shared into the InFARM IT platform and associated interactive data visualizations will be accessible to specifically authorized FAO personnel, including the InFARM coordination team and selected personnel in decentralized offices with the purpose of efficiently managing and improving the IT platform as well as supporting the implementation of AMR surveillance activities in participating countries

[ix] InFARM uses the United Nations "Standard Country or Area Codes for Statistical Use" (M49) methodology to assign country names, geographical regions, and subregions. https://unstats.un.org/unsd/methodology/m49/

Countries are encouraged to share AMR data at levels II and III, preferably at level III, to make the best use of the AMR data shared as a global public good. All data shared at public levels (II and III) will be eventually migrated respecting the chosen level of confidentiality to the upcoming Quadripartite GISSA platform.

3.3 InFARM IT PLATFORM INTERFACES AND INTERACTIVE DATA VISUALIZATIONS

To ensure implementation of the different levels of confidentiality for AMR data files and associated interactive data visualizations, the InFARM IT platform has three different interfaces:

- **Private interface**. Exclusively accessible to users with credentials to access the InFARM system and its IT platform (i.e. InFARM-FPs in a same country and authorized FAO personnel). This interface provides countries with functionalities to manage submissions of AMR data files, and to access their country-level interactive data visualizations produced with data at "*Validated*" status in complete privacy.
- **Preview of the global public interface**. On an annual basis, after closing the annual open call for data, the AMR data with "*Validated*" status shared at public levels II and III will be promoted to data status "*pre-published*", enabling a migration of data from the private interface to the preview of the global public interface. This interface enables countries to preview in privacy the interactive data visualizations produced with data received at levels II and III from all countries. This includes data visualizations at country level (for AMR data at level III) and visualizations aggregating information from countries at subregional, regional, and global levels (for AMR data at levels II and III). The preview of visualizations will be available for a limited time allowing for validation and confirmation by InFARM-FPs before making the visualizations publicly available in the global interface. Countries reporting AMR data files only at private level I will not be able to access this interface as their information would not be shared globally.
- **Global public interface**. Upon validation and confirmation of visualizations in the preview of the public interface by countries sharing data at public levels II and III, the AMR data with data status "*pre-published*" will be promoted to "*published*" status. This will produce a migration of visualizations from the preview of the public interface to the global interface. Interactive data visualizations in the global interface will be produced on an annual basis and will be accessible without credentials to the public through the InFARM IT platform website https://infarm.fao.org/.

One of the key features of the InFARM IT platform is the automatic generation of interactive data visualizations across three interfaces, tailored to the levels of confidentiality in AMR data reporting. The visualizations in the InFARM dashboards offer a descriptive analysis of the AMR data submitted by countries, covering frequency distributions and summary statistics for AMR across a wide range of metadata, including animal species, sample types, sampling sites, and microorganisms. The countries would also be able to use such data visualizations to create their own technical reports and risk communication material as needed.

4. Contribution of AMR data in animals and food for One Health integrated surveillance

Integrated AMR and AMU surveillance is the continuous, collaborative, coordinated, and systematic collection, collation, analysis, interpretation, communication, and sharing of AMR and AMU data, and associated metadata. This includes data from various sectors, such as humans, animals, and products thereof, plants/crops and products thereof, and the environment, to produce harmonized information which can be used to inform decisions and actions aimed at reducing the burden of AMR and preserving the efficacy of antimicrobial agents.

Despite the recognition of the importance of AMR integrated surveillance to support a One Health response, sector-specific surveillance of AMR and AMU and sharing and comparability of data across different areas, currently face a significant number of challenges and gaps. Resource constraints and disparities in sector-specific surveillance systems, along with data unavailability, create substantial gaps in cross-sector data, hindering the realization of a comprehensive global One Health surveillance system for AMR.[4] To address this, the Quadripartite organizations have established standardized core and supplementary indicators for monitoring the implementation of the Global Action Plan on AMR across all sectors.[24] The Quadripartite Joint Secretariat has also established a technical group to provide advice and guidance on the development of global and context-appropriate regional and country-level systems for integrated surveillance. This group is called the Quadripartite Technical Group on AMR and Use Integrated Surveillance (QTG-AIS).[x] Finally, the Quadripartite is also developing the GISSA platform designed initially as a repository of data from the FAO-InFARM, WHO-GLASS, WOAH-ANIMUSE systems.

InFARM aims at addressing the existing gaps in availability of global AMR data in animals and food and is designed to act as a conduit for sharing these data for global surveillance into the GISSA platform. This will be an initial crucial step towards gaining a holistic evidence base for garnering political support, securing funding, and facilitating well-informed decision-making in the fight against AMR.

[x] https://www.who.int/groups/quadripartite-technical-group-on-integrated-surveillance-on-antimicrobial-use-and-resistance

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Annexes

Annex 1
InFARM data model for preparation of AMR data files

Download the InFARM data model in Excel here.*

The data model for the InFARM IT platform outlines the organization and structure of AMR data in alignment with the InFARM framework to be submitted and hosted on the IT platform. This model encompasses essential variables, their corresponding codes, and standardized options, all designed to streamline the sharing of harmonized AMR data in animals and food. Data files conforming to this data model can be created either by manual entry (Excel or CSV), or automatically using data management software such as WHONET and BacLink. Additionally, locally-adapted Laboratory Information Management Systems (LIMS) can be configured to align with the InFARM data model specifications. In this Annex, the process of AMR data preparation and submission is elaborated in further detail.

1.1 COLLECT AND COLLATE AMR DATA

The InFARM focal point(s) are well-equipped to efficiently collect and collate AMR data in a structured manner to create files that align with the InFARM IT platform requirements.

This process involves grouping the AMR data based on attributes and corresponding categories in alignment with the InFARM framework as indicated below (codes of the categories are indicated in brackets for subsequent use in naming the files):

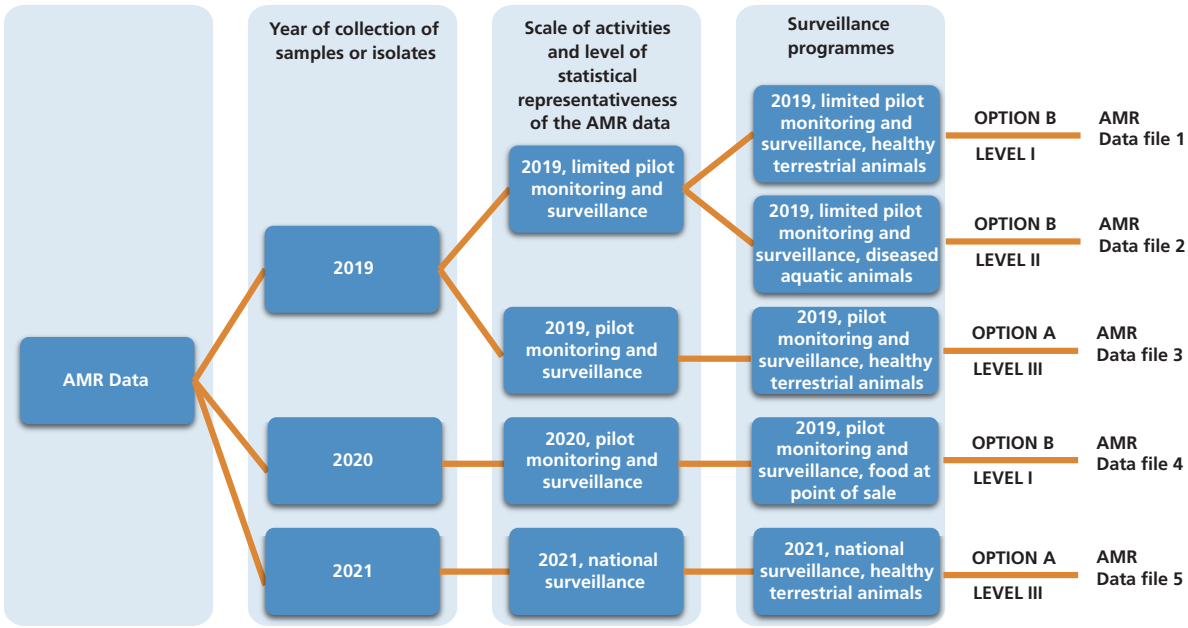
- **Year of sample collection**: data generated from samples collected as early as 2015 can be compiled for submission into the InFARM IT platform.
- **Scale of activities and statistical representativeness**: to reflect the level at which accurate AMR prevalence estimates can be drawn from the data, AMR data prepared for InFARM submission needs to be sorted into these three groups:
  - Limited pilot surveillance activities (e.g. point prevalence survey) representing a local level population (e.g. using non-probability sampling methods) (*Code:* ***PILOTLOC***)
  - Pilot surveillance (e.g. point prevalence survey) representing a national level population (e.g. using probability sampling methods) (*Code:* ***PILOTNAT***)
  - National surveillance (i.e. performed systematically and regularly) representing a national level population (e.g. following a national surveillance strategy that uses probability sampling methods) (*Code:* ***SYSTEMATIC***)
- **Surveillance purpose and programme**: AMR data intended for InFARM submission should be classified into these categories to reflect the type of surveillance data collected in food and agriculture:
  - Programme for healthy terrestrial animals (potentially expanded to cover their production environment) (*Code:* ***ANIMPH***)

* https://www.fao.org/docs/corporatenavigationlibraries/infarm/annex-1-infarm-datamodel.xlsx

- Programme for healthy aquatic animals (potentially expanded to cover their production environment) (*Code:* ***AQUAPH***)
- Programme for food at processing and/or point of sale (*Code:* ***FOODPH***)
- Programme for diseased terrestrial animals (*Code:* ***ANIMAH***)
- Programme for diseased aquatic animals (*Code:* ***AQUAAH***)

Next, all AMR data falling under the same categorization (e.g. AMR data from samples collected in 2022 through national surveillance of healthy terrestrial animals at farm or slaughterhouse level) should be gathered to form an individual *AMR data file*. Figure A1.1 below presents an example of how data should be collated in separated AMR data files for submission into the InFARM IT platform.

Figure A1.1
An example of how countries can categorize and collate their national AMR data to create InFARM data files



Source: Authors' own elaboration.

1.2 InFARM AMR DATA MODEL

Once the data is collated, InFARM focal points need to decide on the level of confidentiality and the reporting format for this individual AMR data file. The InFARM data model offers two reporting options:

- **Option A**: Involves reporting AST data at the isolate level, with each row of the AMR data file corresponding to a distinct isolate, providing specific information. (*Code for naming the file:* ***OPTA***)
- **Option B**: Entails reporting aggregated AST data, where each row in the file represents the count of isolates categorized as R, I, S, WT, NWT (resistant, intermediate, susceptible, wild type, non-wild type), for attributes including specimen, bacterial isolate, AST method, antimicrobial, and supplementary metadata. (*Code for naming the file:* ***OPTB***)

Core variables common for both model options (A and B)

Both data model options share some **core variables** displayed in Table A1.1 below.

TABLE A1.1

InFARM core variables in both data model option A and B. (Mandatory variables to be completed are written in italics and in blue)

VARIABLES ON LOCATION		
Variable name	**Description**	**Example**
YCOORD	• Latitude where samples were generated. If data contains multiple sampling locations, specify the different latitude/longitude combinations for every sample. If detailed location is not available, a proxy can be used for country, and/or lower country geographical administrative units (province, city, zip code, etc.). • Data type: floating-point number. • The response is user defined.	Costa Rica Latitude= 9.748917
XCOORD	• Longitude where samples were generated. If data contains multiple sampling locations, specify the different latitude/longitude combinations for every resistance rate as much as possible. If detailed location is not available, a proxy can be used for country, and/or lower country geographical administrative units (province, city, zip code, etc.). • Data type: floating-point number. • The response is user defined.	Costa Rica Longitude=-83.753428
ID_SITE	• Identification number/code of the sampling site, this is related to the origin variable or place where the sample was recovered/obtained? • Data type: text (max 20 characters). • The response is a user defined.	FARM28
VARIABLES ON THE ORIGIN OF THE SAMPLES/SPECIMENS/ISOLATES		
Variable name	**Description**	**Example**
ORIGIN	• Place where the sample/isolate was recovered. • Data type: categorical. • Follow predefined codes for ***ORIGIN***	SLA (= slaughterhouse)
ORIGIN_NOTES	• Additional notes, when 'Other' category is chosen from InFARM predefined codes. • Data type: text. • The response is user defined.	
SPECIES	• Animal species or food products where samples/ isolates were collected. • Data type: categorical. • Follow predefined codes for ***SPECIES***.	PIC (= Pigs-commercial)
SPECIES_NOTES	• Additional notes, when 'Other' category is chosen. • Data type: text. • The response is user defined.	
SPECIES_SCALE	• Scale of production. • Data type: categorical. • Follow predefined codes for **SPECIES_SCALE**.	BACK (= backyard type)

VARIABLES ON THE ORIGIN OF THE SAMPLES/SPECIMENS/ISOLATES		
Variable name	**Description**	**Example**
SPECIES_SCALE_NOTES	• Additional notes, when 'Other' category is chosen. • Data type: text. • The response is user defined.	
SPECIES_PROD	• Animal product (related to SPECIES). • Data type: categorical. • Follow predefined codes for **SPECIES_PROD**.	DAI (=Dairy)
SPECIES_PROD_NOTES	• Additional notes, when 'Other' category is chosen. • Data type: text. • The response is user defined.	
MARKET_CAT	• Market category. • Data type: categorical. • Follow predefined codes for **SPECIES_PROD**.	DOM (= Domestic)
MARKET_CAT_NOTES	• Additional notes, when 'Other' category is chosen. • Data type: text. • The response is a user defined.	
REASON	• Reason for taking the sample. • Data type: categorical. Follow predefined codes for **REASON**.	DX (= Diagnostic)
REASON_NOTES	• Additional notes, when 'Other' category is chosen. • Data type: text. • The response is a user defined.	
SPECIMEN	• Nature of the samples taken from animals or food from which isolate is recovered. • Data type: categorical. • Follow predefined codes for ***SPECIMEN***.	FAECES (=faeces)
SPECIMEN_NOTES	• Additional notes, when 'Other' category is chosen. • Data type: text. • The response is a user defined.	
VARIABLES ON BACTERIAL IDENTIFICATION		
Variable name	**Description**	**Example**
MICROORG	• Microorganism species identification. • Data type: categorical. • Follow predefined codes for ***MICROORG***.	ESCCOL (= *Escherichia coli*)
MICROORG_ SEROTYPE	• Serotype of isolates. • Data type: categorical. • Follow predefined codes for **MICROORG_SEROTYPE**.	SAL_TYP (= *Salmonella Typhimurium*)
RES_PHENOTYPE	• Resistance phenotypes. • Data type: categorical. • Follow predefined codes for **RES_PHENOTYPE**.	MRSA (=methicillin-resistant *Staphylococcus aureus*)

VARIABLES ON AST		
Variable name	**Description**	**Example**
GUIDELINE	• Guideline used to compare AST results against breakpoints. • Data type: categorical. • Follow predefined codes for *GUIDELINE*.	CLSI
GUIDELINE_VERSION	• Version of the guideline. • Data type: text. • The response is a user defined.	V09 2019
GUIDELINE_NOTES	• Additional notes, when 'Other' category is chosen. • Data type: text. • The response is a user defined.	
MET_AST	• Method for AST. • Data Type: categorical. • Follow predefined codes for *MET_AST*.	DD (= Disk diffusion)
INT_CRITERIA	• AST interpretation criteria (ECOFFs or ECVs CBPs). • Data type: categorical. • Follow predefined codes for *INT_CRITERIA*.	EC (= Epidemiological cut-off values)

Specific variables on data model Option A

In addition to the **core variables**, the variables below in Table A1.2 are specific for reporting AMR data following option A.

Please note that when there are duplicated isolates, the isolate with the most reliable result shall be included in the AMR data file for data model *option A* removing the duplicates. Nonetheless, it is possible to include duplicated isolates that were tested using different AST methods in the AMR data files.

TABLE A1.2
List of specific variables in the data model Option A and response example (mandatory variables to be completed are written in italics and in blue)

Variable name	Description	Example
ID_LAB	• Identification number/code of the laboratory where AST was done. The country should create encrypted codes for laboratories to anonymize the identity of the laboratory. • Data type: text. • The response is a user defined.	AH15
ID_ANIMAL	• Identification number/code of the animal from which the samples are taken. • Data type: text. • The response is a user defined.	CAT02
ID_SAMPLE	• Identification number/code for the sample from which isolates are obtained (for extrapolation of number of samples and number of positives in case targeted bacteria not detected is reported). • Data type: text. • The response is a user defined.	BRO_28

Variable name	Description	Example
ID_ISOLATE	• Identification number/code of the isolate. • Data type: date. • The response is a user defined.	I26
SPECIMEN_DATE	• The specimen collection date. • Data type: date. • The response is DD/MM/YYYY	20/01/2023
POOLED_SAMPLE	• Isolate recovered from pooled sample. • Data type: categorical. • The response is binary (Yes/No)	YES
CLONE_STRAIN	• Clone or strain. • Data type: categorical. • Follow predefined codes for **CLONE_STRAIN**.	MLST_ST (= Sequence type)
STRAIN_NOTES	• Additional information when selecting 'Other' for serotype, resistance phenotype or clone/strain. • Data type: text. • The response is a user defined.	
VALUE_XXX (XXX=antibiotic code in code list for ANTIBIOTIC)	• The antimicrobial susceptibility testing result (AST) value for antibiotic XXX. Value of MIC (µg/mL) or zone diameter (mm). The unit of the value will be automatically generated based on the MET_AST. • Data type: floating-point number. • **Important notes:** As this is a numeric variable it will not recognize special symbols, therefore please remove the mathematical symbols from the maximum and minimum range of dilutions. To do this, for the lowest concentration keep the original dilution, for example <0.5 to 0.5, while for the maximum dilution record the subsequent value in the dilution range, for example >64 to 128. Disc diffusion diameters have continuous numeric values while dilutions are discrete numeric values (0.015, 0.03, 0.06, 0.125, 0.25, 0.5, 1, 2, 4, 8, 16, 32, 64, 128, 256, 512, 1024, 2048).	VALUE_AMP = 10 (mm for DD method) VALUE_CTA = 0.25 (µg/mL for broth dilution method)
INT_XXX (XXX=antibiotic code in code list for ANTIBIOTIC)	• The antimicrobial susceptibility testing result interpretation for antibiotic XXX. • Data type: categorical. Follow predefined codes for ***INT_XXX***. • **Important note:** The interpretation based on epidemiological cut-off values should be Non-Wild Type (INT=NWT) and Wild Type (INT=WT). The interpretation based on clinical breakpoints should be Susceptible (INT=S), Intermediate (INT=I), and Resistant (INT=R)	INT_CIP_CODE = WT (for the isolate interpreted using epidemiological cut-off value) INT_CHL_CODE = R (for isolate interpreted using clinical breakpoints)

Specific variables on data model Option B

In addition to the core variables, the variables below in Table A1.3 are specific for reporting AMR data following option B.

In model B, when there are duplicated isolates, only the isolate with the most reliable result should be included in the AMR data file, removing duplicates.

TABLE A1.3
List of variables in the data model Option B and response example. (Mandatory variables to be completed are written in italics and in blue)

Variable name	Description	Example
ANTIBIOTIC	• Name of the antimicrobial compound used for susceptibility testing. • Data type: categorical. • Follow predefined codes for ***ANTIBIOTIC***.	AMP (= AMPICILIN)
CONCG	• Concentration of antimicrobial used for AST. For dilutions methods, this is the concentration expressed in µg/mL. For diffusion methods, this is the potency of the drug expressed in µg. In the case of antimicrobial mixtures, report the sum of the two concentrations. • Data type: floating-point number. • The response is user defined.	
BREAKPOINT	• Breakpoint used for AST. For diffusion methods, the breakpoint is expressed as <= the diameter value in mm of the growth inhibition zone. For dilution methods, the breakpoint is expressed as >= the value of the concentration µg/mL of bacterial growth inhibition. • Data type: floating-point number. • The response is user defined.	
S	• The number of susceptible isolates (a mandatory field if INT_CRITERIA is clinical breakpoint). • Data type: Numerical. • The response is user defined.	54
I	• The number of intermediate isolates (a mandatory field if INT_CRITERIA is clinical breakpoint). • Data type: Numerical. • The response is user defined.	10
R	• The number of resistant isolates (a mandatory field if INT_CRITERIA is clinical breakpoint). • Data type: Numerical. • The response is user defined.	62
WILD	• The number of wild type isolates (a mandatory field if INT_CRITERIA is epidemiological cut-off value). • Data type: Numerical. • The response is user defined.	0
NON_WILD	• The number of non-wild type isolates (a mandatory field if INT_CRITERIA is epidemiological cut-off value. • Data type: Numerical. • The response is user defined.	0

Variable name	Description	Example
UNK_NO_AST	• The number of isolates with unknown AST results/no AST performed. • Data type: Numerical. • The response is user defined.	5
UNK_NO_BP	• The number of no interpretation isolates. • Data type: Numerical. • The response is user defined.	21
N_SAMPLES	• The number of samples from animals or food commodities for isolation of bacteria and AST. • Data type: Numerical. • The response is user defined.	200
N_POSITIVE	• The number of samples from animals or food commodities with bacterial isolation. • Data type: Numerical. • The response is user defined.	126
N_AST	• The number of bacterial isolates tested for AST. • Data type: Numerical. • The response is user defined. • **Important notes:** we strongly recommend countries to fill in the information. If the total number of isolates is not known, the highest number of tests for specific antibiotic should be used instead.	126

Code lists for variables in Option A and B

The following code lists for variables are provided for informational purposes only. Please be aware that they may be expanded in future open calls based on country needs. For the most up-to-date code lists, please refer to the data model in Excel available at the following link: https://www.fao.org/docs/corporatenavigationlibraries/infarm/annex-1-infarm-datamodel.xlsx

TABLE A1.4
InFARM code lists for variables in model A and B

Variable ANTIBIOTIC ***(data model option B)***	**Name of the antimicrobial compound used for susceptibility testing**
Code	**Description**
AMC	Amoxicillin + clavulanic acid
AMX	Amoxicillin
AMP	Ampicillin
AZM	Azithromycin
PEN	Benzylpenicillin (Penicillin G)
CHL	Chloramphenicol
CIP	Ciprofloxacin
CLI	Clindamycin
COL	Colistin
FEP	Cefepime
CTX	Cefotaxime

Variable ANTIBIOTIC *(data model option B)*	Name of the antimicrobial compound used for susceptibility testing
Code	**Description**
TIO	Ceftiofur
CRO	Ceftriaxone
CAZ	Ceftazidime
LEX	Cefalexin
CZO	Cefazolin
FOX	Cefoxitin
DAN	Danofloxacin
DAP	Daptomycin
DOX	Doxycycline
ENR	Enrofloxacin
ETP	Ertapenem
ERY	Erythromycin
FLR	Florfenicol
FOS	Fosfomycin
GEN	Gentamicin
IPM	Imipenem
KAN	Kanamycin
LNZ	Linezolid
MAR	Marbofloxacin
MEM	Meropenem
NAL	Nalidixic acid
NEO	Neomycin
NOR	Norfloxacin
OXA	Oxacillin
OXY	Oxytetracycline
QDA	Quinupristin/Dalfopristin
RIF	Rifampicin
SOX	Sulfisoxazole
SMX	Sulfamethoxazole
SPT	Spectinomycin
STR	Streptomycin
TEC	Teicoplanin
TCY	Tetracycline
TIA	Tiamulin
TGC	Tigecycline
TIL	Tilmicosin

Variable ANTIBIOTIC *(data model option B)*	**Name of the antimicrobial compound used for susceptibility testing**
Code	**Description**
TMP	Trimethoprim
SXT	Trimethoprim/Sulfamethoxazole
TUL	Tulathromycin
TYL	Tylosin
VAN	Vancomycin
Variable MET_AST *(data model options A and B)*	**Antimicrobial susceptibility testing (AST) method**
Code	**Description**
AD	Agar gel dilution
AUTO	Automated instruments (VITEK, Phoenix)
BD	Broth macrodilution
BMICRO	Broth microdilution (Sensititre, MicroScan)
CGT	Concentration gradient test (ETEST)
DD	Disk diffusion
O	Others
UNK	Unknown
Variable CLONE_STRAIN *(data model option A)*	**Clone or strain**
Code	**Description**
MLST_ST	Sequence type
O	Other
Variable GUIDELINE *(data model options A and B)*	**Guideline**
Code	**Description**
CLSI	CLSI
EUCAST	EUCAST
O	Other (e.g. SFM)
Variable INT_XXX *(data model option A)*	**Interpretation code**
Code	**Description**
S	Susceptible
I	Intermediate
R	Resistant
NI	No interpretation
NS	Non-susceptible
WT	Wild type
NWT	Non-wild type

Variable INT_CRITERIA *(data model options A and B)*	AST interpretation criteria
Code	**Description**
CLIN	Clinical breakpoints human
CLIN_ANI	Clinical breakpoints animal
EC	Epidemiological cut-off values (ECOFF/ECVs)
Variable MARKET_CAT *(data model options A and B)*	**Market category**
Code	**Description**
DOM	Domestic
EXP	For exportation
IMP	Imported
MIX	Mixed
UNK	Unknown
O	Other
Variable MICROORG *(data model options A and B)*	**Microorganism**
Code	**Description**
ACIBAU	*Acinetobacter baumanii*¶
ACTPLE	*Actinobacillus pleuropneumoniae*¶
AERCAV	*Aeromonas caviae*#§†
AERHYD	*Aeromonas hydrophila*#§†
AERSAL	*Aeromonas salmonicida*#§†
AERSOB	*Aeromonas sobria*#§†
AERSPP	*Aeromonas* spp.#§†
AERVER	*Aeromonas veronii*#§†
AVBPAR	*Avibacterium paragallinarum*¶
CAMCOL	*Campylobacter coli**§¶
CAMJEJ	*Campylobacter jejuni**§¶
CAMSPP	*Campylobacter* spp.*§¶
CLOBOT	*Clostridium botulinum*§¶#
CLODIF	*Clostridium difficile*¶
CLOPER	*Clostridium perfringens*§¶
CLOSPP	*Clostridium* spp.§¶#
EDWANG	*Edwardsiella anguillarum*#
EDWICT	*Edwardsiella ictaluri*#
EDWPIS	*Edwardsiella piscicida*#
EDWSPP	*Edwardsiella* spp.#
EDWTAR	*Edwardsiella tarda*#
ENTFCL	*Enterococcus faecalis**¶§

Variable MICROORG *(data model options A and B)*	Microorganism
Code	**Description**
ENTFCM	*Enterococcus faecium*[*¶§]
ENTSPP	*Enterococcus* spp.[*¶§]
ESCCOL	*Escherichia coli*[*¶§†#]
KLEPNE	*Klebsiella pneumoniae*[¶]
LISMON	*Listeria monocytogenes*[§†]
MANHAE	*Mannheimia haemolytica*[¶]
MYCOSPP	*Mycobacterium* spp.[*†§ ¶#]
MYCGAL	*Mycoplasma gallisepticum*[¶]
MYCHYO	*Mycoplasma hyopneumoniae*[¶]
MYCSPP	*Mycoplasma* spp.[¶]
PASMUL	*Pasteurella multocida*[¶]
PSEUAER	*Pseudomonas aeruginosa*[¶]
PSEUSPP	*Pseudomonas* spp.[¶]
SALSPP	*Salmonella* spp.[*¶†§]
STAAUR	*Staphylococcus aureus*[¶]
STAHYI	*Staphylococcus hyicus*[¶]
STAPSE	*Staphylococcus pseudintermedius*[¶]
STREPAGA	*Streptococcus agalactiae*[¶#†]
STREPDYS	*Streptococcus dysgalactiae*[¶#†]
STREPHO	*Streptococcus phocae*[#†]
STREPIN	*Streptococcus iniae*[#†]
STREPSPP	*Streptococcus* spp.[#†¶]
STREPSUI	*Streptococcus suis*[¶]
STREPUBE	*Streptococcus uberis*[¶]
VIBALG	*Vibrio alginolyticus*[#]
VIBANG	*Vibrio anguillarum*[#]
VIBCHO	*Vibrio cholerae*[#†§]
VIBPAR	*Vibrio parahaemolyticus*[#†§]
VIBSPP	*Vibrio* spp.[#†§]
VIBVUL	*Vibrio vulnificus*[#†§]
YERRUS	*Yersinia ruckeri*[#]
ND	Targeted bacteria non detected
O	Other microorganism

Variable MICROORG_SEROTYPE *(data model options A and B)*	
Code	**Description**
SAL_CHOL	*Salmonella* Choleraesuis
SAL_DUB	*Salmonella* Dublin
SAL_ENT	*Salmonella* Enteritidis
SAL_HEI	*Salmonella* Heidelberg
SAL_INF	*Salmonella* Infantis
SAL_KEN	*Salmonella* Kentucky
SAL_TYP	*Salmonella* Typhimurium
O	Other
Variable ORIGIN *(data model options A and B)*	**Place where the sample was recovered (e.g. farm, slaughterhouse)**
Code	**Description**
FAR	Farm[*†¶#]
HOM	Home[*†§¶#]
LAB	Laboratory[¶#]
MAR	Outdoor market[§]
PET	Pet store[¶#]
SLA	Slaughterhouse[*§]
STO	Food store[§]
VEH	Veterinary hospital[¶#]
VET	Veterinary clinic[¶#]
WIL	Wild animals[*†¶#]
UNK	Unknown
O	Other
Variable REASON *(data model options A and B)*	**Reason for taking the sample**
Code	**Description**
DX	Diagnostic
FUP	Follow-up
OUT	Outbreak investigation
RES	Research
ROU	Routine screening
SP	Special screening
UNK	Unknown
O	Other

Variable RES_PHENOTYPE *(data model options A and B)*	
Code	**Description**
CARB	Carbapenemases-producing organism
CREC	Colistin-resistant *E. coli*
CRSAL	Colistin-resistant *Salmonella*
ESBL	Extended spectrum beta-lactamase producing Enterobacterales/Enterobacteriaceae
MRSA	Methicillin-resistant *Staphylococcus aureus*
VRE	Vancomycin-resistant Enterococci
O	Other
Variable SPECIES *(data model options A and B)*	**Animal species or food products where samples/isolates were collected**
Code	**Description**
AMP	Amphibians[§#]
BEE	Bees[¶]
BRO	Broilers – commercial production for meat[*¶§]
BUF	Buffaloes (not *Syncerus caffer*)[*¶§]
CAM	Camelidae[§]
CAN	Dog[¶]
CAT	Cattle[*¶§]
CER	Cervidae (farmed)[*¶§]
CRU	Crustaceans-Penaeids (e.g. shrimp)[§†#]
DUC	Duck[*¶§]
EQU	Equidae (Horse, Donkey, Mule)[*¶*¶§]
FCI	Fish-Cichlids (e.g. tilapia)[§†#]
FCY	Fish-Cyprinids (e.g. carp)[§†#]
FEL	Cat[¶]
FMA	Fish-Marine[§†#]
FSA	Fish-Salmonids (e.g. salmon, trout)[§†#]
FSI	Fish-Siluriformes (e.g. catfish)[§†#]
GOA	Goats[*¶§]
INS	Insect[*¶§]
LAY	Layers – commercial production for eggs[*¶§]
MOL	Molluscs (e.g. shellfish)[§†#]
OAA	Other aquatic food-producing animals[§†#]
OANF	Other aquatic non-food-producing animals[#]
OPO	Other commercial poultry[*¶§]
OTA	Other terrestrial food-producing animals[*¶§]
OTNF	Other terrestrial non-food-producing animals[¶]

Variable SPECIES *(data model options A and B)*	Animal species or food products where samples/isolates were collected
Code	**Description**
PIB	Pigs-backyard[*¶§]
PIC	Pigs-commercial[*¶§]
POB	Poultry – backyard[*¶§]
PROA	Animal processed food products[§]
PROP	Plant food products[§]
RAB	Rabbits[*¶§]
REP	Reptiles (e.g. crocodiles)[§#]
SHE	Sheep[*¶§]
SHG	Sheep and goats (mixed flocks)[*¶§]
TUR	Turkey[*¶§]
O	Others
UNK	Unknown
Variable SPECIES_PROD *(data model options A and B)*	**Animal product**
Code	**Description**
BREE	Breeding
DAI	Dairy
EGG	Egg
FUR	Fur
MEAT	Meat producing
MUL	Multipurpose
PET	Companion animals
RAC	Racing
RES	Research
WIL	Wild
WOO	Wool
WOR	Working
ZOO	Zoo animal
UKN	Unknown
O	Other

Variable SPECIES_SCALE *(data model options A and B)*	Scale of production
Code	**Description**
BACK	Backyard-type
EXT	Extensive
FREE	free range
INT	Intensive
SMINT	Semi intensive
O	Other
Variable SPECIMEN *(data model options A and B)*	**Nature of the samples taken from animals or food from which isolate is recovered**
Code	**Description**
BLOOD	Blood[¶#]
BRAIN	Brain[¶#]
CARCASS	Meat carcasses[§]
CECUM	Caecum[*¶]
EAR	Ear[¶]
EGGS	Eggs[§]
ELIT	Litter and bedding[*]
EMAN	Manure (environment)[*]
ESOI	Soil[*]
EWAS	Animal wastewater or sewage[*]
EWAT	Water[#*†]
EYE	Eye[¶#]
FAECES	Faeces[*¶]
FRESH	Fresh or ice preserved products (aquatic products)[§]
HEMO	Hemolymph[#]
HEPA	Hepatopancreas[#]
INN	Inner organ (lungs, liver, spleen, kidney)[¶#]
INTESTINE	Intestine/gut[¶#*]
KIDNEY	Kidney[¶#]
LIVER	Liver[¶#]
LIVS	Live specimen (fish)[†]
LUNGS	Lungs[¶#]
LYMPH	Lymph nodes[¶#*]
MEAT	Meat[§]
MEATP	Processed meat[§]
MILK	Milk[§]
MILKP	Processed milk product[§]

Variable SPECIMEN *(data model options A and B)*	Nature of the samples taken from animals or food from which isolate is recovered
Code	**Description**
PFRU	Fruits[§]
PVEG	Vegetables[§]
RIN	Meat rinsates[§]
SKIN	Skin[¶#§]
SPLEEN	Spleen[¶#]
URINE	Urine[¶]
UNK	Unknown
O	Other

For relational purposes with surveillance programmes

[*] Healthy terrestrial animals (potentially expanded to cover their production environment)

[†] Healthy aquatic animals (potentially expanded to cover their production environment)

[§] Food at processing or point of sale

[¶] Diseased terrestrial animals

[#] Diseased aquatic animals

1.3 NAMING AND VALIDATING INFARM AMR DATA FILES

AMR data files should be named using the attributes and codes in Annex section 1.1 and section 1.2. corresponding to the year of sample collection, scale of activities and level of statistical representativeness, and surveillance programme, along with the chosen reporting option (A or B). Additionally, the file name should begin with the ISO country code, which can be found at this link: https://unstats.un.org/unsd/methodology/m49/.

For instance, if the AMR data belongs to Italy, the samples were collected in 2022, as part of national surveillance for healthy terrestrial animals, and data is reported through option A, the name of the AMR data file should be named as follows: ITA_2022_SYSTEMATIC_ANIMPH_OPTA.

Before sending the data, focal points are requested to review and validate AMR data files. The validation procedure includes both a visual inspection and a technical check to ensure compliance with the InFARM IT platform's specifications before electronically submitting the data.

Table A1.5 provides some critical checkpoints for validating the InFARM AMR data files.

TABLE A1.5
Summary of checkpoints for validating the AMR data file according to InFARM requirements.

Checkpoints	Description	Comments
Consistency of monitoring and surveillance purposes with reported origin of samples/isolates and surveillance sites	Check if the purpose and programme of AMR monitoring and surveillance are consistent with the origin of the samples/isolates and ensure that it is reflected in the number of surveillance sites from which samples originated, in alignment with the InFARM framework.	If the samples/isolates are from diseased animals, the samples should be from diagnostic laboratories or farms, not from slaughterhouses or food points of sale. If the samples/isolates are from healthy terrestrial animals, the surveillance sites should be from farms and/or slaughterhouses and not from diagnostic laboratories or food points of sale. If the samples/isolates are from food at processing or point of sale, the surveillance sites should be slaughterhouses or food points of sale.
Reporting on mandatory data model variables	As a minimum, ensure that all mandatory data variables are completed.	The mandatory variables in both data model options A and B include origin, animal species, specimens, microorganisms, antibiotics, guideline used, guideline version, AST method, and selected interpretation criteria. For data model option A, it is required to complete the values of AST (MIC in µg/mL, or zone diameter in mm) and the interpretation results for at least one antibiotic. For data model option B, it is required to complete the sets of numbers for aggregated interpretation results (number of resistant, intermediate and susceptible isolates or number of isolates classified as wild or non-wild type when).

Checkpoints	Description	Comments
Alignment between the purpose of monitoring and surveillance and AST interpretation criteria used	Ensure the recommended interpretation criteria is selected and aligned with the monitoring and surveillance purpose and programme as per table 1 in the main text of this manual.	For the healthy terrestrial and aquatic animals, as well as for food at processing and/or point of sale, it is recommended to use human clinical breakpoints or epidemiological cut-off values. For diseased terrestrial and aquatic animals, it is recommended to use animal clinical breakpoints or epidemiological cut-off values when specific animal breakpoints are unavailable. Furthermore, it is advisable to adhere to international standards such as CLSI or EUCAST and use the latest available versions whenever possible.
Alignment between the interpretation criteria selected and the categorization of AST results	Ensure the consistency or correspondence between the AST criteria used to interpret AST results and their categorization.	For data model option A, when the interpretation criteria selected are clinical breakpoints, the interpretation results should be categorized as Susceptible (S), Intermediate (I), and Resistant (R). When the interpretation criteria are epidemiological cut-off values, the results should be categorized as Wild Type (WT) and Non-Wild Type (NWT). For data model Option B, when the interpretation criteria selected are clinical breakpoints, the variables to report on are the number of Susceptible, Intermediate, and Resistant isolates. When the interpretation criteria are epidemiological cut-off values, the number of isolates should be completed under the variables to report on number of Wild Type and Non-Wild Type isolates.

Annex 2
Enrolment request form

Download the enrolment form here.*

FAO has developed this enrolment request form to join the International FAO Antimicrobial Resistance (InFARM) system. The questionnaire allows countries to identify national focal point(s) (InFARM-FPs) responsible for reporting data to InFARM and express the needs and commitment for progressively strengthening monitoring and surveillance capacities.

The InFARM-FPs are requested to fill and return this enrolment request form to FAO-AMR-InFARM@fao.org. Upon FAO internal validation, the focal point(s) will receive the credentials and instructions necessary to access the InFARM IT platform and further guidance on the next steps for submission of AMR surveillance information and InFARM AMR data files.

* https://www.fao.org/docs/corporatenavigationlibraries/infarm/annex-2-infarm-enrollment-questionnaire.docx

Annex 3

Monitoring and surveillance components and implementation questionnaire

Download the surveillance questionnaire here.*

The purpose of the monitoring and surveillance components and implementation questionnaire is to collect information on the monitoring and surveillance activities on antimicrobial resistance (AMR) in food and agriculture sectors undertaken by countries enrolled in the InFARM system. The information gathered will also provide a contextualized interpretation of the interactive data visualizations produced from the AMR data submitted by countries. The surveillance questionnaire is intended to be filled online by nominated InFARM-FPs with access to the private interface of the InFARM IT platform.

* https://www.fao.org/docs/corporatenavigationlibraries/infarm/annex-3-infarm-surveillance-questionnare.docx

Resource partners:

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