Food and Agriculture
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THE INTERNATIONAL FAO ANTIMICROBIAL RESISTANCE MONITORING (InFARM) SYSTEM

Handbook with additional instructions to participate
in the data call 2025

Updates to the enrolment process, enhancements to the data model, expanded guidance for AMR data preparation and submission, and strengthened validation checks

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1. Introduction

This document has been developed for national InFARM focal points (FP's), national AMR surveillance data managers, and national AMR data analysts or epidemiologists involved in data preparation and submission to the InFARM IT platform during the 2025 data call.

It describes the updated enrollment process, additions to the InFARM data model, including additions to its code list, priority combinations of variables and codes specific to surveillance programmes, and validation checks.

This document expands upon the already existing methods and list of variables available in the manual for implementation of InFARM[1].

The updated materials are available in the following links and in the website https://www.fao.org/antimicrobial-resistance/resources/infarm-system/en/:

- InFARM Data Model https://www.fao.org/docs/corporatenavigationlibraries/infarm/annex-1-infarm-datamodel.xlsx
- InFARM enrolment request https://www.fao.org/docs/corporatenavigationlibraries/infarm/annex-2-infarm-enrollment-questionnaire.docx
- InFARM surveillance implementation questionnaire. https://www.fao.org/docs/corporatenavigationlibraries/infarm/annex-3-infarm-surveillance-questionnare.docx

2. Updates in the enrolment process

Focal points will no longer be required to accept the Terms of Use (ToU) through the enrollment questionnaire. Instead, submitting the enrollment request with the contact details of focal points will be sufficient to generate credentials and grant access to the IT platform. Acceptance of ToU will be requested in the first log-in into the IT platform.

Below is a detailed description of the updated enrollment process for the InFARM data call 2025:

i. FAO sends an invitation to countries to join the data call through official channels (e.g. Chief Veterinary Officers Network, Codex Alimentarius Focal Points, INFOSAN and others) reaching Ministries of Agriculture (and Ministries of Fisheries and Aquaculture if existing), Food Safety Authorities and Ministries of Health where applicable.
ii. Country officials respond to the invitation by completing the enrollment request with names, position and email address of InFARM Focal Point(s) per surveillance programme and submit it to FAO-AMR-InFARM@fao.org.
iii. FAO will validate the enrollment request and send the credentials to access the InFARM IT platform to the email address/es of designated InFARM focal point(s).
iv. Upon first access to the InFARM IT platform, InFARM focal point(s) will be prompted to accept the InFARM ToU.
v. After accepting the ToU, focal point's accounts will be automatically enrolled in the platform and will be able to participate by completing surveillance questionnaire and reporting AMR data files.

3. Enhancements to the InFARM data model

Based on data quality checks of previous AMR data submissions and requests from countries during the 2024 InFARM data call, the InFARM data model has been updated to allow the submission of additional variable categories, enhancing the overall comprehensiveness of data received by the InFARM IT platform. The newly added variable categories allow countries to submit additional results regarding the antibiotics tested, interpretation criteria, microorganisms, and specimen types.

Additionally, the following codes have been removed from the code list under MICROORGANISM, codes *ND* and *O;* and under SPECIMEN, codes *UNK* and *O* in programmes with public health purposes but retained in programmes with animal health purpose). As guidance in selecting the appropriate specimen when not in the list, it is encouraged that countries use the closest option available as proxy. For example, a surface swab from surfaces covered with fecal material or manure from farms could be categorized as FAECAL. Please send an email to FAO-AMR-InFARM@fao.org if you would like further guidance or to request the inclusion of additional codes for both MICROORGANISM and SPECIMEN.

Table 1. New category codes in existing variables of the InFARM data model

Data model option	Existing variable	Newly added codes	Corresponding labels (*description*)
A and B	**ANTIBIOTIC**	AVI	Avilamycin
		BAC	Bacitracin
		FLM	Flumequine
		LVX	Levofloxacin
		OXO	Oxolinic acid
A and B	**INT_CRITERIA**	O	Other[a]
A and B	**MICROORG**	BORBCH	*Bordetella bronchiseptica*
		BRAHYO	*Brachyspira hyodysenteriae*
		BRAPIL	*Brachyspira pilosicoli*
		BRASPP	*Brachyspira spp.*
		ENTCEC	*Enterococcus cecorum*
		ENTHIR	*Enterococcus hirae*
		ERYRHU	*Erysipelothrix rhusiopathiae*
		FLAPSY	*Flavobacterium psychrophilum*
		FLACOL	*Flavobacterium columnare*
		GALANA	*Gallibacterium anatis*
		GLAPAR	*Glaesserella parasuis*
		MORBOV	*Moraxella bovis*
		MYCBOV	*Mycoplasma bovis*
		MYCSYN	*Mycoplasma synoviae*
		ORNRHI	*Ornithobacterium rhinotracheale*
		PROSPP	*Proteus* spp.
		STAXYL	*Staphylococcus xylosus*
		STASPP	*Staphylococcus* spp.

Data model option	Existing variable	Newly added codes	Corresponding labels (*description*)
		TRUPYO	*Trueperella (Arcanobacterium) pyogenes*
A and B	**MICROORG_SEROTYPE**[b]	SAL_AGO	*Salmonella* Agona
		SAL_ANA	*Salmonella* Anatum
		SAL_CER	*Salmonella* Cerro
		SAL_DER	*Salmonella* Derby
		SAL_JAV	*Salmonella* Java
		SAL_JAN	*Salmonella* Javiana
		SAL_JHN	*Salmonella* Johannesburg
		SAL_LON	*Salmonella* London
		SAL_MBA	*Salmonella* Mbandaka
		SAL_MON	*Salmonella* Montevideo
		SAL_MUE	*Salmonella* Muenchen
		SAL_MSR	*Salmonella* Muenster
		SAL_NEW	*Salmonella* Newport
		SAL_READ	*Salmonella* Reading
		SAL_SCZ	*Salmonella* Schwarzengrund
		SAL_SPL	*Salmonella* Saintpaul
		SAL_STA	*Salmonella* Stanley
		SAL_THM	*Salmonella* Thompson
		SAL_UGA	*Salmonella* Uganda
		SAL_VIR	*Salmonella* Virchow
A and B	**ORIGIN**	STO	Food store and retail outlets
A	**RES_PHENOTYPE**	KPC	*Klebsiella pneumoniae* carbapenemase[c]
A and B	**SPECIES**	CAM	Camelidae (camels)
		OPO	Other poultry (backyard, native breeds, dual-purpose breeds)
A and B	**SPECIMEN**	BOOTS	Boot swabs, boot socks
		CLOACAL	Cloacal swabs
		RECTAL	Rectal swabs

[a] For locally generated guidelines (breakpoints which are not CLSI or EUCAST) for interpreting antimicrobial susceptibility test results.

[b] These are commonly isolated serotypes as reported in various national AMR surveillance programs.

[c] *Klebsiella pneumoniae* (KLEPNE) carbapanemase-producing (a specific Enterobacterales carbapenemase-producing organism).

4. Expanded guidance for preparing and submitting antimicrobial resistance (AMR) data files to the InFARM IT platform

During the first InFARM open call for data in 2024, AMR data were submitted from national surveillance systems at various stages of development and using different data structures. Submissions also included historical data from local and national pilot projects that had not previously been validated, analyzed, or used for reporting and communication. Due to the diversity of data sources, several challenges emerged while providing technical support to countries during the preparation and submission of AMR data files to the IT platform.

Below are common errors identified in the AMR data files, as detected by the platform, due to non-compliance with the technical specifications outlined in the InFARM manual:

- Surveillance Programme vs. Variable SPECIMEN: In some cases, the selected surveillance programme did not match the type of specimens collected. For example, surveillance of healthy terrestrial animals typically involves fecal or cecal samples—not organ samples (e.g., liver, intestines) obtained from necropsied diseased animals.
- Surveillance Programme vs. Variable ORIGIN: In several instances, the selected surveillance programme was inconsistent with the origin of the samples. For example, surveillance of diseased animals requires samples from laboratories—not from homes, stores, or markets.
- Mandatory Variables: Omissions of one or more mandatory InFARM variables were detected in both Option A (isolate-level) and Option B (aggregated) reporting. For instance, in Option A submissions, key variables such as minimum inhibitory concentration (MIC) values, inhibition zone diameters (in mm), and their corresponding interpretations (R, I, S) were frequently missing.

To improve the quality of data submitted to the InFARM IT platform, this section provides targeted guidance for InFARM focal points on reporting key combinations of variables and category codes tailored to specific surveillance programmes. It also includes recommendations for focusing AMR isolate reporting on specific sets of antibiotics (i.e., antibiotic panels). This approach supports better alignment with international AMR surveillance standards and guidance documents on AMR in animals and food [2-5 ,6,7,8], fosters greater data harmonization, enhances cross-country comparability, and enables more accurate global AMR estimates.

4.1. Recommended combinations of variable categories for focused reporting on the different surveillance programmes

To reduce errors and ensure compliance with the InFARM technical specifications—and to support globally harmonized and integrated AMR data reporting across sectors, tables 2 to 6 provide detailed guidance for focused reporting. These recommendations outline priority combinations of variables and category codes that are specific to each surveillance programme.

Countries are encouraged to prioritize the submission of specific combinations of the mandatory variables ORIGIN, SPECIES, SPECIMEN, and MICROORGANISMS, as presented in the following tables. While not prescriptive, these recommended combinations offer a structured approach to achieving a more comprehensive and coherent overview of AMR across production chains, animal species, and commonly collected sample types.

4.1.1. Healthy terrestrial animals programme

The table below presents recommended combinations of categories for the variables ORIGIN, SPECIES, SPECIMEN, and MICROORGANISMS to guide **focused AMR data reporting for healthy terrestrial animals**. These combinations are aligned with international guidelines [5,7] to ensure harmonized data collection across countries and enable robust comparison and analysis at national, regional, and global levels.

Table 2. Recommended combinations of variable categories for focused reporting of AMR data files under the healthy terrestrial animals surveillance programme

Variable Name	**Acceptable categories - their codes and descriptions**
ORIGIN	FAR – farm SLA - slaughterhouse/abattoir (MAR - outdoor market[a])
SPECIES	**Any terrestrial/land animals (typically food animal species):** BRO- broilers, CAT- cattle LAY - layers OPO - other poultry (native or local breeds) PIB – pigs - backyard PIC – pigs - commercial POB - poultry-backyard
SPECIMEN	**Farm-sourced:** FAECES, CLOACAL, RECTAL, ELIT, EMAN, (EGGS, MILK[b]) **Slaughter plant-sourced:** CAECUM (*and cecal content*[c]), FAECES[d], CLOACAL, RECTAL, ELIT, EMAN, EWAS, (LYMPH) **Outdoor market-sourced:** CAECUM, FAECES, CLOACAL, RECTAL
MICROORG	ESCCOL, SALSPP, CAMCOL, CAMJEJ, CAMSPP, ENTFCL, ENTFCM, ENTSPP

[a] Outdoor market such as live bird market where live birds are sold or slaughtered on site.

[b] Raw unpasteurized milk such as those collected directly from animals or bulk tank.

[c] The whole cecum/ceca (poultry) may be collected for transport to the laboratory or cecal content (pigs, cattle) collected aseptically directly from the organ during the evisceration stage.

[d] When faecal samples are collected from transport trucks because of logistical reasons.

4.1.2. Healthy aquatic animals programme

The table below presents recommended combinations of categories for the variables ORIGIN, SPECIES, SPECIMEN, and MICROORGANISMS to guide **focused AMR data reporting for healthy aquatic animals**. These combinations are aligned with international guidelines [4, 6, 9] to ensure harmonized data collection across countries and enable robust comparison and analysis at national, regional, and global levels.

Table 3. Recommended combinations of variable categories for focused reporting of AMR data files under the healthy aquatic animals surveillance programme

Variable Name	Acceptable categories - their codes and descriptions
ORIGIN	FAR - Farm WIL – Natural habitat[a]
SPECIES[b]	CRU - crustaceans-penaeids (e.g., shrimp) FCI - fish-cichlids (e.g., tilapia) FCY - fish-Cyprinids (e.g., carp) FMA - fish-Marine (e.g., tuna) FSA - fish-Salmonids (e.g., salmon, trout) FSI - fish-Siluriformes (e.g., catfish) MOL - molluscs (e.g., clam, oyster)
SPECIMEN	EWAT - water FRESH - fresh or ice-preserved aquatic products
MICROORG[c]	SALSPP, ESCCOL, ENTSPP, AERSPP, EDWSPP, VIRSPP

[a] Origin of wild-caught fishes or molluscs such as rivers, lakes, oceans or other natural bodies of water.

[b] The exact fish species, tilapia, carp or molluscs could be specified in the optional variable SPECIES_NOTES.

[c] Non-exhaustive list and options/other microorganisms are listed elsewhere. [9]

4.1.3. Diseased terrestrial animals programme

The table below presents recommended combinations of categories for the variables ORIGIN, SPECIES, SPECIMEN, and MICROORGANISMS to guide **focused AMR data reporting for diseased terrestrial animals**. These are based on guidance for harmonized AMR surveillance and monitoring,[5] previous InFARM submissions (2024), and those reported by national AMR surveillance programs (prioritized animal pathogens isolated from diseased terrestrial animals). [10-13]

Table 4. Recommended combinations of variable categories for focused reporting of AMR data files under the diseased terrestrial animals surveillance programme

Variable Name	**Acceptable categories and codes**
ORIGIN	FAR – farm LAB – laboratory PET – pet store VEH – veterinary hospital VET – veterinary clinic
SPECIES	**Any terrestrial/land animals indicated in SPECIES for healthy animals (Table 2), plus the following non-food producing animal species:** CAN – dog EQU – Equidae – horses and mules FEL – cat REP – reptiles (e.g., crocodiles)
SPECIMEN	**Laboratory-sourced[a]:** EAR, EYE, INN, KIDNEY, LIVER, LUNGS, LYMPH, SKIN, SPLEEN, URINE **Farm-sourced:** BLOOD, CLOACAL SWABS, EGGS, FAECES, MILK (e.g., unpasteurized or mastitic milk), URINE
MICROORG[b]	**Commonly tested from diverse host species**: ESCCOL, SALSPP,[5] STAAUR, STASPP, STREPSPP, PASMUL[5] **Common pathogenic bacteria**: **Pigs:** ACTPLE - *Actinobacillus pleuropneumoniae*[5] STREPSUI - *Streptococcus suis* **Poultry-various species:** AVBPAR - *Avibacterium paragallinarum* **Cattle:** MANHAE - *Mannheimia haemolytica*[5]

[a] Acceptable specimens collected from laboratories or field necropsy (i.e., if farm-sourced).

[b] Non-exhaustive list, included in Annex 1 and target pathogens tested by national AMR surveillance programmes.[11-14]

4.1.4. Diseased aquatic animals programme

The table below presents recommended combinations of categories for the variables ORIGIN, SPECIES, SPECIMEN, and MICROORGANISMS to guide **focused AMR data reporting for diseased aquatic animals**. The recommended priority categories are based on guidance for harmonized AMR surveillance and monitoring,[4] previous InFARM submissions (2024), and those reported by national AMR surveillance programs (prioritized animal pathogens isolated from diseased aquatic animals).[6, 10]

Table 5. Recommended combinations of variable categories for focused reporting of AMR data files under the diseased aquatic animals surveillance programme

Variable Name	**Acceptable categories - their codes and descriptions**
ORIGIN	FAR – farm LAB – laboratory PET- pet store
SPECIES[2]	AMP - amphibians CRU - crustaceans-penaeids (e.g. shrimp) FCI - fish-cichlids (e.g. tilapia) FCY - fish-Cyprinids (e.g. carp) FMA - fish-Marine (e.g., tuna) FSA - fish-Salmonids (e.g. salmon, trout) FSI - fish-Siluriformes (e.g. catfish) MOL - molluscs (e.g. shellfish-shrimp, lobster, clam)
SPECIMEN	EWAT – water, HEMO – hemolymph, HEPA - hepatopancreas, KIDNEY, LIVER, SKIN, SPLEEN
MICROORG	**WOAH list**[a] : VIBPAR, LISMON, SALSPP **Other**[b]: AERSPP, EDWSPP, ESCCOL[c], VIBCHO, VIBSPP

[a] Listed in World Organization for Animal Health (WOAH) Aquatic Animal Health Code.[4]

[b] Please refer to the InFARM code list for the species belonging to the following genera: *Aeromonas, Edwardsiella* and *Vibrio*.

[c] *E. coli* is used as an indicator of cross-contamination in aquaculture production.

4.1.5. Food at processing and point of sale programme

The table below presents recommended combinations of categories for the variables ORIGIN, SPECIES, SPECIMEN, and MICROORGANISMS to guide **focused AMR data reporting for food at processing and point of sale**. The recommended priority categories listed below are based on guidance for harmonized AMR surveillance and monitoring [2, 3, 7] previous InFARM submissions (2024), and those reported by national AMR surveillance programs (prioritized list of microorganisms in AMR surveillance programs in animals and food from food production/farm to point of sale/retail continuum).[2, 3, 7, 11, 12, 15-16]

Table 6. Recommended combinations of variable categories for focused reporting of AMR data files under the food at processing and point of sale surveillance programme

Variable Name	Acceptable categories - their codes and descriptions
ORIGIN	MAR - outdoor market SLA - slaughterhouse/abattoir STO – food stores and retail outlets
SPECIES	Species sampled under healthy terrestrial and healthy aquatic animals used for food. Please refer to Table 2 and Table 3
SPECIMEN	CARCASS, EGGS (table eggs), LIVS (live specimen), MEAT, MILKP, PFRU (fruits), PVEG (vegetables), SKIN
MICROORG[a]	CAMCOL, CAMJEJ, CAMSPP, ENTFCL, ENTFCM, ENTSPP, ESCCOL, SALSPP

[a] In many national AMR surveillance programmes with comprehensive sampling across the food production to retail continuum, the same microorganisms are used in every production phase to track the dissemination of antimicrobial resistance.

4.2. Recommended panels of antibiotics for focused reporting on the different surveillance programmes

The InFARM data model has a fixed list of antimicrobials and follows the WHONET 3-letter acronym.[17]
Please note carefully:

- In the data model Option A, the order of the antimicrobial-specific variables (VALUE_XXX and INT_XXX) is extremely important. Antimicrobials tested by the country but not present in the current version of the data model option A should not be inserted into the data template. Similarly, antibiotics that are not present in the code list for the variable ANTIBIOTIC in option B should not be reported.
- Minimum inhibitory concentration (MIC) data should be floating-point numbers (numbers with fractions or decimal points). Inhibition zones in mm are typically fixed-point numbers. Remove embedded formulas or calculations within cells.

This section includes recommendations for focusing AMR isolate reporting on specific sets of antibiotics (i.e., antibiotic panels).

4.2.1. Antibiotic panel for programmes with primarily public health purpose (healthy terrestrial animals, healthy aquatic animals and food at processing and point of sale).

National AMR surveillance programmes use a standardized panel of antimicrobials to monitor AMR in common microorganisms from animals and food.[3] Countries are encouraged to report AMR data files utilizing antimicrobials such as those shown in table 7 below.

Table 7. Antimicrobial panel in microorganisms used in surveillance programmes with prevailing public health purpose

E. coli* and *Salmonella[a]	***Enterococcus* spp.**[b]	***Campylobacter* spp.**[c]
Defined panel[8] Cefpodoxime alone (*or ceftazidime in combination with one of either cefotaxime or ceftriaxone*)* Ciprofloxacin Ampicillin Tetracycline Chloramphenicol Gentamicin Trimethoprim-sulfamethoxazole Nalidixic acid (optional) Colistin (*optional, include isolates tested using microbroth dilution only*)	Erythromycin Teicoplanin Vancomycin Ampicillin Gentamicin Streptomycin Tigecycline Linezolid Quinupristin/dalfopristin Chloramphenicol Tetracycline	Ciprofloxacin Erythromycin Gentamicin Nalidixic acid Streptomycin Tetracycline *Other antimicrobials*: Azithromycin Chloramphenicol Clindamycin Florfenicol Florfenicol Meropenem

[a] Enterobacterales are intrinsically resistant to the following antimicrobials/classes and inclusion in the panel should be avoided: clindamycin, fusidic acid, glycopeptides (e.g., vancomycin), macrolides (clarithromycin and erythromycin), rifampin.

[b] *Enterococcus* spp. isolates are intrinsically resistant to the following antimicrobials/classes and inclusion in the panel should be avoided: aminoglycosides, cephalosporins, clindamycin, fusidic acid, trimethoprim, and trimethoprim-sulfamethoxazole. *Enterococcus faecalis* isolates are instrinsically resistant to streptogramins (quinupristin-dalfopristin).

[c] *Campylobacter jejuni* are intrinsically resistant to the following (inclusion to the panel should be avoided): cephalothin, fusidic acid, streptogramins, and trimethoprim.

* Defined panel of antimicrobials, specific requirements for 3rd generation cephalosporins: cefpodoxime alone, or ceftazidime in combination with cefotaxime, or ceftazidime in combination with ceftriaxone.[8]

4.2.2. Antibiotic panel for programmes with primarily animal health purpose (diseased terrestrial and diseased aquatic animals)

The antimicrobial panel may vary between countries. These panels generally include veterinary antimicrobials; however, their inclusion in the AST panel may be limited by the lack of quality control strains and the absence of established breakpoints. Table 8 serves as an example only.

Table 8. Antimicrobial panel in microorganisms used in surveillance programmes with prevailing animal health purpose

Terrestrial animals		
***Staphylococcus* spp.**	***Streptococcus* spp.**	***Pasteurella multocida*[a]**
Cefoxitin Enrofloxacin Erythromycin Florfenicol Gentamicin Lincomycin Neomycin Penicillin Tetracycline Trimethoprim-sulfamethoxazole Tylosin	Enrofloxacin Erythromycin Gentamicin Kanamycin Lincomycin Marbofloxacin Oxacillin Streptomycin Tetracycline TMPS Tylosin	Amoxicillin Amoxicillin-clavulanic acid Ceftiofur Cephalexin Doxycycline Enrofloxacin Florfenicol Flumequine Gentamicin Marbofloxacin Nalidixic acid Spectinomycin Streptomycin Tetracycline
Aquatic animals[b]		
***Aeromonas salmonicida*[c]**	***Vibrio* spp.[d]**	
Ampicillin Enrofloxacin Erythromycin Florfenicol Gentamicin Oxytetracycline Oxolinic acid Trimethoprim-sulfamethoxazole	Cefotaxime Ceftazidime Meropenem Ciprfloxacin Levofloxacin Erythromycin Doxycycline Tetracycline Trimethoprim-sulfamethoxazole	

[a] The antimicrobials are commonly used for the treatment and control of localized and systemic pathogenic bacterial infections. Antimicrobials to include should consider known resistance mechanisms (exclude those antimicrobials where intrinsic resistance is expressed).

[b] Quality control strains for testing certain pathogens and breakpoints may be unavailable for most microorganisms from aquatic animals (including amphibians).

[C] From CLSI Vet03-ED2:2020.[18]

[d] Based on the panel included in the EUCAST Clinical Breakpoints for *Vibrio* spp.[19]

5. Strengthened validation checks during submission of AMR data to the InFARM IT platform

When creating records for uploading AMR data files and during the actual upload process, the InFARM IT platform automatically performs validation checks to detect inconsistencies and ensure compliance with technical requirements.

Focal points are required to complete the Context Data section (i.e. creating a record for submission with a unique identifier or primary key) before uploading any AMR data files. The following built-in validation rules must be observed when entering context data for each surveillance programme:

- For Healthy Terrestrial Animals enter the number of Farms and/or Slaughterhouses.
- For Healthy Aquatic Animals enter the number of Farms.
- For Food at Processing enter the number of Slaughterhouses and/or Retail Stores.
- For Diseased Terrestrial Animals enter the number of Farms and/or Laboratories.
- For Diseased Aquatic Animals enter the number of Farms and/or Laboratories.

AMR data files that do not comply with the technical specifications outlined in Annex 1 – InFARM Data Model (link to Annex 1) will be automatically rejected by the platform. Focal points will not be able to proceed with the submission process until the identified errors are corrected.

To support users in addressing these issues, Tables 9, 10 and 11 below provide a list of common error messages encountered when submitting data under Option A (isolate-level) and/or Option B (aggregated), along with the corresponding corrections required to ensure successful validation and submission. All Mandatory variables should be filed correctly.

Table 9. Common errors in submitting AMR data files using InFARM data model options A and B and the corrections required

Error description	**Fix instructions**
X Coordinates must be between -90 and 90	Fix the values. For simplicity, a proxy for country could be used instead of per sampling location/origin.
Y Coordinates must be between -180 and 180	Fix the values. For simplicity, a proxy for country could be used instead of per sampling location/origin.
Origin code is not valid [a]	Mandatory variable and should not be blank/null. Check and replace with a correct ORIGIN code. See Annex 1 from the manual.
The selected origin is not suitable for surveillance purposes under *Healthy terrestrial animals* [b]	Check Annex 1, under the 'ORIGIN' code list, and refer to the 'Purpose' column; Tip! This also pertains to the location where the samples were collected.
The selected origin code is currently unavailable from the InFARM code list	Please contact the InFARM team - FAO-AMR-INFARM@fao.org - and provide the AMR data file.
Origin notes cannot exceed 256 characters [c]	Truncate the text entered in ORIGIN_NOTES (up to 256 characters).
The selected species is not suitable for surveillance purposes under *Healthy terrestrial animals* [b]	Check Annex 1, under the 'SPECIES' code list, and refer to the 'Purpose' column; Tip! these entries are intended for food.

Error description	**Fix instructions**
The selected species code is currently unavailable in the InFARM code list	Please contact the InFARM team - FAO-AMR-INFARM@fao.org - and provide the AMR data file.
The selected specimen is not suitable for surveillance purposes under *'Healthy terrestrial animals* [b]	Check Annex 1, under the 'SPECIMEN' code list, and refer to the 'Purpose' column.
The selected specimen code is currently unavailable in the InFARM code list	Please contact the InFARM team - FAO-AMR-INFARM@fao.org - and provide the AMR data file.
Microorganism code is not valid	Check and replace with a correct MICROORG code. See Annex 1 from the manual. Any microorganism not on the list will not be accepted.
The selected microorganism is not suitable for surveillance purposes under *'Healthy terrestrial animals* [b]	Check Annex 1, under the 'MICROORG' code list, and refer to the 'Purpose' column; if not on the code list' recommended purpose, please do not include the data in the submission.
The selected microorganism code is currently unavailable in the InFARM code list.	Please contact the InFARM team - FAO-AMR-INFARM@fao.org - and provide the AMR data file.
Microorganism serotype code is not valid.	Check and replace with a correct MICROORGANISM_SEROTYPE code. See Annex 1 from the manual.
Resistance phenotype code is not valid.	Check and replace with a correct RESISTANCE_PHENOTYPE code. See Annex 1 from the manual.
Guideline code is not valid.	Mandatory variable and should not be blank/null. Check and replace with a correct GUIDELINE code. The acceptable are CLSI, EUCAST and O (others, such as local/regional guideline).
Guideline version cannot exceed 15 characters	Truncate the text entered in GUIDELINE_VERSION (up to 15 characters). Acceptable values are the version/guideline publication year (e.g., M100 2025, EUCAST v15 2025).
AST method code is not valid	Mandatory variable and should not be blank/null. Check and replace with a correct AST_METHOD code. See Annex 1 from the manual.
Interpretation criteria code is not valid	Mandatory variable and should not be blank/null. Check and replace with a correct INTERPRETATION code. See Annex 1 from the manual.

[a] The same error message may appear for other optional variables that require standardized codes, including Species scale code, Species product code, Market category code, and Reason code.

[b] The same error message may appear for other programmes: Healthy aquatic animals (potentially expanded to cover their production environment), Food at processing and/or point of sale, Diseased terrestrial animals, and Diseased aquatic animals.

[c] This applies to other optional free-text variables or fields including the following: Species scale notes, Species product notes, Market category notes, Reason notes, Guideline notes, Species notes, Specimen notes. Values entered in these fields must be limited to fewer than 256 characters. Please review and truncate any text that exceeds this limit to ensure compatibility with the InFARM requirements.

Table 10. Common errors in InFARM data model option A and corrections required

Error Description	Fix Instructions
Site Id cannot exceed 20 characters[a]	Follow the character length requirement; generate new codes or truncate the existing identifiers entered.
Lab Id must exist, and it cannot exceed 20 characters	Mandatory variable and should not be blank/null. Follow the character length requirement; generate new codes or truncate the existing identifiers entered.
Isolate Id must exist, and it cannot exceed 20 characters	Mandatory variable and should not be blank/null. Follow the character length requirement; generate new codes or truncate the existing identifiers entered.
Pooled sample must be a Boolean	Provide TRUE or FALSE (not YES or NO, or binary 1 or 2).
Clone or strain code is not valid	Check and replace with a correct CLONE_STRAIN code. See Annex 1 from the manual.
Strain notes cannot exceed 256 characters	Truncate the text entered in STRAIN_NOTES (up to 256 characters).
No submission present for any antibiotic	Mandatory. Please provide results in at least one antimicrobial (for example VALUE_AMC and INT_AMC).

[a] The same applies for Animal id and Sample id if these optional fields are available in your submission/s.

Table 11. Common errors in InFARM data model option B and corrections required

Error Description	Fix Instructions
Antibiotic code is not valid.	Check and replace with a correct ANTIBIOTIC code. See Annex 1 from the manual. If the antibiotic is not on the list, please contact FAO-AMR-InFARM@fao.org .
Susceptible Isolates are mandatory and must be an integer [a]	If there are no Susceptible isolates, enter 0.
Bacterial Isolates Number must be an integer greater or equal to zero [b]	Enter a positive integer value.
Concentration must be greater or equal to zero	Enter a positive value.
Breakpoint must be greater or equal to zero	Enter a positive value.
Since Interpretation Criteria is EC, then Susceptible Isolates, Intermediate Isolates and Resistant Isolates must be 0 [c]	Enter 0. Should not be blank/null.
Since Interpretation Criteria is CLIN, then Wild Types Isolates Number must be 0 [d]	Enter 0. Should not be blank/null.

[a] The same error message may appear for the following variables: Intermediate Isolates, Resistant Isolates, Wild Types Isolates, Non Wild Types Isolates, Unknown AST Results Isolates, No Interpretation Isolate. Enter a positive integer value or 0, the fields cannot be left blank.

[b] The same error message may appear for Samples Number and Positive Samples Number.

[c] The same error message may appear for Intermediate Isolates and Resistant Isolates.

[d] The same error message may appear for Non Wild Types Isolates.

Notes

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Animal Production and Health Division
Natural Resources and Sustainable Production
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