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SCIENTIFIC OPINION

Occurrence and spread of carbapenemase-producing Enterobacterales (CPE) in the food chain in the EU/EFTA. Part 1: 2025 update

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The declarations of interest of all scientific experts active in EFSA's work are available at https://open.efsa.europa.eu/experts

Abstract

Carbapenemase-producing Enterobacterales (CPE) have been reported in the food chain in 14 out of 30 EU/EFTA countries. Commonly reported genes are bla_{VIM-1}, bla_{OXA-48} and $bla_{OXA-181}$, followed by bla_{NDM-5} and bla_{IMI-1}. *Escherichia coli,* target of most of the studies, *Enterobacter cloacae* complex, *Klebsiella pneumoniae* complex and *Salmonella* Infantis are the most frequent CPE. *E. coli* isolates show a high clonal diversity. IncHI2 (bla_{VIM-1} and $bla_{OXA-162}$), IncC (bla_{VIM-1} and bla_{NDM-1}), IncX3 (bla_{NDM-5} and $bla_{OXA-181}$), IncI and IncL (bla_{OXA-48}) plasmids are frequently reported. Most reports are from terrestrial food-producing animals and their environments – mainly pigs, followed by bovines and poultry and with occasional reports of meat thereof (targets of the EU monitoring and follow up trace back investigations). Few studies have investigated foods of aquatic animal origin and of non-animal origin, finding a great CPE diversity. A notable increase in the number of CPE detections has been observed, predominantly from pigs, with a surge in certain countries in 2021 ($bla_{OXA-181}$, Italy) and 2023 (bla_{OXA-48}, Spain; $bla_{OXA-181}$, bla_{OXA-48}, $bla_{OXA-244}$ and bla_{NDM-5}, Portugal). Very few data points to circumstantial evidence of CPE transmission, clonal and/or horizontal gene spread within the food chain and from/to humans. Various methods are used in the EU/EFTA countries to detect and characterise CPE in the food chain. Improvement of their sensitivity should be investigated. Ten out of 30 EU/EFTA countries have specific contingency plans for CPE control, being epidemiological investigations (e.g. trace-back) a common action included in those plans. Overall, data remain scarce for the bacterial species and sources beyond those systematically monitored. Recommendations to fill data gaps on other bacterial species and sources, dissemination pathways and optimisation of detection methods are given. A One Health approach to address the drivers of CPE spread in the food chain is needed.

KEYWORDS

antimicrobial resistance, carbapenem, clone, detection methods, food-producing animals, molecular epidemiology, plasmid, whole-genome sequencing

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SUMMARY

Since the first description of carbapenemase-producing Enterobacterales (CPE) in the food chain in the European Union (EU) in 2011, concerns about their occurrence has grown. In 2013, the EFSA BIOHAZ Panel published a scientific opinion on 'Carbapenem resistance in food animal ecosystems', highlighting the need for vigilance in monitoring this emerging threat. Since then, studies have reported the occurrence of CPE in the food chain in the EU and the European Food trade Association (EU/EFTA). Given the evolving scientific landscape, the BIOHAZ Panel initiated a self-task to update its former assessment. More specifically, EFSA was asked to address, the following Terms of Reference (ToRs):

ToR1: To collect information from EU/EFTA countries reporting data to EFSA for the EU AMR monitoring regarding ongoing or planned studies, investigations and existing contingency plans and/or control measures related to CPE;

ToR2: to collaborate with countries to generate new data, with the following objectives: (a) developing higher sensitivity protocols for CPE isolation, detection and characterisation; (b) conducting epidemiological investigations to elucidate sources and dissemination pathways; (c) performing in-depth genetic analysis of available CPE and investigate multidrug resistance; (d) carrying out comparative genomics analyses of CPE from different sources.

ToR3: To review all new data and literature to provide scientific advice on the sources and dissemination pathways of CPE detected in food-producing animals, products derived thereof and the food-producing environment.

The present scientific opinion addresses the aspects outlined in ToR1 and ToR3. This update is based on a review of scientific literature up to February 2025, data provided by EU/EFTA countries to EFSA under the EU AMR monitoring programme, and additional information gathered from these countries.

CPE have been detected in 14 of 30 EU/EFTA countries, namely, Austria, Belgium, Czechia, Germany, Greece, Hungary, Italy, Norway, the Netherlands, Portugal, Romania, Spain, Sweden and Switzerland. Most isolates were identified through the EU and national AMR monitoring programmes.

The most commonly reported genes are *bla*$_{\text{VIM-1}}$, *bla*$_{\text{OXA-48}}$ and *bla*$_{\text{OXA-181}}$, followed by *bla*$_{\text{NDM-5}}$ and *bla*$_{\text{IMI-1}}$. Less common genes include *bla*$_{\text{NDM-1}}$, *bla*$_{\text{OXA-162}}$, *bla*$_{\text{GES-5}}$, *bla*$_{\text{IMI-3}}$ and *bla*$_{\text{KPC-3}}$, while other genes (e.g.*bla*$_{\text{OXA-244}}$), or co-occurrence of multiple genes within single isolates being rarely detected.

E. coli is the primary species reported but also the main focus of both research studies and EU monitoring. Other species were also detected, including isolates from the *Enterobacter cloacae* complex, the *Klebsiella pneumoniae* complex and *Salmonella* Infantis. Additionally, sporadic reports have identified species from the *Klebsiella oxytoca* complex, non-Infantis *Salmonella enterica* serovars and various other genera. In general, limited data are available beyond *Escherichia coli*.

E. coli isolates show the highest clonal diversity, with *E. coli* ST23-complex (ST88, ST410), ST101-complex (ST5229, ST101), ST10-complex (ST10, ST48, ST744) and ST542 and *Salmonella* Infantis ST32 isolates being detected across multiple food chain sources and/or countries. Additionally, *Salmonella* Infantis ST32, *K. pneumoniae* ST307 and ST525 isolates were also detected. The most frequently reported plasmid types are IncHI2 (*bla*$_{\text{VIM-1}}$ and *bla*$_{\text{OXA-162}}$), IncC (*bla*$_{\text{VIM-1}}$ and *bla*$_{\text{NDM-1}}$), IncX3 (*bla*$_{\text{NDM-5}}$.and *bla*$_{\text{OXA-181}}$), IncI and IncL (*bla*$_{\text{OXA-48}}$).

CPE have been detected throughout the EU/EFTA food chain. Most reports come from terrestrial food-producing animals and their environments – mainly pigs, followed by bovines and poultry – via the EU AMR monitoring programme and trace back investigations. Occasional findings have been noted in meat products. Although only a few studies have investigated foods of aquatic animal origin and foods of non-animal origin, those studies have nonetheless reported the presence of CPE. Overall, data remain scarce for sources beyond the systematically monitored food-producing animals. In the case of Sweden, the reported CPE were isolated from feed mills, but not from food production animals or foods.

In terrestrial food-producing animals, the distribution of carbapenemase genes varies by species: pigs exhibit the greatest gene variety (predominantly *bla*$_{\text{VIM-1}}$, with *bla*$_{\text{OXA-48}}$, *bla*$_{\text{OXA-181}}$ and *bla*$_{\text{NDM-5}}$), bovines mainly harbour *bla*$_{\text{OXA-181}}$ and *bla*$_{\text{NDM-5}}$, and broilers predominantly show *bla*$_{\text{VIM-1}}$. In contrast, food derived from aquatic animals – including imported products – displays not only a higher frequency of CPE detections but also a broader diversity of Enterobacterales species and carbapenemase genes (including *bla*$_{\text{OXA-48}}$, *bla*$_{\text{VIM}}$, *bla*$_{\text{IMI-1}}$, *bla*$_{\text{IMP}}$ and bla$_{\text{KPC}}$), often with detection of multiple genes per isolate. Similarly, although based on few studies, food of non-animal origin (including imported products) has a greater gene diversity (including *bla*$_{\text{OXA-48}}$, *bla*$_{\text{VIM}}$, *bla*$_{\text{IMI-1}}$, *bla*$_{\text{IMP}}$ and *bla*$_{\text{KPC}}$), often with multiple genes per isolate.

The timeline of CPE emergence in the EU/EFTA food chain began with *bla*$_{\text{VIM-1}}$ in pigs in Germany (2011). Since then, there has been an increase in the number of CPE detections, especially in pigs, but also for all other types of food-producing animals and foods. From 2015 to 2024, several gene variants were reported, with *bla*$_{\text{NDM-5}}$, *bla*$_{\text{OXA-48}}$, *bla*$_{\text{OXA-181}}$ and *bla*$_{\text{VIM-1}}$ being repeatedly detected across the years and/or detected in multiple countries. Looking exclusively at the data from the harmonised EU monitoring, an increase in the number of reports was seen in 2021–2023. This was mostly explained by an increase in pigs for *bla*$_{\text{OXA-181}}$ and *bla*$_{\text{OXA-48}}$ in Italy and Spain, respectively, together with the first CPE reports, with several genes and gene combinations, identified in Portugal in 2023. In general, when considering all available data (scientific literature and harmonised monitoring), an increase in CPE reports may partially reflect an increase in testing.

Evidence of CPE transmission within livestock production is well-documented in Germany, Italy and Spain. In Germany, genomic and epidemiologic data showed that *bla*$_{\text{VIM-1}}$-IncHI2-carrying *E. coli* ST88 and *Salmonella* Infantis ST32 persisted and occasionally spread within pig production. In Italy, *E. coli* ST5229 carrying *bla*$_{\text{OXA-181}}$ on IncX3/IncX1 plasmids were found in pigs, bovines and turkeys. Transmission was observed from breeding to fattening pigs and linked to dairy calves, with *E. coli* ST5229-*bla*$_{\text{OXA-181}}$-IncX1 also identified in a farm worker, suggesting local spill over between animals and humans. In Spain, IncL plasmids carrying *bla*$_{\text{OXA-48}}$ contributed to the spread of this gene throughout the pig production system. Several *E. coli* types common in the food chain (e.g. ST10, ST38, ST48, ST101 and ST410) have also been linked to

human cases of carbapenemases producers. However, limited whole-genome sequencing data prevent a clear confirmation of connection with the food chain. Additionally, the emergence of human cases of carbapenemase-producing *S. enterica* in the EU in 2022 and 2023 suggests a food-producing origin, even though such CPE was not detected in the food chain during the same period. In some cases, common plasmids have been found in both animal and human bacteria. For example, the bla_{OXA-48}-IncL plasmid, which has long circulated in human bacteria, has now been detected in livestock.

The identified risk factors associated with CPE emergence and spread include the co-resistance to different antimicrobials and/or metals, movement and trade of CPE-positive animals and CPE-contaminated food products, and human carriers involved in animal or food production who may introduce CPE into the food chain.

EU/EFTA laboratories use a range of methods for CPE detection and characterisation, including various selective media, PCR-protocols and whole-genome sequencing (WGS) workflows. No single culture-based method can detect all CPE and culture-independent methods have not yet been thoroughly evaluated. Official specific monitoring protocols to detect ESBL, AmpC and carabepanemases rely on a pre-enrichment culture followed by isolation on selective media, balancing sensitivity, specificity and cost; however, these methods primarily target *E. coli*, leaving other relevant Enterobacterales unaddressed. While these methods have successfully isolated CPE and detected increased occurrences in some regions, their sensitivity could be improved. Enhanced protocols using selective enrichment with low carbapenem concentrations, PCR and metagenomic approaches have been developed for specific situations. Additionally, at least 24 EU/EFTA countries have laboratories capable of WGS, although their ability to identify clusters and plasmids varies.

Ten out of the total of 30 EU/EFTA have specific contingency plans for CPE control. From these 10 countries, Germany, Italy, The Netherlands, Norway, Sweden and Spain already had CPE findings, whereas Denmark, Finland, Lithuania, Malta and have not yet reported the occurrence of any CPE. In four of those countries, these plans are part of mandatory programmes included in legislation, whereas for the other six, they are voluntary programmes. Epidemiological investigations, especially trace back investigations, are the most frequent actions reported. Other measures reported were the identification and isolation of CPE carriers, reduction of antimicrobial use and implementation of biosecurity measures. Seven countries reported to include inter-sectorial communication between agencies or departments in their contingency plans. Several bottlenecks were identified to monitor and control CPE in the food chain.

The recommendations focus on understanding how to prevent or minimise the occurrence and spread of CPE in food ecosystem/ food chain. Recommendations were done to fill the knowledge gaps in the bacterial species and sources not targeted in the current official monitoring, transmission pathways, detection methods and types of studies needed to optimise the CPE detection. A One Health approach, integrating human, animal and environmental health, is needed to address effectively the drivers of carbapenem resistance in the food chain worldwide.

1 | INTRODUCTION

1.1 | Background and Terms of Reference as provided by the requestor

Carbapenems are broad-spectrum, last-resort, β-lactam antimicrobials used for the treatment of serious bacterial infections in humans. Resistance to carbapenems is mainly due to the production of carbapenemase enzymes and is considered a serious public health concern for the EU and globally. Carbapenem-resistant infections, which are often healthcare-associated, are difficult to treat and may have poor outcomes.

In the last years, several published studies have reported the sporadic occurrence of carbapenemase-producing bacteria in food-producing animals and their environment, including in the EU. In addition, data from the EU harmonised antimicrobial resistance (AMR) monitoring recently showed the presence of carbapenemase-producing bacteria in several EU Member States and other countries reporting data to EFSA, and from several animal sectors, as indicated below. Carbapenemase genes are often located in genetic elements (plasmids, transposons, integrons), which bear other AMR genes conferring resistance to several antimicrobial classes, i.e. multi-drug resistance. Thus, although carbapenems are not (and have never been) authorised for use in food-producing animals in the EU, carbapenemase-producing bacteria, if introduced into farm-animals production systems, may be co-selected by the use/selective pressure of other antimicrobials, in both animals and the environment. The plasmids and other mobile genetic elements which encode the production of carbapenemase enzymes, could also be transferred to other bacteria by horizontal gene transfer. The importance of the spread and further establishment of carbapenemase genes and of carbapenemase-producing Enterobacterales such as *E. coli* carrying $bla_{\text{NDM-5}}$ in humans in several EU/EEA countries, is recognized as a significant concern by ECDC (2023).[1] Likewise concerns related to the finding of carbapenem resistance in bacteria from food and food-producing animals are also being raised worldwide.[2]

According to Commission Implementing Decision (EU) 2020/1729, which applies from 1st January 2021 and until December 2027, monitoring of AMR is mandatory in *Salmonella*, *Campylobacter* and indicator commensal *E. coli*, in the major domestically produced food-producing animal populations and their derived meat. Routine monitoring of indicator *E. coli* and *Salmonella* spp. as well as the specific monitoring of ESBL-/AmpC–/carbapenemase-producing *E. coli* in caecal samples of food-producing animals and their meat products is therefore now mandatory. In addition, monitoring of *E. coli* in caecal samples of fattening pigs and bovine animals under 1 year of age, as well as in pig meat and bovine meat gathered at retail and border control posts became mandatory in 2021, whereas monitoring of *E. coli* in caecal samples of broilers, fattening turkeys and in fresh broiler meat sampled at retail and border control posts became mandatory in 2022.

Before 2021, bacterial isolates were categorised as presumptive ESBL-, AmpC- or carbapenemase-producing based on the phenotype. Since 2021, whole-genome sequencing (WGS) is authorised as an alternative method. Countries which identify ESBL-, AmpC- or carbapenemase-producing isolates based on genotypic results using WGS no longer need to report the phenotypic results. In 2022, six Member States (Czechia, Germany, Finland, Italy, The Netherlands and Sweden) and one EFTA country (Norway) reported genotypic results (the last four countries reported also phenotypic AMR results).

In a previous BIOHAZ Panel Opinion on "*Scientific Opinion on Carbapenem resistance in food animal ecosystems*",[3] dating back to 2013, EFSA provided advice on this emerging threat. Among the measures recommended to prevent and control the spread of carbapenem resistance in bacteria from livestock were:

- *"Where the presence of carbapenemase-producing strain is confirmed,* ***detailed epidemiological investigations*** *should be started immediately;*
- *the* ***most sensitive methods*** *should be used for their detection, and carbapenemase-producing isolates should be genetically characterized for allowing comparisons;*
- ***control measures should be proactively implemented*** *at national and international levels, and should involve* ***inter-departmental communication between human and veterinary authorities;***
- *as carbapenemase-producing bacteria can spread from the hospital environment to the animal population by a variety of routes (wastewater, human/animal contact,* etc.*), measures addressing such routes of transmission,* ***minimising the potential spill-over of carbapenemase-producing organisms from humans to food-producing animals*** *are therefore particularly important;*
- ***at the farm level, these measures could include*** *identification and isolation of carriers, animal quarantine through to destruction of infected flocks/herds, restrictions in the movement of personnel between farms, increased biosecurity, controls on animal and animal by-products trade, or by improving hygiene throughout the food chain;*
- *in cases where containment measures are taken,* ***targeted surveys*** *should be started to verify the efficiency of the measures taken."*

Data reported to EFSA from the AMR harmonised monitoring revealed the presence of carbapenemase-producing *E. coli* in several Member States and animal sectors during the last years:

[1] https://www.ecdc.europa.eu/sites/default/files/documents/Increase-E-coli-isolates-blaNDM-5-EU-EEA-may2023.pdf.

[2] Huang et al. (2023). Carbapenem resistance in the food supply chain. Journal of Food Protection, 86, 100108. https://doi.org/10.1016/j.jfp.2023.100108.

[3] https://efsa.onlinelibrary.wiley.com/doi/10.2903/j.efsa.2013.3501.

- In **2015** and **2017**, 2 isolates reported by **Germany** from **pigs** were confirmed as carrying ***bla*$_{\text{VIM-1}}$**. Also in 2015, **Belgium** informed EFSA about the finding of 1 ***bla*$_{\text{VIM-1}}$**-carrying isolate from **minced pork** (collected from a national monitoring).
- In **2016**, **Romania** reported 2 isolates from **broilers** and 1 from **broiler meat**, which were confirmed as carrying ***bla*$_{\text{OXA-162}}$** (*bla*$_{\text{OXA-48}}$-like).
- In **2019**, 3 isolates were reported by **Germany** were confirmed to carry ***bla*$_{\text{VIM-1}}$** (**pig meat**), ***bla*$_{\text{OXA-48}}$** (**pigs**) and ***bla*$_{\text{GES-5}}$** (**pigs**), respectively.
- In **2020**, 1 isolate reported **by Austria** from **broilers** was confirmed as carrying ***bla*$_{\text{VIM-1}}$**.
- **In 2021**, there were reports from:

  - **Hungary:** 2 isolates from **bovine meat** and 1 isolate from **pig meat**, were confirmed as ***bla*$_{\text{NDM-5}}$** carriers.
  - **Spain:** 2 isolates from pigs were confirmed as ***bla*$_{\text{OXA-48}}$** carriers.
  - **Italy:** WGS revealed **26 *E. coli*** isolates, 21 from **pigs** and 5 from **bovines**, confirmed as carrying ***bla*$_{\text{OXA-181}}$** (four isolates from calves and 20 from fattening pigs), ***bla*$_{\text{OXA-48}}$** (one isolate from a fattening pig) or ***bla*$_{\text{NDM-5}}$** (one isolate from a calf).
  - **Czechia:** WGS revealed 3 isolates from **pigs**, which were confirmed as carrying ***bla*$_{\text{NDM-5}}$**.

- **In 2022** (these results will be included in 2022 EUSR on AMR, which is currently under preparation):

  - 1 isolate reported by **Italy**, from **broilers**, harboring the ***bla*$_{\text{VIM-1}}$** gene, as well as 2 isolates from **fattening turkeys** confirmed as carrying ***bla*$_{\text{OXA-181}}$**.
  - 2 isolates from **broilers**, reported by **Austria**, were confirmed as carrying ***bla*$_{\text{VIM-1}}$**.

- In **2023:**

  - **Norway** informed EFSA about the finding on 1 **cattle** isolate, confirmed as ***bla*$_{\text{NDM-5}}$**.
  - **Czechia** also informed about the presence of another carbapenemase-producing isolate from **pigs**.
  - **Italy** informed of the further isolation on ***bla*$_{\text{OXA-181}}$** from **pigs** and **bovine animals**.

As a consequence of the increase of the number of countries reporting the detection of carbapenemase-producing bacteria in the last years, as well as the involvement of different animal species, and due to the relevance of the genetic determinants found, following EFSA's initiative in liaison with the EURL-AR, several Member States have expressed their willingness to engage, with EFSA, in thoroughly investigating the emergence and spread of carbapenemase-producing Enterobacterales, going beyond the information collected through the current EU AMR monitoring in food-producing animals and derived meat.

TERMS OF REFERENCE

The BIOHAZ Panel is asked to initiate a self-task to supervise the production and review of new data and evidence generated by the Member States, as well as any new scientific literature published from 2013 until present, and that would allow to investigate the sources and dissemination pathways of carbapenemase-producing Enterobacterales detected in food-producing animals, products derived thereof and the food-producing environment, as well as to better characterise the magnitude of their occurrence.

It is envisaged that the Panel will issue one or more scientific opinion(s) on the current status of the occurrence and spread of carbapenemase-producing Enterobacterales in the food chain in the EU/EFTA (depending on the issues detected). This will be done in close liaison with ECDC, as well as consulting informing other EU Agencies (European Medicines Agency (EMA), EEA) as appropriate.

More specifically, EFSA is requested to address the following terms of reference (ToRs):

1. To gather information from countries reporting data to EFSA for the AMR monitoring (EU Member States, EFTA countries, as well as possibly EU candidate countries) on (i) ongoing or planned studies/investigations spanning from recent surveillance findings (carbapenemase-producing Enterobacterales in the food-chain), as well as on (ii) contingency plans and/or control measures implemented/planned to halt the spread of carbapenemase-producing Enterobacterales in the food chain.
2. To collaborate with the above-mentioned countries and with the EURL-AR with the purpose of generating new data (beyond those already collected through the current AMR monitoring) through a specific project (outsourcing, 2024 to 2026). Countries interested in participating could express their interest in one or several of the work packages with the following objectives:

   a. To design a high sensitivity protocol for the isolation and/or detection and characterization of specific carbapenemase-producing *E. coli* and other Enterobacterales to be used for targeted studies within the food chain and/or the environment.

b. To perform epidemiological investigations (e.g. traceback/longitudinal/trace forward/network, other) of carbapenemase-producing *E. coli* and other Enterobacterales using intensive targeted exploratory sampling and testing, with the aim of elucidating possible sources and dissemination pathways.
c. To perform in-depth genetic analysis (clonality, plasmids, ISs, Tns, ICEs) of available *E. coli* isolates from official monitoring and newly obtained isolates of carbapenemase-producing *E. coli* and other Enterobacterales. In addition, to also investigate the occurrence of multi-drug resistance in these isolates, that could contribute to the co-selection by use of other antimicrobial classes/metals.
d. To perform comparative genomics analyses of the isolates gathered in this project from different countries/regions/animal species including isolates from different sources such as humans and pets.

3. To review all new data/evidence generated by the Member States and the EURL-AR, as well as any new scientific literature published from 2013 in order to provide scientific advice on the sources and dissemination pathways of carbapenemase-producing bacteria detected in food-producing animals, products derived thereof and the food-producing environment, by issuing at least two scientific opinion(s) targeting the different topics identified in ToRs 1 and 2.

   Deadline 30 June 2027.

1.2 | Interpretation of the Terms of Reference

The state of knowledge regarding carbapenemase-producing Enterobacterales (CPE) in the food chain up to February 2025 is presented in this scientific opinion, Part 1, that addresses ToR1 and the review of new scientific literature and data mentioned in ToR3. Information was gathered by means of: (i) a review of the literature and available data since 2011, when the first findings of CPE in the European Union (EU) food chain took place (EFSA BIOHAZ Panel, 2013); (ii) targeted surveys sent to the EU Member States[4] and countries belonging to the European Food Trade Association (EFTA)[5] reporting data to EFSA for AMR monitoring. Deadline of this Part 1 opinion is 31 March 2025.

The main objective of the literature review was to collect information on:

- CPE detected in the food chain, terrestrial and aquatic animals, food of animal and non-animal origin, and food-producing related environments;
- transmission routes and risk factors for CPE spread;
- microbiological and molecular methods used for CPE detection and characterisation.

The review focused primarily on EU/EFTA countries, while also considering relevant global findings. It covers food production and consumption (including retail and border posts) within these regions. The review encompasses all stages of the production and processing of foods of both animal and non-animal origin.

The main objectives of the targeted surveys were to collect information on:

- ongoing and planned studies/investigations regarding CPE;
- CPE-positive findings since 2011;
- laboratory methods currently in use for the detection and characterisation of CPE in the EU;
- existing contingency plans and control measures aimed at preventing or minimising the emergence and spread of CPE in the food chain.

The assessment was conducted in close collaboration with the European Centre for Disease Prevention and Control (ECDC), with input from the European Medicines Agency (EMA) and in a continuous dialogue with the European Commision (EC) DG-SANTE representatives. The resulting findings offer a comprehensive overview of the current status of CPE occurrence and dissemination in the food chain within the EU/EFTA, providing a basis for future evaluations and recommendations.

Each ToR was translated into an assessment question (AQ) and, if applicable, into sub-assessment questions (SQ1), as follows:

AQ1. What is the current status of carbapenemase-producing Enterobacterales (CPE) in the food chain in the EU/EFTA since the last EFSA opinion?

SQ1.1 What carbapenemase-encoding genes have been found?
SQ1.2 What are the bacterial species in which they were found?

[4] https://european-union.europa.eu/principles-countries-history/eu-countries_en.

[5] EFTA countries performing the EU AMR monitoring are: Norway, Switzerland and Iceland. The United Kingdom (UK) left the European Union on 31 January 2020. For all data presented in this scientific opinion, the 'EU' acronym refers to 28 Member States including UK until 31 January 2020 and to 27 Member States from 1 February on, and for EFTA, the three countries mentioned above.

SQ1.3 What are the CPE clones?
SQ1.4. What are the mobile genetic elements associated with the carbapenemase-encoding genes?
SQ1.5 What are the sources (animals, food of animal and non-animal origin and food production environments)?
SQ1.6 What is the geographical and temporal distribution?

AQ2: What are the transmission dynamics of CPE in the food chain in the EU/EFTA?

SQ2.1 What are the documented transmission/dissemination routes?
SQ2.2 What are the risk factors identified for their emergence and spread?

AQ3: What are the methods in use for CPE detection and characterisation?
AQ4: What contingency/mitigation/control plans to control spread or potential spread of CPE in the food chain do currently exist in the EU/EFTA?

SQ4.1 What contingency plans, if any, are available for preparedness?
SQ4.2 What mitigation/control measures, if any, are currently in place?
SQ4.3 In which circumstances are the contingency/mitigation/control strategies applied?

For the purpose of generation of new data requested in ToR2, a Framework Partnership Agreement (FPA GP/EFSA/BIOHAW/2024/01) was signed in December 2024 with 18 Institutions included in the EFSA Article 36 list[6] and hosting National Reference Laboratories for Antimicrobial Resistance (NRLs-AR) that are involved in the official EU antimicrobial resistance monitoring described in this document (see Section 3.1.4). The project will be coordinated by the Danish Technical University (Copenhagen, Denmark), which hosts the European Reference Laboratory EURL_AR),[7] and will last until end of 2027. The data generated, covering ToR2a-d and further updates of the literature (also part of ToR3), will be used for the preparation of a new scientific opinion with an update of the situation up to 2027.

1.3 | Additional information

1.3.1 | Carbapenems

In the EU, the main carbapenems in use include meropenem, imipenem and ertapenem. These beta-lactam antibiotics are primarily employed to treat nosocomial infections caused by multidrug-resistant (MDR) Gram-negative bacteria, including extended-spectrum beta-lactamase (ESBL) and AmpC-producing Enterobacterales, as well as resistant strains of *Acinetobacter* species and *Pseudomonas aeruginosa* (Tamma et al., 2024). More recently, meropenem-vaborbactam and imipenem-relebactam were approved for clinical use in human medicine. The addition of these newly developed beta-lactamase inhibitors helps to overcome resistance mechanisms, particularly those involving Ambler class A (such as KPC) and C beta-lactamases (see Section 3.1.1.1). This makes these drug combinations effective against certain carbapenem-resistant pathogens, providing a crucial treatment option for infections with limited alternatives (Vázquez-Ucha et al., 2020).

Carbapenems are classified by the World Health Organization (WHO) as 'Highest Priority Critically Important Antimicrobials' (HPCIA) in human medicine (WHO, 2024). Within the WHO's 'Access, Watch, Reserve (AWaRE)' framework for evaluating and monitoring antibiotic use, all carbapenems (classified under WHO Anatomical Therapeutic Chemical – ATC - group J01DH) fall under the 'Watch' category, except for meropenem-vaborbactam and imipenem-cilastatin-relebactam. 'Watch' antibiotics, with their broad-spectrum of activity, should be used with stewardship measures to limit empirical use to treat infections that are more likely to be resistant to 'Access' antibiotics. In contrast, 'Reserve' antibiotics are last-resort treatments for infections caused by multidrug-resistant organisms (MDROs) and should be preserved for such cases (WHO, 2023). These include new carbapenem combinations with beta-lactamase inhibitors, such as meropenem-vaborbactam and imipenem-relebactam.

1.3.2 | Carbapenem consumption in humans

Globally, while carbapenem consumption in humans remains low compared to other antibiotic classes, it increased by 74% between 2016 and 2023, mostly driven by increased consumption in middle-income countries, whereas consumption in high-income countries did not show major changes during this period (Klein et al., 2024). In the EU/European Economic Area (EEA), carbapenem consumption in humans is monitored through the European Surveillance of Antimicrobial Consumption Network (ESAC-Net), coordinated by the European Centre for Disease Prevention and Control (ECDC). More information on data collection and analysis is available from the ESAC-Net reporting protocol (ECDC, 2024a) and the ESAC-Net annual

[6] https://www.efsa.europa.eu/en/partnersnetworks/scorg.
[7] https://www.food.dtu.dk/english/topics/antimicrobial-resistance/eurl-ar.

epidemiological report (ECDC, 2024b), and data on carbapenem consumption are publicly available through the online ECDC antimicrobial consumption dashboard (ECDC, 2024c). In 2023, the total (community and hospital sectors combined) population-weighted mean carbapenem consumption in the EU/EEA was low compared to other antibiotic classes, with 0.06 defined daily doses (DDD) per 1000 inhabitants per day, ranging from 0.015 in the Netherlands to 0.195 DDD per 1000 inhabitants per day in Greece. The majority (98%) of carbapenem consumption occurred within the hospital sector, and all carbapenems consumed during this period were for parenteral use.

For the EU/EEA overall, no statistically significant trend in the population-weighted mean carbapenem consumption was observed between 2019 and 2023 (Figure 1). At country level, statistically significant increasing trends were observed for Croatia, Estonia, Lithuania, Spain and Portugal, and statistically significant decreasing trends for Belgium and Denmark.

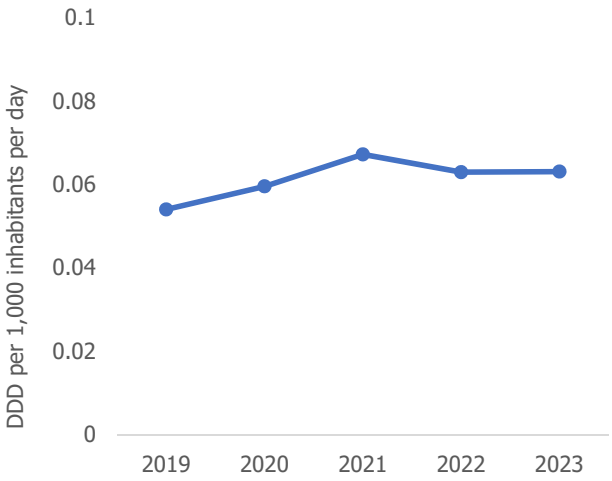

FIGURE 1 Total consumption of carbapenems in humans, EU/EEA, 2019–2023.* *Source:* ESAC-Net, ECDC, 2024. *DDD, defined daily doses. Total consumption corresponds to consumption in the community and hospital sectors combined. Carbapenems represent group J01DH of the Anatomical Therapeutic Chemical (ATC) classification system. EU/EEA refers to the population-weighted mean consumption, based on data from the 26 EU/EEA countries (Austria, Belgium, Bulgaria, Croatia, Czechia, Denmark, Estonia, Finland, France, Greece, Hungary, Iceland, Ireland, Italy, Latvia, Lithuania, Luxembourg, Malta, the Netherlands, Norway, Poland, Portugal, Romania, Slovakia, Slovenia and Spain) that continuously reported data to ESAC-Net on total antimicrobial consumption in humans for 2019–2023.

The latest ECDC point prevalence survey of healthcare-associated infections and antimicrobial use in European acute care hospitals 2022–2023 showed considerable variation in carbapenem use across hospitals in EU/EEA countries. The percentage of hospitalised patients receiving at least one carbapenem on the day of the survey ranged from 0.6% of patients in France to 11.6% in Cyprus (ECDC, 2024d). Carbapenems represented about 6% of all prescribed antimicrobials. These data underscore the importance of interventions to optimise carbapenem use in humans, thereby addressing the selective pressure that contributes to the development of MDROs including those resistant to carbapenems. Notably, previous ECDC analyses have observed statistically significant positive associations, at country level, between carbapenem consumption in humans and carbapenem resistance in invasive *E. coli* and *Klebsiella pneumoniae* isolates in the EU/EEA (ECDC, EFSA and EMA, 2024).

1.3.3 | Carbapenem use in animals

Carbapenems have never been authorised for use in animals in the EU/EFTA. Regulation (EU) 2019/6 on Veterinary Medicinal Products[8] recognised antimicrobial resistance as a major global public health threat, requiring urgent action using a One Health approach. Consequently, a range of risk management measures aimed at tackling AMR was introduced, including provisions to reserve certain antimicrobials for human use only, in order to preserve their efficacy.

Carbapenems were designated as antimicrobials reserved for human treatment as they met all three mandatory and cumulative criteria outlined in the Commission Delegated Regulation (EU) 2021/1760.[9] These criteria are:

- Criterion A: carbapenems are of high importance for preserving human health and should therefore be reserved for use in human medicine only.

[8]Regulation (EU) 2019/6 of the European Parliament and of the Council of 11 December 2018 on veterinary medicinal products and repealing Directive 2001/82/EC (Text with EEA relevance). https://eur-lex.europa.eu/legal-content/EN/TXT/PDF/?uri=CELEX:32019R0006.

[9]Commission Delegated Regulation (EU) 2021/1760 of 26 May 2021 supplementing Regulation (EU) 2019/6 of the European Parliament and of the Council by establishing the criteria for the designation of antimicrobials to be reserved for the treatment of certain infections in humans (Text with EEA relevance). OJ L 353, 6.10.2021, p. 1–5. https://eur-lex.europa.eu/legal-content/EN/TXT/PDF/?uri=CELEX:32021R1760.

- Criterion B: their use in animals could accelerate the spread of AMR by facilitating the transmission of resistance from animals to humans.
- Criterion C: they do not represent an essential need for animal health, and their absence in veterinary medicine would not have a significant impact on animal health or a major impact on animal welfare and public health.

As a result, the Commission Implementing Regulation (EU) 2022/1255 of 19 July 2022[10] designated carbapenems as one of the groups of antimicrobials reserved for the treatment of certain infections in humans, in accordance with Regulation (EU) 2019/6 of the European Parliament and of the Council.

Despite the absence of carbapenem use in animals, other antimicrobials to which CPE are also resistant could act as selective agents, particularly 3rd generation cephalosporins. According to the ESVAC report (EMA, 2023) between 2017 and 2022, the sales of 3rd- and 4th-generation cephalosporins decreased by 33.8% (from 0.19 mg/PCU to 0.13 mg/PCU). However, sales were unevenly distributed across countries submitting data.

2 | DATA AND METHODOLOGIES

2.1 | Data

2.1.1 | Data from the scientific literature

Scientific literature published from 2011 (first description of CPE in the food chain in the EU) to February 2025, as described in 2.2.2, was considered for the current opinion. Several of the reviewed publications referred to data collected through the EU monitoring, for which information was available at EFSA (2.1.2.) and/or directly gathered from the countries through the survey on CPE-positive findings (data included in supplementary information in Annex C). These data were thoroughly analysed and combined to avoid duplication.

2.1.2 | Data available at EFSA

Data reported to EFSA by EU/EFTA countries as part of the EU AMR monitoring programme, in accordance with Commission Implementing Decision 2013/652/EU[11] and 2020/1729[12] (see Section 3.1.4) were considered for this opinion. The following data sources were used:

- European Summary Reports on AMR in zoonotic and indicator bacteria from humans, animals and food (EUSR-AMR). Data on CPE-positive findings published in the EUSR-AMR for the monitoring programmes run from 2015 to 2023[13] (EFSA and ECDC, 2017, 2018, 2019, 2021, 2022, 2023, 2024, 2025).
- EFSA Data Warehouse – raw AMR monitoring data submitted to EFSA by EU/EFTA countries (source of the data published in the EUSR-AMR summary reports mentioned above).

For the current opinion, only isolates confirmed by molecular methods as CPE were included. Additional isolates exhibiting phenotypic resistance to carbapenems, though not yet confirmed, were excluded from the current assessment.

2.1.3 | Data from targeted surveys

Data for this opinion was collected through targeted surveys provided by EU/EFTA countries as indicated in 2.2.3. The data includes information on:

- Activities beyond official EU AMR monitoring: responses from 30 EU/EFTA countries on activities performed in addition to the official EU AMR monitoring programme, as required under Commission Implementing Decision (EU) 2020/1729.
- CPE-positive findings: data from 11 EU/EFTA countries with CPE-positive findings since 2011, both obtained within and outside the scope of the official EU AMR monitoring programme. A few countries already provided data through the survey for isolates collected within the 2024 EU monitoring, in advance to the official reporting period to EFSA (April–May 2025).[14]

[10]Commission Implementing Regulation (EU) 2022/1255 of 19 July 2022 designating antimicrobials or groups of antimicrobials reserved for treatment of certain infections in humans, in accordance with Regulation (EU) 2019/6 of the European Parliament and of the Council (Text with EEA relevance). https://eur-lex.europa.eu/legal-content/EN/TXT/PDF/?uri=CELEX:32022R1255.

[11]Commission Implementing Decision of 12 November 2013 on the monitoring and reporting of antimicrobial resistance in zoonotic and commensal bacteria (notified under document C(2013) 7145). (2013/652/EU). OJ L 303, 14.11.2013, p. 26–39. https://eur-lex.europa.eu/legal-content/EN/TXT/PDF/?uri=CELEX:32013D0652

[12]Commission Implementing Decision (EU) 2020/1729 of 17 November 2020 on the monitoring and reporting of antimicrobial resistance in zoonotic and commensal bacteria and repealing Implementing Decision 2013/652/EU. OJ L 387, 19.11.2020, p. 8–21. https://eur-lex.europa.eu/legal-content/EN/TXT/PDF/?uri=CELEX:32020D1729

[13]https://www.efsa.europa.eu/en/data-report/biological-monitoring.

[14]https://www.efsa.europa.eu/en/resources/data-collection-zoonoses.

- Laboratory methods: information from 30 EU/EFTA countries on the laboratory methods in use in EU/EFTA for isolating and characterising carbapenem-resistant Enterobacterales (CRE), CPE and/or carbapenemases in monitoring and research activities.
- Contingency plans and mitigation measures: details from 30 EU/EFTA countries on existing contingency plans and mitigation/control measures to address the spread of CPE in the food chain.

2.1.4 | Data provided by ECDC and other international institutions

Data provided by ECDC and/or published by other relevant institutions supporting the assessment of antimicrobial resistance across the EU/EEA included:

- EARS-Net: https://www.ecdc.europa.eu/en/about-us/networks/disease-networks-and-laboratory-networks/ears-net-data
- EARS-Net Annual Epidemiological Report: https://www.ecdc.europa.eu/en/publications-data/surveillance-antimicrobial-resistance-europe-2022
- EARS-Net Reporting Protocol: https://www.ecdc.europa.eu/en/publications-data/antimicrobial-resistance-amr-reporting-protocol-2024
- Assessing the health burden of infections with antibiotic-resistant bacteria in the EU/EEA, 2016-2020 Revised estimates of burden of disease for antimicrobial resistance: https://www.ecdc.europa.eu/en/publications-data/health-burden-infections-antibiotic-resistant-bacteria-2016-2020
- WHO Regional Office for Europe (WHO/Europe). Antimicrobial resistance dashboard. Copenhagen: WHO/Europe; 2023. Available at: https://worldhealthorg.shinyapps.io/WHO-AMR-Dashboard/
- European Centre for Disease Prevention and Control (ECDC). Antimicrobial consumption dashboard. Stockholm: ECDC; 2024. Available from: https://www.ecdc.europa.eu/en/antimicrobial-consumption/surveillance-and-disease-data/database

2.2 | Methodologies

2.2.1 | Approach to answer the ToRs

The approach to answer the ToRs was defined in advance and is described in the protocol (Annex A). It covers both the problem formulation (i.e. what the assessment aims to address) and which methods will be used for addressing the problem. The problem formulation ('what') includes the clarification of the mandate (see further refined in Section 1.2) and consists of the steps (1) translation of the mandate into scientifically answerable AQs, and (2) the selection of the approach for the assessment. The planning of the methods for conducting the assessment ('how') consists of specifying the evidence needs and the methods for answering each AQ, including the uncertainty analysis. Protocol development followed the draft framework for protocol development for EFSA's scientific assessments (EFSA Scientific Committee, 2023).

2.2.2 | Literature search and expert knowledge

A qualitative assessment was undertaken, based on the available literature and expert knowledge within the working group (WG) as detailed in the protocol (Annex A). The search strategy (search strings and databases) is included in Table A.1 (Appendix A). Literature searches were extended using the 'footnote chasing' method (White et al., 1992) and supplemented with citation contributions from WG members and members of the EFSA BIOHAZ Panel. The relevance of the records for providing information was assessed by screening titles and abstracts, as well as through the knowledge and expertise of the WG members. This review included international reports, EFSA scientific opinions and reports, scientific review papers, book chapters, peer-review articles and other documents known by the experts or retrieved through non-systematic searches.

2.2.3 | Survey

The surveys indicated in Section 2.1.3, created in the EU-surveys platform[15] were distributed to the EU/EFTA countries to gather information on CPE with the following objectives:

1. To provide basic information of ongoing and planned studies and activities on CPE in EU, that are funded from sources other than EFSA.
2. To summarise CPE-positive findings since 2011 within and beyond official EU monitoring, including information on plasmids, clones and other molecular characteristics.

[15] https://ec.europa.eu/eusurvey/home/welcome.

3. To provide an overview on the laboratory methods currently used for the detection and characterisation of CPE in the EU.
4. To outline contingency plans and control measures for CPE control that are currently in place across the EU to prevent or minimise the emergence and spread of CPE in the food chain, along with the challenges faced in their implementation or development.

Surveys were sent to the representatives of the AMR Subgroup of the Scientific Network for Zoonoses Monitoring,[16] which consulted the National Reference Laboratories for Antimicrobial Resistance[17] and national risk managers.

Questions included in the surveys are included in Annexes B1 (basic information), B2 (methods) and B3 (control options).

With regards to the CPE-positive findings, for those countries that had indicated to have CPE findings in the first survey (Annex B1), an excel sheet containing the EU-Monitoring data described in 2.1.2 and/or identified in the published literature/presentations for each EU/EFTA country was shared with the respective country requesting to ensure accuracy and to provide additional information, if available, for those isolates (sequence types, plasmids, etc.). Countries were also asked to provide information on additional isolates collected outside the EU-monitoring (e.g. research projects, trace back investigations, etc.). The information received was included in Table B.1 (Appendix B) and Supplementary information in Annex C.

2.2.4 | Uncertainty analysis

The need for an uncertainty analysis was considered, as recommended by the EFSA guidance and related principles and methods on uncertainty analysis in scientific assessments (EFSA Scientific Committee, 2018a, 2018b), and described in the protocol (Annex A). Since this scientific opinion describes what has been observed and what current practices are, it was agreed that an uncertainty analysis and the expression of the impact of the overall uncertainty in the answer to the terms of reference was not needed. However, the main sources of uncertainty related to ToR1 were identified by the experts and briefly reported in conclusions.

3 | ASSESSMENT

3.1 | Introduction

3.1.1 | Carbapenem resistance mechanisms

Resistance to carbapenems in Enterobacterales can arise from different mechanisms (please see Section 3.1.1.2), differing in terms of frequency from species to species, but with carbapenem-hydrolyzing enzymes (so-called carbapenemases) playing the most significant role. Apart from acquired production of carbapenem-hydrolyzing beta-lactamases, decreased susceptibility to carbapenems may result from production of beta-lactamases that are not categorised as carbapenemases, combined with permeability defects (mainly loss or modifications of outer membrane proteins). Those beta-lactamases being non-carbapenemases but possibly playing a role in carbapenem resistance are either some Ambler class A extended-spectrum beta-lactamases (such as CTX-M enzymes) or class C broad-spectrum beta-lactamases. In fact, those beta-lactamases may possess a very weak capacity to hydrolyze (or just to bind to) carbapenems, which is not sufficient to lead to reduced susceptibility to carbapenems in-vitro if not associated with a permeability defect. Likewise, those latter permeability defects may slightly affect the penetration of carbapenems into the bacterial cell but without impact on the susceptibility if not associated to a beta-lactamase. As an example, resistance to the carbapenem ertapenem may occur through production of acquired CTX-M-type ESBLs combined with permeability defects in *E. coli* (Girlich et al., 2008, 2009). Moreover, resistance to imipenem in *Enterobacter cloacae* is often due to a permeability defect combined with overexpression of the intrinsic AmpC-encoding gene in that species (Lee et al., 1991).

To summarise, both traits (production of certain beta-lactamases and permeability defects) are necessary to confer reduced carbapenem susceptibility or resistance but are not sufficient on their own. This contrasts with carbapenemases that may confer resistance to carbapenems per se, as they typically possess a significant capacity to hydrolyse the corresponding substrates directly.

The focus on CPE in both human medicine and the food chain is paramount due to their significant public health implications. CPE are not only sources of difficult-to-treat infections but also pose a substantial risk for further dissemination of resistance traits, primarily because carbapenemase genes are often plasmid-encoded (Bush & Bradford, 2020). This characteristic enables rapid spread between bacterial species and across different environments, including the food chain (Huang et al., 2023).

By contrast, combination of non-carbapenemase beta-lactamases together with permeability defects, that latter feature being chromosomally-encoded and consequently not readily transferable, implies that this resistance mechanism is less relevant in terms of infection control and prevention. This explains why only patients infected or colonised with carbapenemase-producing microorganisms are considered high risk for further dissemination in clinical settings, leading

[16] https://www.efsa.europa.eu/en/science/scientific-committee-and-panels/data.
[17] https://www.food.dtu.dk/english/topics/antimicrobial-resistance/eurl-ar/participants.

to the implementation of infection control measures (cohorting, contact precaution, isolation in dedicated rooms, reinforcement of hand hygiene, etc.). This feature explains also why carbapenemase-producing microorganisms are among the most serious threats for public health.

CPE relevance extends beyond healthcare settings into the food chain, explaining the dedicated focus made in this overall document. CPE have been detected in various food types, food-producing animals and their environments (EFSA BIOHAZ Panel, 2021), but also in general environmental sources (e.g. water, soil), providing a significant public health risk, as they provide additional routes for human exposure to and colonisation by CPE. Studies have highlighted the ability of plasmid-encoded carbapenemases to target multiple bacterial species, creating additional reservoirs not only within hospital settings but also in food-producing animals and food products (Falgenhauer et al., 2017; Gijón et al., 2020). This cross-species transfer potential further emphasises the critical need for comprehensive control and prevention strategies targeting CPE dissemination throughout the entire food chain, from farm to fork. Given these factors, the control and prevention of CPE dissemination is of utmost importance in both clinical and food safety contexts.

3.1.1.1 | *Carbapenemases*

Carbapenemases hydrolyse all ß-lactams including the carbapenems, except for monobactams (aztreonam). Based on their hydrolytic properties, carbapenemases are classified into two distinct groups, namely the serine carbapenemases (with an active site serine) and the metallo-β-lactamases (MBL) (requiring Zinc [Zn] ions in their active site). The group of serine carbapenemases includes beta-lactamases that belong to the molecular classes A and D, while the metallo-enzymes belong to class B of the Ambler classification (Table 1). According to the updated functional classification scheme (Bush & Jacoby, 2010), carbapenemases belong to subgroups 2f (class A), 2df (class D), 3a and 3b (class B).

Class A Carbapenemases

Among the class A carbapenemases, the most commonly identified in human medicine are the KPC- and GES-type enzymes. As of January 2025, a total of 245 different **KPC**-type enzymes have been identified (beta-lactamase database, http://bldb.eu/Enzymes.php). All KPC-type enzymes can be considered carbapenemases, although certain variants, such as those selected under the pressure of ceftazidime-avibactam use, may exhibit significantly reduced carbapenemase activity. Those variants may differ from a single amino acid substitution compared to the original enzyme, those mutations occurring in the omega loop (amino acid positions 164–179), with Asp179Tyr substitution being the most commonly identified (as observed in the KPC-33 sequence) (Lai et al., 2024), eventually leading to enhanced affinity toward ceftazidime and reduced binding of avibactam. Other variants may also exhibit amino acid insertions, such as for KPC-41 and KPC-50 (Mueller et al., 2019; Poirel et al., 2020). Worryingly, those isolates producing KPC variants being sources of resistance to ceftazidime-avibactam also show resistance to cefiderocol, the first siderophore antibiotic. This is particularly concerning because cefiderocol, designed to overcome resistance in multidrug-resistant pathogens, is hydrolyzed at higher level once such variants are produced (Poirel et al., 2022).

KPC-type beta-lactamases are most commonly reported from *K. pneumoniae*, but have been reported in almost all types of Enterobacterales. In addition, they have been, although rarely, identified in *P. aeruginosa*.

A total of 59 **GES-type** enzymes have been identified (beta-lactamase database, http://bldb.eu/Enzymes.php). The GES family of enzymes does only include a limited number of variants being categorised as carbapenemases. Indeed, the original variant GES-1 as well as many other GES variants are pure ESBLs, significantly hydrolyzing broad-spectrum cephalosporins but lacking any carbapenemase activity, while only some GES variants, through specific amino acid substitutions, additionally possess the capacity to compromise the efficacy of carbapenems.

By contrast, GES-type beta-lactamases are commonly identified from *P. aeruginosa* and *Acinetobacter baumannii* strains, and also *Aeromonas* spp. from environmental sources, but less commonly in Enterobacterales.

Class B Carbapenemases

Among the class B carbapenemases, the most commonly identified are the NDM, VIM and IMP enzymes. They all possess the capacity to hydrolyse significantly all beta-lactams, except aztreonam and are not inhibited by currently available beta-lactamase inhibitors. They do require zinc ions to be functional and their hydrolytic action can therefore be antagonised by different metal chelating agents, such as EDTA. Most of the time, acquisition of those MBL-encoding genes is plasmid-related and therefore additional resistance genes to other antibiotics are frequently co-acquired.

In particular, **NDM**-encoding plasmids have been identified in many diverse Gram-negative species, as a consequence of a high diversity of plasmid backbones on which the corresponding gene might be located. This diversity increases the likelihood of a plasmid being compatible with a given host, thereby facilitating the dissemination of bla_{NDM} genes at a higher rate. As of January 2025, there are 69 NDM variants being identified (http://bldb.eu/Enzymes.php). All those NDM variants possess a very similar hydrolysis profile, with some nuance observed in terms of catalytic efficiencies against carbapenems for some variants. NDM-1 is predominating and NDM-5 is increasingly reported and considered as an emerging threat, either in hospital settings or in the community, of NDM-5-producing *E. coli* isolates. Those isolates, often co-producing AmpC beta-lactamases of the CMY type and exhibiting modifications in their PBP3 protein, are resistant to the aztreonam-avibactam combination. The currently uniquely available beta-lactam-based therapeutic option can no

longer be considered for treating infections caused by those NDM-5-producing strains (Chakraborty et al., 2021; Sadek, Ruppé, et al., 2021). Hence, emergence of those NDM-5-producing *E. coli* strain backgrounds represents currently one of the major threats with respect to carbapenemase-producing microorganisms.

VIM enzymes, with 92 variants being reported so far (January 2025, http://bldb.eu/Enzymes.php), also constitute a homogeneous group of enzymes with respect to their hydrolysis profile, which is basically very similar to that of NDM enzymes. In terms of distribution, VIM enzymes are mainly found in *P. aeruginosa* and Enterobacterales in Europe.

Finally, the group of **IMP** enzymes gathers today a total of 106 variants, mainly found in South-East Asia and Australia, even though their identification in Europe is not so rare. Nevertheless, they are less predominant than the two former groups, namely NDM and VIM. As observed for VIM enzymes, they are mainly found in *P. aeruginosa* and less frequently in Enterobacterales.

Class D Carbapenemases

Among the class D beta-lactamases, a huge diversity exists, both in terms of amino acid sequence as in terms of hydrolysis profiles (Evans & Amyes, 2014). Despite more than 1200 OXA enzymes have been identified so far, only some subgroups exhibit carbapenemase activitiy. Many of those latter are intrinsic to some specific species, such as OXA-51-like enzymes being encoded by chromosomal genes of *A. baumannii* or OXA-50-like enzymes being intrinsic to *P. aeruginosa*. The most problematic OXA are those being acquired (most often through plasmid acquisition) and possessing carbapenemase activity. In Enterobacterales, OXA-48 and its derivatives are of major concern, since they have been identified worldwide, in a large array of species (Boyd et al., 2022). So far, a total of 57 variants of OXA-48 have been identified (http://bldb.eu/alignment.php?align=D:OXA-48-like). When looking at the epidemiology of class D carbapenem-hydrolyzing beta-lactamases, and even if OXA-48-like enzymes are still the almost only concerning ones, some evolutions have been observed during the last decade. Although OXA-48 was once the predominant variant, nowadays, many different OXA-48 derivatives (such as OXA-181, OXA-232, OXA-244 and OXA-484) have emerged. While sharing a similar hydrolytic pattern (hydrolyzing penicillins at high level, sparing broad-spectrum cephalosporins) these derivatives exhibit unique features. For instance, the hydrolytic activity toward carbapenems may be significantly weaker, hence conferring lower levels of resistance/reduced susceptibility to carbapenems and consequently being more difficult to be detected (Emeraud et al., 2020; Hoyos-Mallecot et al., 2017). Hence, some of the OXA-244-producing *E. coli* isolates may for instance still exhibit susceptibility to carbapenems, though they are often very close to the resistance breakpoints and/or the epidemiological cut-off values (ECOFFs).[18] As a result, they may go undetected when relying on selective media supplemented with carbapenem molecules. Such 'silent' spread of enzymes with carbapenemase properties is of significant concern, as it could lead to an increase frequency of carbapenem-based treatment failures when infections are caused by these underrecognised threats.

The corresponding genes are located onto plasmids possessing different backgrounds, with the pOXA-48a plasmid of the IncL type (previously named IncL/M; Poirel et al., 2012; Carattoli et al., 2015) being considered as epidemic and self-conjugating at high frequency.

The other carbapenem-hydrolysing class D beta-lactamases (CHDLs) of concern are the OXA-23, OXA-40 and OXA-58 subgroups of enzymes (Evans & Amyes, 2014). All these share the same hydrolysis pattern as the OXA-48-like enzymes, but the $bla_{\text{OXA-23}}$ gene is mostly found as chromosomally integrated in *A. baumannii*, contrasting with the more common plasmid-borne $bla_{\text{OXA-58}}$ and $bla_{\text{OXA-40}}$ (Grosso et al., 2011, 2012). Noteworthy, the $bla_{\text{OXA-23}}$ gene is intrinsic to the *Acinetobacter radioresistens* species, in which it is systematically identified. Interestingly, this gene is increasingly reported as being acquired in *Proteus mirabilis*, where it confers reduced susceptibility to carbapenems (Lombes et al., 2022). It represents one of the rare examples of a CHDL-encoding gene being found as acquired in an Enterobacterales species, as well as in the non-fermenting *A. baumannii* species.

TABLE 1 Acquired carbapenemases in clinically-relevant bacterial species.

Molecular class	Acquired carbapenemases	Bacterial species[a]
Class A	BIC	*Pseudomonas fluorescens*
	BKC	*Klebsiella pneumoniae, Enterobacter hormaechei* subsp. *xiangfangensis*
	FLC	*Enterobacter cloacae* complex
	FRI	*Enterobacter cloacae* complex
	GES	*Klebsiella pneumoniae, Escherichia coli, Serratia marcescens* *Acinetobacter baumannii, Pseudomonas aeruginosa*
	GPC	*Pseudomonas aeruginosa*
	KPC	Almost all clinically-relevant Enterobacterales species[b] *Pseudomonas aeruginosa, Pseudomonas putida*
	IMI	*Enterobacter cloacae* complex
	VCC	*Vibrio cholerae, Aeromonas caviae*

(Continues)

[18] https://mic.eucast.org/.

TABLE 1 (Continued)

Molecular class	Acquired carbapenemases	Bacterial species[a]
Class B	CAM	*Pseudomonas aeruginosa*
	DIM	*Pseudomonas stutzeri, Pseudomonas aeruginosa*
	FIM	*Pseudomonas aeruginosa*
	GIM	*Escherichia coli, Klebsiella pneumoniae, Enterobacter cloacae* complex *Pseudomonas aeruginosa*
	IMP	Almost all clinically-relevant Enterobacterales species,[b] *Shigella flexneri* *Acinetobacter baumannii, Pseudomonas aeruginosa, Achromobacter xylosoxydans*
	NDM	Almost all clinically-relevant Enterobacterales species,[b] *Acinetobacter baumannii, Pseudomonas aeruginosa*, other non-Enterobacterales
	SIM	*Acinetobacter baumannii, Pseudomonas aeruginosa*
	SPM	*Pseudomonas aeruginosa*
	TMB	*Enterobacter hormaechei, Citrobacter freundii* *Acinetobacter* spp., *Pseudomonas aeruginosa, Achromobacter xylosoxydans*
	VIM	Almost all clinically-relevant Enterobacterales species[b] *Acinetobacter baumannii, Pseudomonas aeruginosa*, other non-Enterobacterales
Class D	OXA-23-like[c]	*Acinetobacter baumannii* *Proteus mirabilis*
	OXA-48-like[c]	Almost all clinically-relevant Enterobacterales species[b]
	OXA-58-like[c]	*Acinetobacter baumannii*
	OXA-134-like[c]	*Acinetobacter baumannii*
	OXA-143-like[c]	*Acinetobacter baumannii*

[a]Enterobacterales species are written in black, while non-Enterobacterales species are shown in grey.

[b]*Klebsiella pneumoniae, Klebsiella aerogenes, Klebsiella oxytoca, Escherichia coli, Enterobacter cloacae* complex, *Salmonella enterica, Citrobacter freundii* complex, *Serratia marscescens, Raoultella* spp.

[c]Members and protein alignments can be seen in BLDB: http://bldb.eu/Enzymes.php (Naas et al., 2017): for OXA-23-like: http://bldb.eu/alignment.php?align=D:OXA-23-like; OXA-48-like: http://bldb.eu/alignment.php?align=D:OXA-48-like; OXA-58-like: http://bldb.eu/alignment.php?align=D:OXA-58-like; OXA-134-like: https://bldb.eu/alignment.php?align=D:OXA-134-like.

3.1.1.2 | *Carbapenem resistance due to other mechanisms*

While carbapenemases remain the primary mechanism of carbapenem resistance in Gram-negative bacteria, several other significant mechanisms can contribute to carbapenem non-susceptibility. However, the complex interplay of these mechanisms can make it challenging to definitively identify all contributing factors in a given isolate. These additional mechanisms include: (a) ESBL or AmpC hyperproduction, (b) reduced hydrolysis of carbapenems, particularly ertapenem, by ESBLs, e.g. CTX-M-15, (c) outer membrane impermeability due to porin alteration or loss by point mutations or deletions, (d) decreased permeability due to pleiotropic mutations that influence the expression levels of porins or non-specific efflux, (e) overexpression of efflux pumps and (f) modifications in penicillin-binding proteins (PBPs).

3.1.2 | Significance and public health threat of human infections with carbapenemase-producing Enterobacterales (CPE)

In a recent update of its rapid risk assessment (RRA), ECDC reiterated that carbapenem-resistant Enterobacterales represents a significant threat to patients and healthcare systems in EU/EEA countries due to their associated high mortality, primarily caused by delays in administration of effective antimicrobial therapy and the limited number of alternative and easily available treatment options, despite the existence of newly approved antimicrobials (ECDC, 2025). Carbapenem-resistant *K. pneumoniae* alone was estimated to be responsible for 38,668 (95% uncertainty interval (UI): 34,020 – 43,658) infections and 4076 (95% UI: 3565– 4585) attributable deaths in the EU/EEA in 2020 (Annex 1 of ECDC, 2022).

Since the previous ECDC RRA in 2019, there have been various signs that the epidemiological situation in the EU/EEA continues to deteriorate (ECDC, 2025). These signs include:

- an increase in the incidence of carbapenem-resistant *K. pneumoniae* bloodstream infections in 23 EU Member States due to continued transmission of high-risk lineages of carbapenem-resistant *K. pneumoniae* in hospitals;
- convergence of virulence and resistance in *K. pneumoniae*, including healthcare-associated spread of hypervirulent *K. pneumoniae* ST23 carrying carbapenemase genes;
- newly emerging Enterobacterales species (e.g. *Providencia stuartii*) carrying carbapenemase genes;
- plasmid-mediated spread of carbapenemase genes causing outbreaks within hospitals and across healthcare networks; and

– increasing detection of isolates (including isolated cases and clusters) of high-risk lineages of *E. coli* carrying carbapenemase genes with a risk of spreading in the community.

ECDC considered the risk for further spread of carbapenem-resistant Enterobacterales in the EU/EEA as high-to-very-high due to frequent cross-border importation events after patient transfer between countries, large regional outbreaks, and the fact that implementation of infection prevention and control (IPC) measures is suboptimal in many hospitals and has so far been insufficient to achieve sustained control of high-risk lineages of carbapenem-resistant *K. pneumoniae* and other Enterobacterales (ECDC, 2025).

According to EARS-Net data from 2023, the EU incidence of carbapenem-resistant *K. pneumoniae* bloodstream infections was estimated at 3.97 per 100,000 population (country range: 0.00–21.44). This was 57.5% higher than in 2019 (baseline year), with a statistically significant increasing trend between 2019 and 2023 (ECDC, 2024e). Spread of carbapenemase-producing *K. pneumoniae* has been primarily associated with the spread of high-risk clones in hospital networks in EU/EEA countries (David et al., 2019). The most frequent carbapenemase-producing *K. pneumoniae* sequence types (STs) detected in the European Survey of carbapenemase-producing Enterobacteriaceae (EuSCAPE) in 2013/2014 were ST11, ST15, ST101 and ST258/512 (David et al., 2019). While these STs remained widespread across European hospitals in 2019 (ECDC carbapenem- and/or colistin-resistant Enterobacterales, CCRE survey, report in preparation), additional *K. pneumoniae* STs emerged, such as ST147, ST307 and ST39. Frequent transmission events within hospitals are driving the repeated emergence and rapid spread of new high-risk clones throughout healthcare systems (Tryfinopoulou et al., 2023).

Hypervirulent carbapenem-resistant *K. pneumoniae* (hvKp) poses an additional threat with a potential for cross-border dissemination. While previously hvKp were only rarely observed in the EU/EEA, sustained healthcare-associated spread of hvKp ST23 carrying carbapenemase genes has now been reported in Ireland (Brennan et al., 2022). ECDC considers the risk for further spread and establishment of hvKp carrying carbapenemase genes in healthcare settings in EU/EEA countries with consequent significant impact on morbidity and mortality as high (ECDC, 2024f).

Despite the rapid dissemination of carbapenemase-producing high-risk clones of *K. pneumoniae*, carbapenem resistance in *E. coli* had so far remained low. Carbapenem-resistant *E. coli* was estimated to be responsible for 1987 (95% UI: 1662–2361) infections and 157 (95% UI: 129–185) attributable deaths in the EU/EEA in 2020, much less than for carbapenem-resistant *K. pneumoniae* (Annex 1 of ECDC, 2022). In 2023, the EU incidence of carbapenem-resistant *E. coli* bloodstream infections was estimated at only 0.14 per 100,000 population (country range: 0.00–0.73) (ECDC, 2024e). However, there are now various examples of increasing spread of carbapenemase-producing *E. coli* in the EU/EEA involving various combinations of high-risk STs and carbapenemase genes, including *E. coli* ST167, ST361, ST405, ST410 and ST648 carrying $bla_{\text{NDM-5}}$ (ECDC, 2023; Linkevicius et al., 2023) and *E. coli* ST38 carrying $bla_{\text{OXA-244}}$ (ECDC, 2021). In addition, the predominant extraintestinal pathogenic *E. coli* (ExPEC) high-risk lineage ST131 can acquire carbapenemase genes. *E. coli* ST131 is frequently resistant to several antibiotic groups and has been a main driver of the global dissemination of the $bla_{\text{CTX-M-15}}$ ESBL gene (Mathers et al., 2015). There is a high risk that *E. coli* ST131 may play a similar role in the dissemination of carbapenemase genes. WGS and epidemiological data from 17 national reference laboratories participating in the European Antimicrobial Resistance Genes Surveillance Network (EURGen-Net) showed that *E. coli* ST131 had acquired 18 different carbapenemase genes, most frequently $bla_{\text{OXA-244}}$ and $bla_{\text{OXA-48}}$. In particular, *E. coli* ST131 isolates carrying $bla_{\text{OXA-244}}$ increased rapidly since 2021 with large multi-country clusters (Kohlenberg et al., 2024). ExPEC have been identified in non-human reservoirs including food, companion and food-producing animals, sewage and other environmental sources (Manges & Johnson, 2015). They can be transmitted via the faecal-oral route, sexual contact, foodborne exposure or within household environments (Manges et al., 2019) making it difficult to control their spread within the human population. Further spread of ExPEC carrying carbapenemase genes would mean that carbapenems could no longer be reliably effective for empiric treatment of severe *E. coli* infections. The increasing detection of *E. coli* isolates carrying carbapenemase genes is therefore a significant public health concern urgently requiring public health action.

Besides the increasing spread of the most frequent species, i.e. *K. pneumoniae* and *E. coli*, carrying carbapenemase genes, an ECDC survey from 2023 showed that other carbapenemase-producing Enterobacterales species are being detected in EU/EEA countries including *Citrobacter freundii* complex, *E. cloacae* complex, *K. oxytoca*, *Proteus* spp., *P. stuartii* and *Serratia marcescens* (ECDC, unpublished data). Especially NDM-producing *P. stuartii* recently received attention due to cross-border spread related to medical transfers from Ukraine (Witteveen et al., 2024). Further investigation provided evidence for a wider dissemination of NDM-producing *P. stuartii* in Eastern Europe and the Balkan region including in Bulgaria, Greece, Hungary, North Macedonia and Serbia (ECDC, 2024g; Linkevicius et al., 2024). While carbapenemase-producing *K. pneumoniae* and *E. coli* remain the main public health threat in the EU/EEA, carbapenemase-producing *P. stuartii* and other carbapenemase-producing Enterobacterales species will require enhanced surveillance in the coming years.

3.1.3 | Epidemiology of CPE in the food chain outside EU/EFTA countries

Although the focus of this document is on the EU/EFTA food chain, it is worth mentioning other reports of CPE findings worldwide. Indeed, it has been shown that import products might also constitute significant sources of CPE for the EU/EFTA. Hence, considering the extra-EU/EFTA epidemiology is therefore crucial for accurate surveillance and monitoring, and accordingly, some examples are included below.

In recent years, the number of reports of CPE in the food chain has increased across various countries and continents. This rise is likely due in large part to a growing number of studies on this topic worldwide, but it may also reflect an actual

increase in the occurrence of these CPE globally. In any case, this trend in terms of number of studies and reports clearly indicates that carbapenem resistance is a substantial issue in many regions outside the EU/EFTA (Huang et al., 2023; Kot & Witeska, 2024; Ramírez-Castillo et al., 2023).

China represents the country with the highest number of reported CPE in the food chain (Huang et al., 2023; Ramírez-Castillo et al., 2023). However, it is important to acknowledge that China has also conducted and published the most comprehensive number of studies investigating this issue, probably creating a surveillance bias in the global epidemiological data.

Among the published studies focussing on primary animal production and food at retail (e.g. local markets), the most common CPE reported were *E. coli* and *Klebsiella* spp.. However, *Salmonella enterica, Proteus* spp. and other Enterobacterales species, have also been identified. Reports of CPE in the food chain originate mainly from Asian and African countries, but there are also several reports from the Middle East. On the top of that, a few reports from South America (e.g. Brazil, Peru, others) have been published, emphasising that the issue of CPE in the food chain calls for a global perspective.

It is noteworthy that in the aforementioned countries outside Europe, CPE have been identified not only in terrestrial food-producing animals and their environments, but also in the meat thereof, foods of aquatic animal origin and in foods of non-animal origin, mainly vegetables. The occurrence of CPE in livestock, poultry, seafood and fresh produce/vegetables indicates widespread contamination and thereby a risk of human exposure across all regions. The evidence is highest for vegetables, meat (especially poultry) and pigs as common sources of CPE in the food chain (Huang et al., 2023; Ramírez-Castillo et al., 2023; Sugawara et al., 2019; Taggar et al., 2020). Although several sources have been identified, it remains difficult to appreciate the extent of CPE contamination. Indeed, methodologies may significantly vary from country to country, including sampling methods and detection tools (screening approach and determination of the resistance mechanisms among others).

Analysis of the published studies show that occurrence of carbapenemases in non-EU/EFTA areas vary depending on the type of animals, with particularly high levels observed in *E. coli* from poultry and pigs in Asia (eg. China, India, Pakistan, South Korea, others) (bla_{KPC-2}, bla_{NDM}, bla_{IMP}, bla_{VIM}, bla_{OXA-48}) and Africa (bla_{NDM-5}, $bla_{OXA-244}$) (Hayer et al., 2022; Sadek et al., 2022). Dairy products and bovine animals have been also described as a source of CPE (e.g. Lebanon, Türkiye, Egypt, India). Noteworthy, a high number of CPE have also been described for various aquatic species/aquaculture products in certain countries (shrimps, fish, oysters, eg. from Vietnam, Egypt, Tunisia, etc), including reports on bla_{NDM} (Asia, Africa), bla_{KPC} (Africa) or bla_{OXA-48} (Africa) genes (Das et al., 2019; Hamza et al., 2020). Moreover, food products of non-animal origin (fresh and/or ready-to-eat vegetables from China, Japan, Myanmar, Ghana, others) have been found to carry CPE with bla_{NDM} (Asia, Africa, South America), bla_{KPC} (Asia, South America), bla_{OXA-48}-like (Asia, Africa) genes and bla_{VIM-4} (Africa), with some strains showing links to clinical isolates, suggesting in some instances a human-driven contamination, for instance through handling.

Overall, and even if a great diversity of carbapenemase types have been identified in non-EU countries with large population sizes such as China and India, NDM-like seem to be the predominating enzymes, reflecting the observations in humans, with the NDM-1 variant predominating (Ramírez-Castillo et al., 2023; Taggar et al., 2020). The very concerning occurrence of NDM-5-producing *E. coli*, which is nowadays a major threat reported worldwide in humans, was highlighted through its identification in several Asian countries, e.g. among retail eggs in China (Liu et al., 2023), but also in aquaculture contexts (grass carps) (Lv et al., 2022), vegetables (Lv et al., 2024) and swine, chicken and duck farms (Kuang et al., 2022; Wen et al., 2023; Zheng et al., 2024) in China, and in *Klebsiella* spp. from farmed-fresh water fish in India (Dwivedi et al., 2023).

The Middle East, especially Egypt, has reported the presence of OXA-48-like and NDM carbapenemases in *E. coli* and *K. pneumoniae* isolated from various food sources, including camel meat and poultry (Taggar et al., 2020; Touati & Mairi, 2020a).

In Africa, the countries where the majority of studies dealing with food products or food-producing animals have been conducted are Algeria, Egypt, Nigeria, South Africa and Tunisia (Alonso et al., 2017; Sadek, Poirel, et al., 2020; Sadek, Nariya, et al., 2020; Sadek, Soliman, et al., 2021; Sadek et al., 2022; Touati & Mairi, 2020b). In these countries, a large diversity in carbapenemase-producing species was observed, with Enterobacterales being the most common, often identified in seafood.

From the North and Central American regions, there have been relatively few reports from isolates related to livestock, such as *Raoultella ornithinolytica* isolated from pork sausage samples in the USA, co-harbouring both bla_{KPC-2} and bla_{NDM-5}, and *K. pneumoniae* ST258 isolated from bovine mastitis with bla_{KPC-2} in Mexico (Ballash et al., 2021; Silva-Sánchez et al., 2021). In contrast, other CPE have been found in imported seafood in the USA and Canada (Janecko et al., 2016; Parker et al., 2024; Tate et al., 2022).

In South America (mainly from Brazil), different CPE have been detected, with reports from poultry farms and retail chicken meat (*K. pneumoniae* with bla_{KPC-2} in Brazil, Valiatti et al., 2022; *E. coli* with bla_{KPC-3} in Peru, Murray et al., 2021), calves (eg. bla_{OXA-48} in *Salmonella enterica*, Gabana et al., 2022) and vegetables (bla_{KPC-2} and bla_{NDM-1}, Furlan et al., 2024).

In general, the data suggest a connection between human and animal isolates, irrespective of region, with a major role of certain plasmids in the spread of carbapenemase-encoding genes across various environments. The high rates observed in some countries are concerning and highlight the need for stronger surveillance and mitigation strategies, especially in areas where surveillance and response systems may be lacking. A One Health approach, integrating human, animal and environmental health, is needed to address effectively the drivers of carbapenem resistance worldwide.

3.1.4 | Harmonised EU AMR monitoring targeting carbapenemase-producing Enterobacterales (*E. coli, Salmonella enterica*) in zoonotic and commensal bacteria from food-producing animals and meat thereof

In the EU, the monitoring of AMR in zoonotic and commensal bacteria from food-producing animals and meat thereof is performed yearly by the EU MSs and three EFTA countries in an harmonised way as laid down in the legislation (Directive 2003/99/EC,[19] Commission Implementing Decision 2013/652/EU (1-01-2014 to 21-12-2020) and its update (EU) 2020/1729 (entering into effect on 1 January 2021-ongoing). Accordingly, monitoring of AMR is mandatory in non-typhoidal *Salmonella enterica subsp. enterica* serovars, *Campylobacter jejuni* and indicator commensal *E. coli*, and voluntary in other selected bacteria of public health importance from food-producing animals and their derived meat in the EU MSs.

Apart from the routine monitoring of AMR (AMR MON) for the bacteria mentioned above, the EU monitoring also includes (i) the mandatory specific monitoring of ESBL/AmpC/carbapenemase-producing *E. coli* (ESBL MON, WGS ESBL MON) and (ii) the specific one on carbapenemase-producing *E. coli* (CARBA MON, WGS CARBA MON). On the contrary to the routine one, these last require selective isolation[20,21] and characterisation (antimicrobial susceptibility test and/or WGS gene detection) of the isolates, as well as the non-selective detection and characterisation of indicator commensal *E. coli* and *Salmonella enterica* isolates with resistance to third-generation cephalosporins or carbapenems (see Section 3.4). Both specific monitoring programmes collect isolates derived from randomised sampling in food-producing animals at slaughter, as well as meat at retail and at border control posts. The monitoring focuses on healthy animals belonging to the animal populations to which the consumer is most likely to be exposed through food, such as domestic poultry (mainly broilers and fattening turkeys), fattening pigs and bovine animals under 1 year of age.

The EU monitoring is conducted on a biennial basis, with sampling carried out on a rotating schedule. In odd years, the focus is on fattening pigs, bovine animals under 1 year of age and their derived meat, while in even years, the focus shifts to poultry populations (broilers and fattening turkeys) and their derived meat. Additional information, including sampling sizes and the number of isolates to be tested etc., can be found in Commission Implementing Decision (EU) 2020/1729.

The overview on the progression over time on the countries performing those specific monitoring programmes since the entry in force of Commission Implementing Decision 2013/652/EU and (EU) 2020/1729, till the latest reported year (2023) are shown in Figures 5 and 6.

3.2 | Current status of carbapenemase-producing Enterobacterales in the food chain in the EU/EFTA (AQ1)

This assessment compiles available information on CPE detection in the food chain focusing on their occurrence, geographical and temporal distribution, associated bacterial species and clones, carbapenemase-encoding genes and mobile genetic elements. Data were gathered through an extensive review of scientific literature, EFSA reports and databases and information provided by the MSs, as detailed in Section 2.1.

Positive-findings stem from isolates collected through the EU-monitoring programme (described in Section 3.1.4), national monitoring initiatives and research studies. In some instances, countries with positive detections performed trace back investigations, which increased the number of reports and introduced variability in the sources, bacterial species and other factors.

An overview of the positive carbapenemase-encoding genes and CPE considered in this opinion is presented in Figures 2–4 and Tables 2–3. Detailed information on those positive-findings (380 isolates and 6 additional positive findings from microbiota/microbiome analysis) are provided in Table B.1 (Appendix B) and supplementary information in Annex C. The following sections highlight key insights for all isolates, with additional details on notable individual CPE reports. A dedicated Section (3.2.5) focuses exclusively on data from the EU-monitoring programme.

[19]Directive 2003/99/EC of the European Parliament and of the Council of 17 November 2003 on the monitoring of zoonoses and zoonotic agents, amending Council Decision 90/424/EEC and repealing Council Directive 92/117/EEC. OJ L 325, 12.12.2003, p. 31–40. https://eur-lex.europa.eu/legal-content/EN/TXT/PDF/?uri=CELEX:32003L0099.

[20]https://www.food.dtu.dk/english/-/media/institutter/foedevareinstituttet/temaer/antibiotikaresistens/eurl-ar/protocols/esbl-ampc-and-camrbapenemase-producing-e-coli/esbl_ampc_cpeprotocol_version_caecal_v9_17122024.pdf.

[21]https://www.food.dtu.dk/english/-/media/institutter/foedevareinstituttet/temaer/antibiotikaresistens/eurl-ar/protocols/esbl-ampc-and-camrbapenemase-producing-e-coli/esbl_ampc_cpeprotocol_version_meat_v9_17122024.pdf.

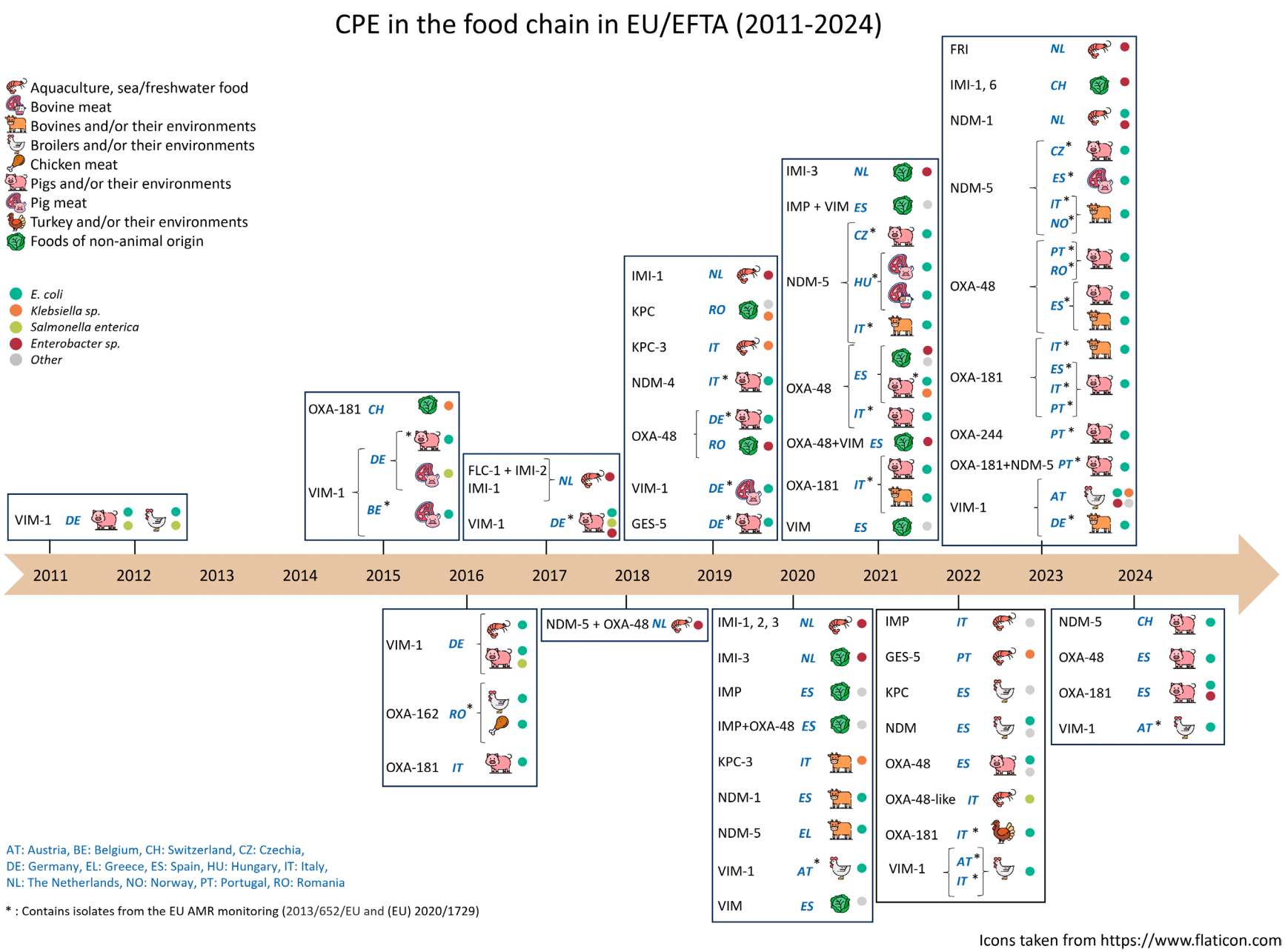

FIGURE 2 Temporal representation of the occurrence of CPE in food-producing animals, their environment and foods of animal and non-animal origin in the EU/EFTA, 2011–2024. Additionally, in 2016 and 2019, OXA-48 and IMI-2 in *Enterobacter* spp. were isolated from fishery lakes and feed mills in Romania and Sweden, respectively. The terms grouped within each matrix are shown in the glossary.

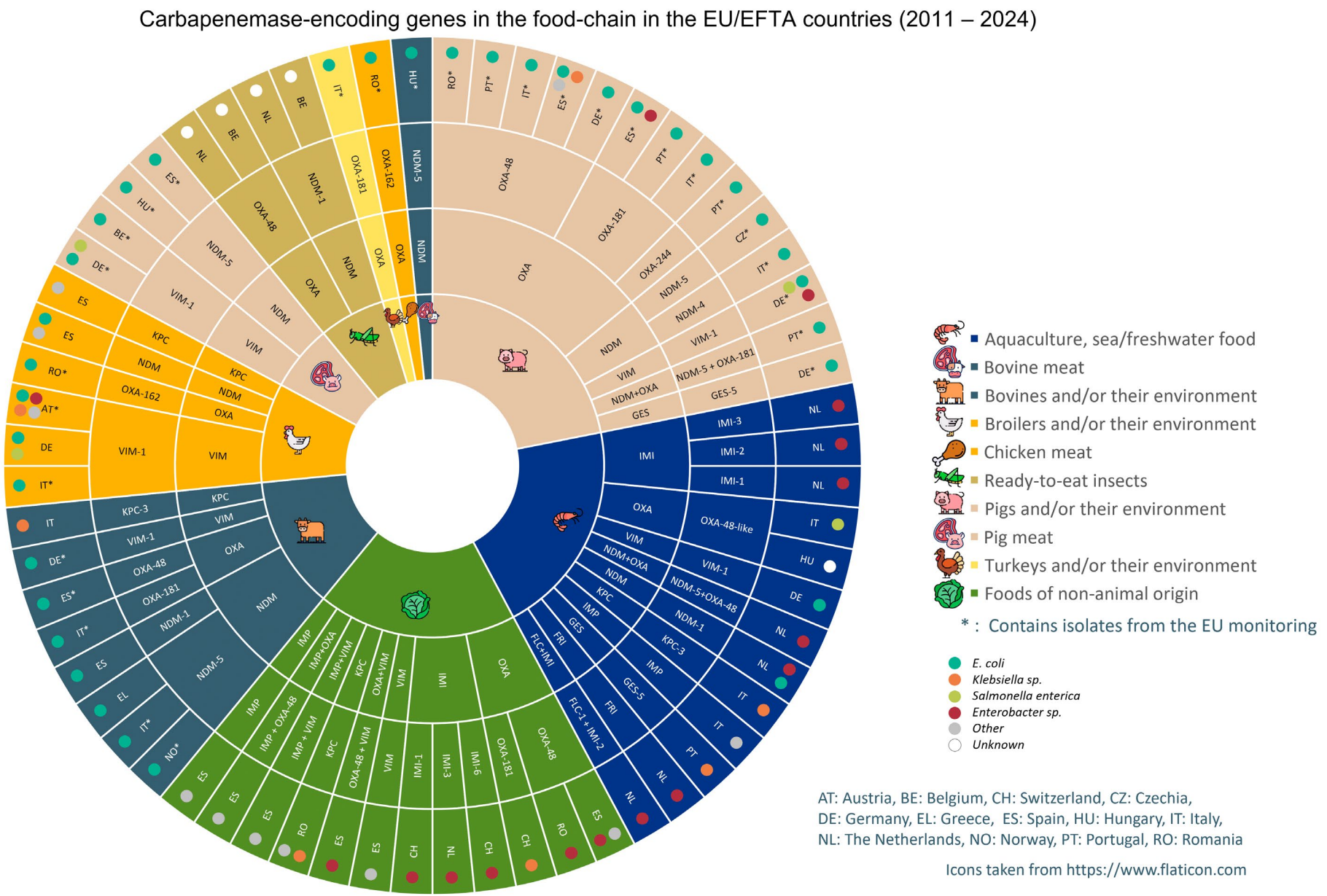

FIGURE 3 Occurrence of carbapenemase-encoding genes in food-producing animals, their environment and food of animal and non-animal origin in the EU/EFTA, 2011–2024. Additionally, IMI-2 and OXA-48 in *Enterobacter* spp. were isolated from feed mills and fishery lakes in Sweden and Romania, respectively. The size of the segments of the circle does not correspond to the number of isolates found, but to the different combinations (countries, genes, gene family, source). The terms grouped within each matrix are shown in the glossary.

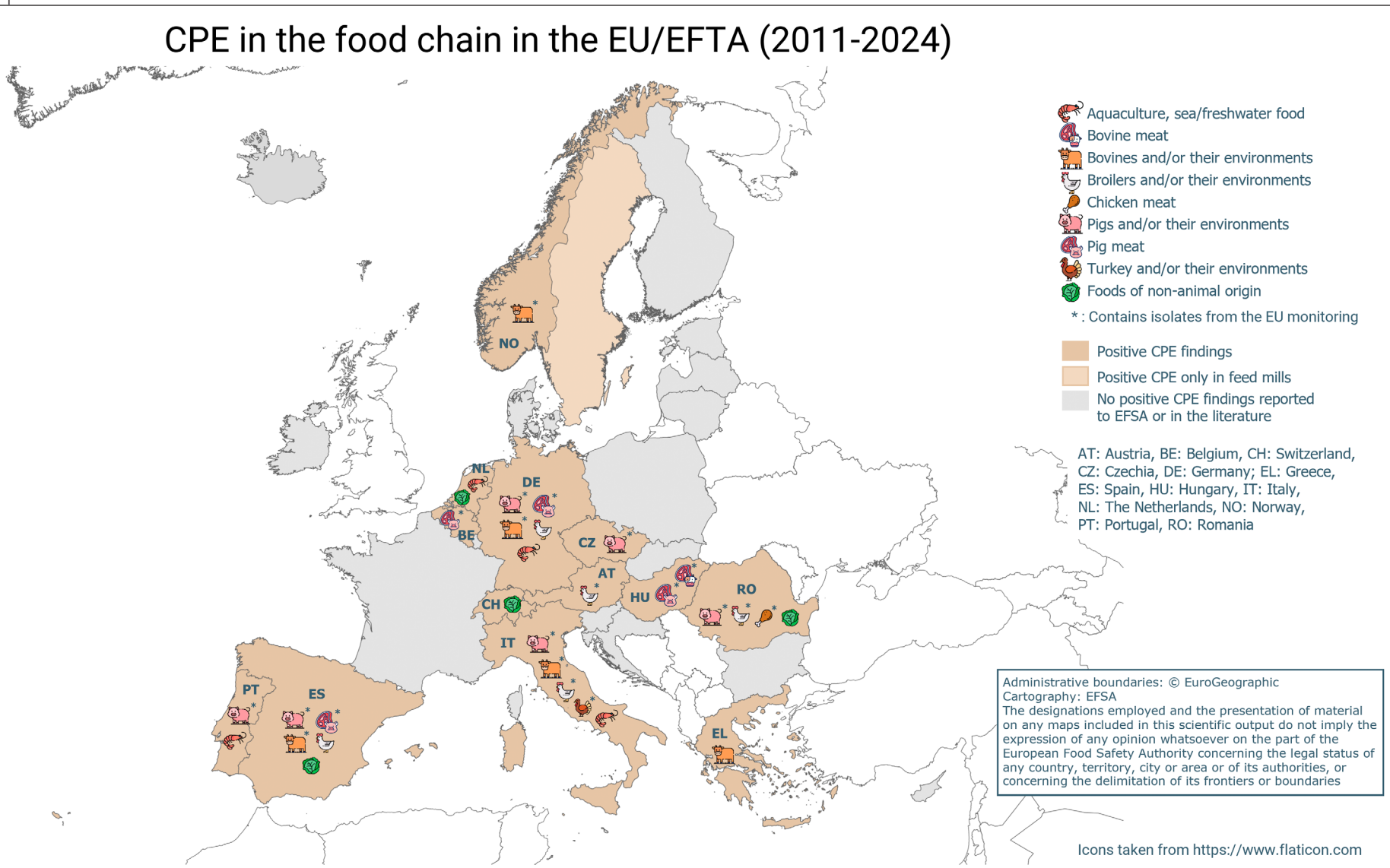

FIGURE 4 Geographical representation for the occurrence of CPE in food-producing animals, their environments and foods of animal and non-animal origin in the EU/EFTA, 2011–2024. Adittionally, CPE were also reported from feed mills in Sweden and fishery lakes in Romania. The terms grouped within each matrix are shown is the glossary. *Kosovo – this designation is without prejudice to positions on status and is in line with United Nations Security Council Resolution 1244 and the International Court of Justice Opinion on the Kosovo Declaration of Independence.

3.2.1 | What carbapenemase-encoding genes, carbapenemase-producing bacterial species and clones were found in the food chain in the EU/EFTA? (SQ1.1-SQ1.3)

At least 22 gene variants belonging to nine carbapenemase families were detected, with *bla*$_{OXA}$, *bla*$_{VIM}$ and *bla*$_{NDM}$ gene families being the most frequent, while the remaining families included *bla*$_{IMI}$, *bla*$_{IMP}$, *bla*$_{KPC}$, *bla*$_{GES}$, *bla*$_{FRC}$ and *bla*$_{FLC}$. The most commonly reported carbapenemase genes were *bla*$_{VIM-1}$, *bla*$_{OXA-48}$ and *bla*$_{OXA-181}$, followed by *bla*$_{NDM-5}$ and *bla*$_{IMI-1}$. Less common genes included *bla*$_{NDM-1}$, *bla*$_{OXA-162}$, *bla*$_{GES-5}$, *bla*$_{IMI-3}$ and *bla*$_{KPC-3}$, with rare instances of other genes like *bla*$_{OXA-244}$ and gene combinations (e.g. bla$_{NDM-5}$ + *bla*$_{OXA-48}$, *bla*$_{NDM-5}$ + *bla*$_{OXA-181}$) (see Figure 2 for occurrence overview and Table B.1 in Appendix B, and supplementary data in Annex C for specific isolates).

Distribution varied along the food chain, as illustrated in Figure 3. There was broader gene variety in foods of aquatic animal origin and foods of non-animal origin than from those from livestock, poultry and meat thereof. Also, pig production showed the greatest gene variety among the terrestrial food-producing animals (details on matrix-gene occurrence is included in Section 3.2.3).

The primary carbapenemase-producing microorganism detected was *E. coli*. However, this is also the species most assays are designed to primarily detect. In addition to *E. coli*, *Enterobacter cloacae* complex (*E. cloacae, E. asburiae* and *E. hormaechei*), *K. pneumoniae* complex (*K. pneumoniae* and *K. variicola*) and *Salmonella Infantis* were also often reported. There were also a few or single reports of *Klebsiella oxytoca complex (K. oxytoca* and *K. michiganensis)*, other *Salmonella enterica* serovars (*S.* Goldcoast and *S.* Enteritidis), *E. vonholyi, Serratia fonticola, Rahnella* spp., *Pantoea* spp., *Raoultella* spp., *Citrobacter* spp., *Kluyvera cryocrescens*, *Morganella morganii* and *Proteus* spp. (Figures 2 and 3, Tables 2 and 3, Table B.1 in Appendix B; and supplementary information in Annex C). *E. coli* isolates were recovered mainly from the different terrestrial food-producing animal species and/or their environments, as well as from meat thereof. Carbapenemase-producing *Enterobacter* spp. strains were mainly isolated from foods of non-animal origin and foods from aquatic animal origin, being sporadically isolated also from pigs and broilers, while *Klebsiella* spp. isolates were collected from aquaculture products, vegetables, pigs, bovines and broilers and/or their environments. In general, limited data were available on bacterial species beyond *E. coli*, which is the primary focus of current systematic monitoring efforts.

For those isolates for which molecular typing data were available, isolates exhibit diverse sequence types (STs) across key genera/species (Tables 2 and 3). *E. coli* showed the highest diversity, with at least 66 STs, 36 of them grouped into 13 ST-complexes[22] (ST-Cplx), followed by *Enterobacter* spp. (at least 10 STs), *Klebsiella* spp. (4 STs) and *Salmonella enterica* (2 STs), though most of these STs are represented by one to three isolates.

Ubiquitous STs, detected across multiple sources and countries, include *E. coli* ST23-Cplx (ST88, ST410), ST101-Cplx (ST5229, ST101) and ST10-Cplx (ST10, ST48, ST744) and ST542, alongside *S.* Infantis ST32 (Table 2).

E. coli ST10 was associated with the broadest variety of carbapenemase genes, including *bla*$_{NDM-5}$, *bla*$_{OXA-181}$, *bla*$_{OXA-48}$, *bla*$_{OXA-162}$ and *bla*$_{VIM-1}$, and has been found in pigs, bovines, chicken meat and seafood, reflecting its widespread presence across animal-derived products. ST101 carries *bla*$_{NDM-5}$, *bla*$_{OXA-181}$, *bla*$_{OXA-48}$ and *bla*$_{VIM-1}$, and was mainly isolated from pigs. ST5229 (also ST101-Cplx) was linked to *bla*$_{OXA-181}$ and *bla*$_{OXA-48}$, and was detected in pigs, bovines and occasionally turkeys, indicating a broad livestock distribution. ST410, from the ST23-Cplx, carries *bla*$_{OXA-181}$ and *bla*$_{OXA-48}$, and was predominantly found in pigs, whereas ST88, also from the ST23-Cplx, was associated mainly with *bla*$_{VIM-1}$ and was found in pigs and their environments, reflecting a more limited resistance and distribution profile. These STs highlight the varying degrees of carbapenemase diversity within *E. coli* CPE sequence types, with ST10 standing out for its extensive carbapenemase gene diversity and source coverage, as illustrated in Table 2.

K. pneumoniae ST307 (*bla*$_{KPC-3}$ in bovine milk filters, Italy), a clinically significant ST and ST525 (*bla*$_{OXA-48}$ in pigs, Spain), an ST also associated with human infection cases (Pitout et al., 2019) were reported, along with *K. michiganensis* ST382 (*bla*$_{KPC-3}$, in seafood, Italy).

S. Infantis ST32 encoding *bla*$_{VIM-1}$ were recovered from poultry environments, pigs and their environments and pig meat.

It is of relevance to note that clonal assignment based on phylogenomic analyses was not conducted in most of the studies considered. Sequence type (ST) and ST complex assignments were generally used instead to infer clonal relationships. Nevertheless, this approach lacks the granularity needed for precise clonal identification, as full sequence data (e.g. WGS) are unavailable for most isolates. This limits detailed insights into identity with public health-relevant clones.

[22]According to Enterobase, STs are arbitrary constructs and natural populations can each encompass multiple, related ST variants. Therefore, 7-gene STs are grouped into ST Complexes in *Escherichia/Shigella* by an eBurst approach and into their equivalent eBurst groups (eBGs) in *S. enterica*. https://enterobase.readthedocs.io/en/latest/enterobase-tutorials/deeper-lineages.html.

TABLE 2 Carbapenemase-encoding genes, bacterial species and sequence types found in the food chain in EU/EFTA countries.

Carbapenemase type[a](n)	Bacteria	Sequence type complex (if available), sequence type (country, number if different than 1)	Reference[b]
FLC-1 + IMI-2 (1)	*Enterobacter* spp.	ST813 (NL)	Brouwer et al. (2019), Survey
FRI (1)	*Enterobacter* spp.	NA (NL)	Bruggemana et al. (2024), Survey
GES-5 (3)	*Escherichia coli*	ST1084 (DE), NA (DE)	Irrgang, Tausch, et al. (2020), EFSA and ECDC (2021)
	Klebsiella spp.	DLV644 (PT)	Freire et al. (2023)
IMI-1 (12)	*Enterobacter* spp.	[ST412, ST477, ST820, ST1516, ST3044, ST3052 (CH)], ST411 (CH, NL), NA (NL)	Tresch et al. (2024), Brouwer et al. (2018), Bruggemana et al. (2024), Survey
IMI-2 (2)	*Enterobacter* spp.	ST657 (SE), NA (NL)	Börjesson et al. (2022), Bruggemana et al. (2024), EFSA and ECDC (2022), Survey
IMI-3 (3)	*Enterobacter* spp.	NA (NL)	Bruggemana et al. (2024), EFSA and ECDC (2022, 2023), Survey
IMI-6 (1)	*Enterobacter* spp.	ST657 (CH)	Tresch et al. (2024)
IMP (8)	Other (*Proteus* spp. *Serratia* spp.)	NA (IT, ES)	Jiménez-Belenguer et al. (2023), Ferri et al. (2023)
IMP + OXA-48 (1)	Other (*Rahnella* spp.)	NA (ES)	Jiménez-Belenguer et al. (2023)
IMP + VIM (2)	Other (*Rahnella* spp.)	NA (ES)	Jiménez-Belenguer et al. (2023)
KPC (3)	*Klebsiella* spp.	NA (RO)	Colosi et al. (2020)
	Other (*Citrobacter* spp., *Morganella* spp.)	NA (RO, ES)	Panera-Martínez et al. (2024), Colosi et al. (2020)
KPC-3 (2)	*Klebsiella* spp.	[ST307, ST382 (IT)]	Simoni et al. (2022), Bonardi et al. (2023)
NDM (20)	*Escherichia coli*	NA (ES, RO)	Panera-Martínez et al. (2024), Lazăr et al. (2021)
	Other (*Serratia* spp.)	NA (ES)	Panera-Martínez et al. (2024)
NDM-1 (7)	*Enterobacter* spp.	NA (NL)	Bruggemana et al. (2024), Survey
	Escherichia coli	ST11626 (ES), NA (NL)	Tello et al. (2022), Bruggemana et al. (2024), EFSA and ECDC (2025), Survey
	NA (microbiota)[c]	NA (BE, NL)	Milanović et al. (2018)
NDM-4 (1)	*Escherichia coli*	ST86 Cplx: ST641 (IT)	Diaconu et al. (2020), EFSA and ECDC (2021), Survey
NDM-5 (26)	*Escherichia coli*	**ST10-Cplx**: [**ST10**, ST3489 (CZ)], [ST617, ST15567 (IT)] ST46-Cplx: ST46 (CZ) **ST101-Cplx**: **ST101** (CZ) ST155-Cplx: ST58 (CZ) ST405-Cplx: ST405 (HU) [ST75, ST898, ST1147, (CZ)], ST361 (EL), NA (NO, ES)	Tsilipounidaki et al. (2022), EFSA and ECDC (2023, 2025), EURL-AR WorkshopMeeting_2023_Ivanova; Survey
NDM-5 + OXA-181 (5)	*Escherichia coli*	NA (PT)	EFSA and ECDC (2025)
NDM-5 + OXA-48 (1)	*Enterobacter* spp.	NA (NL)	Bruggemana et al. (2024), Survey
OXA-162 (3)	*Escherichia coli*	**ST10-Cplx**: **ST10** (RO) ST155-Cplx: ST155 (RO) ST4980 (RO)	Bortolaia et al. (2021), EFSA and ECDC (2018), Survey

TABLE 2 (Continued)

Carbapenemase type[a](n)	Bacteria	Sequence type complex (if available), sequence type (country, number if different than 1)	Reference[b]
OXA-181 (84)	*Enterobacter* spp.	ST134 (ES)	Survey
	Escherichia coli	**ST10-Cplx**: **ST10** (IT, ES), **ST48** (IT, ES), [ST34, ST218, ST744, ST761, ST3489 (IT)], ST5708 (ES) **ST23-Cplx**: **ST410** (IT, ES) ST86-Cplx: ST641 (IT) **ST101-Cplx**: [**ST101**, ST359 (IT)], **ST5229** (IT, ES) ST155-Cplx: ST58 (IT), ST1015 (ES) ST156-Cplx: ST348 (IT) ST165-Cplx: ST165 (IT) ST469-Cplx: ST4623 (ES) [ST117, ST540, ST1152, ST1494, ST244, ST3014, ST4450, ST5752, ST7461 (IT)], ST542 (IT, ES), ST4038 (ES), NA (IT, PT, ES)	Carfora et al. (2022), Pulss et al. (2017), EFSA and ECDC (2023, 2024, 2025); Survey
	Klebsiella spp.	NA (CH)	Zurfluh et al. (2015)
OXA-244 (1)	*Escherichia coli*	NA (PT)	EFSA and ECDC (2025)
OXA-48 (88)	*Enterobacter* spp.	NA (ES, RO)	Jiménez-Belenguer et al. (2023), Colosi et al. (2020)
	Escherichia coli	**ST10-Cplx**: **ST10** (ES), ST34 (ES), **ST48** (ES), ST744 (ES), ST1303 (ES), ST10170 (ES) **ST23-Cplx**: [**ST88**, ST360, ST1725, **ST410**, ST1998 (ES)], ST295 (DE) ST38-Cplx: ST38 (IT) ST46-Cplx: ST46 (ES) ST86-Cplx: [ST453, ST641, ST877, (ES)] ST155-Cplx: ST58 (ES) **ST101-Cplx**: [**ST101**, **ST5229**, (ES)] ST448-Cplx: ST448 (ES) [ST117, ST457, ST542, ST1011, ST1196, ST3014, ST4429, ST4682, ST5759, ST8432, (ES)], NA (PT)	Carfora et al. (2022), Irrgang, Pauly, et al. (2020), EFSA and ECDC (2021, 2023, 2025), Survey
	Klebsiella spp.	ST525 (ES)	Survey
	Other (*Kluyvera* spp., *Pantoea* spp., *Raoultella* spp.)	NA (ES)	Jiménez-Belenguer et al. (2023), Survey
	NA (microbiota)[c]	NA (NL, BE)	Milanović et al. (2018)
OXA-48 + VIM (1)	*Enterobacter* spp.	NA (ES)	Jiménez-Belenguer et al. (2023)
OXA-48-like (2)	*Salmonella enterica*	NA (IT)	Ferri et al. (2023)
	NA (microbiota)[c]	NA (HU)	Libisch et al. (2022)
VIM (5)	Other (*Serratia* spp., *Pantoea* spp., *Rahnella* spp.)	NA (ES)	Jiménez-Belenguer et al. (2023)

(Continues)

TABLE 2 (Continued)

Carbapenemase type[a](n)	Bacteria	Sequence type complex (if available), sequence type (country, number if different than 1)	Reference[b]
VIM-1 (101)	*Enterobacter* spp.	NA (AT, DE)	Roschanski et al. (2019), Survey
	Escherichia coli	**ST10-Cplx**: [**ST10**, **ST48**, (DE)] **ST23-Cplx**: **ST88** (DE) **ST101-Cplx**: **ST101** (AT) ST131-Cplx: ST131 (DE) ST155-Cplx: ST155 (AT) ST469-Cplx: ST679 (AT) [ST847, ST7593, ST5869, (DE)], ST154 (AT), ST216 (IT), ST5869 (BE), ST1196 (AT)	Fischer et al. (2012, 2013, 2017), Roschanski, Friese, et al. (2017, 2017), Roschanski et al., 2018), García-Graells et al. (2020), Irrgang et al. (2017, 2019, 2025), Pauly et al. (2021), EURL-AR WorkshopMeeting_2024_Irrgang; EFSA and ECDC (2017, 2019, 2021, 2022, 2024, 2025); Survey
	Klebsiella spp.	NA (AT)	Survey
	Salmonella enterica	*S*. Infantis ST32 (DE) *S*. Goaldcoast ST358 (DE)	Fischer et al. (2013, 2017), Borowiak et al. (2017), Roschanski et al. (2019), EFSA and ECDC (2019); Survey
	Other (*Citrobacter* spp.)	NA (AT)	Survey

Note: (n): Number of isolates with those genes. ST-Cplx, Multilocus Sequence type complex (for *E. coli*) according to Enterobase https://enterobase.warwick.ac.uk/; ST: multilocus sequence type reported by authors/countries. Those marked in bold represent the most frequently reported.

Abbreviations: AT, Austria; BE, Belgium; CH, Switzerland; DE, Germany; EL, Greece; ES, Spain; HU, Hungary; IT, Italy; NL, The Netherlands; PT, Portugal; RO, Romania; SE, Sweden; NO, Norway.

[a]Although the data were obtained from carbapenemase gene characterisation, the protein designation (e.g. NDM-1 instead of bla_{NDM-1}) is used as a surrogate for the corresponding gene.

[b]Survey: Information received from the EU/EFTA countries with positive findings, and the literature review is included in Table B.1 in Appendix B and supplementary information in Annex C. Presentations provided at the EURL-AR Network Workshops meetings can be accessed at: https://www.food.dtu.dk/english/topics/antimicrobial-resistance/eurl-ar/presentations/workshop-2024 and https://www.food.dtu.dk/english/topics/antimicrobial-resistance/eurl-ar/presentations/workshop-2023

[c]Genes reported from microbiota analyses (qPCR and/or metagenomic), without linking genes to the specific bacterial species.

3.2.2 | What are the mobile genetic elements associated with the carbapenemase-encoding genes? (SQ1.4)

According to the information available (Table 3, Table B.1 in Appendix B, and supplementary information in Annex C), the spread of carbapenemase genes within the food chain is facilitated by mobile genetic elements, such as transposons and integrons that can be transferred among different plasmid types. Conjugative plasmids promote horizontal gene transfer between bacteria of different species circulating in different sources. This section lists plasmid types associated with the most common carbapenemase genes identified in the food chain.

The carbapenemase-encoding genes $bla_{\text{VIM-1}}$ and $bla_{\text{OXA-162}}$ were associated with plasmids belonging to the Incompability group (Inc) IncHI2 in *E. coli* and *Salmonella* from minced pig meat, a sick piglet and slaughter pigs in Germany (Falgenhauer et al., 2017; Fischer et al., 2012, 2013; Roschanski et al., 2018), and *E. coli* from healthy broilers in Romania (Bortolaia et al., 2021). The $bla_{\text{VIM-1}}$ gene was also identified on IncC plasmids in *E. coli* from pig meat in Germany and Belgium (García-Graells et al., 2020; Pauly et al., 2020).

The $bla_{\text{OXA-181}}$ gene has been commonly reported in the food chain, associated with IncX3 plasmids in *E. coli* from Italy and Switzerland (Carfora et al., 2022; Pulss et al., 2017; Zurfluh et al., 2015), while $bla_{\text{OXA-48}}$ was associated with IncL and IncI1 plasmids (Irrgang, Pauly, et al., 2020, EFSA and ECDC, 2025, Table B.1 in Appendix B; and supplementary information in Annex C). The $bla_{\text{NDM-1}}$ gene was detected on IncC plasmids in *E. coli* isolated from cattle in Spain (Tello et al., 2022), $bla_{\text{NDM-4}}$ was located on IncFII plasmids in *E. coli* of pig origin in Italy (Diaconu et al., 2020) and $bla_{\text{NDM-5}}$ was located on IncX3 plasmids in *E. coli* from pigs in Czechia (EFSA and ECDC, 2023, 2025; Table B.1 in Appendix B; and supplementary information in Annex C).

TABLE 3 Distribution of carbapenemase-encoding genes on plasmids in Enterobacterales from the food chain in the EU/EFTA (2011–2024).

Carbapenemase type[a]	Carba gene plasmid-location	Bacterial species (ST)	Source	Year	Country	References[b]
VIM-1	IncHI2 (pST1)	*E. coli* (**ST88**, ST48, ST131, ST593, ST7593), *Salmonella* Infantis (**ST32**), *S.* Goldcoast (ST358), *E. cloacae*	Pigs, pig meat, broiler, including farm-related environments	2011, 2012, 2015, 2016, 2017	DE	Fischer et al. (2012, 2013, 2017), Roschanski, Friese, et al. (2017); Roschanski et al. (2018, 2019), Borowiak et al. (2017), Pauly et al. (2021), EFSA and ECDC (2019), Irrgang et al. (2019), Survey
	IncC	*E. coli* (**ST5869**)	Pig meat	2015, 2019	BE, DE	García-Graells et al. (2020), Pauly et al. (2021), EFSA and ECDC (2017, 2021), Survey
	Untypable plasmid	*E. coli* (ST847)	Bovines	2023	DE	Irrgang et al. (2025), EFSA and ECDC (2025), Survey
	IncY	*E. coli* (ST10)	Seafood	2016	DE	Roschanski et al. (2017)
OXA-48	IncL	*E. coli* (ST34, ST46, ST48, ST58, ST88, **ST101**, ST117, ST295, ST360, **ST410**, ST448, ST457 ST453, ST542, ST525, ST641, ST744, ST877, ST1011, ST1725, ST1998, ST3014, ST4429, **ST5229**, ST8432), *Kluyvera cryocrescens* *K. pneumoniae* (ST525)	Pigs, bovines	2019, 2021, 2022, 2023	DE, ES	Irrgang, Pauly, et al. (2020), EFSA and ECDC (2021, 2025), Survey
	IncI1	*E. coli* (**ST10**, ST34, **ST410**, ST448, ST641, ST877, ST1196, ST1303, ST1998, ST4682, **ST5299**)	Pigs	2021, 2022, 2023, 2024	ES	EFSA and ECDC (2025); Survey
OXA-181	IncX3 (ΔColKP3)	*E. coli* (**ST10**, ST48, ST117, ST218, ST359, **ST410**, ST461, ST542, ST1015, ST3489, ST4038, ST4623, **ST5229**, ST5708, ST7461), *E. cloacae* (ST134), *Klebsiella variicola*	Pigs, spices	2015, 2016, 2021, 2022, 2023, 2024	IT, ES, CH	Carfora et al. (2022), Pulss et al. (2017), Zurfluh et al. (2015), EFSA and ECDC (2023, 2025), Survey
	ColKP3	*E. coli* (**ST10**, **ST410**, nearest ST7941)	Pigs	2023	ES	EFSA and ECDC (2025) Survey
	IncFII	*E. coli* (ST542, **ST5229**)	Pigs	2021	IT	Carfora et al. (2022), EFSA and ECDC (2023), Survey
	IncX1	*E. coli* (**ST5229, ST744**)	Pigs, humans	2021	IT	Carfora et al. (2022), EFSA and ECDC (2023), Survey
OXA-162	IncHI2 (pST4)	*E. coli* (**ST10**, ST155, ST4980)	Broiler, chicken meat	2016	RO	Bortolaia et al. (2021), EFSA and ECDC (2018), Survey
NDM-5	IncX3	*E. coli* (**ST10**, ST46, ST58, ST75, **ST101**, ST3469, ST898, ST1147)	Pigs	2021, 2023, 2024	CZ	EFSA and ECDC (2023, 2025), Survey
	IncFII	*E. coli* (ST361)	Bovines	2020	EL	Tsilipounidaki et al. (2022)
NDM-1	IncC	*E. coli* (ST11626)	Bovines	2020	ES	Tello et al. (2022)
NDM-4	IncFII	*E. coli* (ST641)	Pigs	2019	IT	Diaconu et al. (2020), EFSA and ECDC (2021), Survey
IMI-2, FLC-1	IncFII(Y)	*E. cloacae* (ST813)	Seafood	2017	NL	Brouwer et al. (2019), Survey
IMI-6	IncFII(Yp)	*E. asburiae* (ST657)	Vegetables	2023	CH	Tresch et al. (2024)

TABLE 3 (Continued)

Carbapenemase type[a]	Carba gene plasmid-location	Bacterial species (ST)	Source	Year	Country	References[b]
KPC-3	IncFII	*K. michiganensis* (ST382)	Seafood/aquaculture	2018, 2019	IT	Simoni et al. (2022)
GES-5	ColE	*K. pneumoniae, E. coli* (ST1084)	Seafood, pigs	2019, 2022, 2023	PT, DE	Freire et al. (2023), Irrgang, Tausch, et al. (2020), EFSA and ECDC (2021), Survey

Note: ST: multi-locus sequence type. Those marked in bold represent the most frequent STs reported.

Abbreviations: BE, Belgium; CH, Switzerland; CZ, Czechia; DE, Germany; EL, Greece; ES, Spain; IT, Italy; NL, The Netherlands; PT, Portugal; RO, Romania.

[a]Although the data were obtained from carbapenemase gene characterisation, the protein designation (e.g. NDM-1 instead of bla_{NDM-1}) is used as a surrogate for the corresponding gene.

[b]Survey: Information received from the EU/EFTA countries with positive findings, and the literature review is included in Table B.1 in Appendix B and supplementary information in Annex C.

3.2.3 | What are the sources in which those CPE and carbapenemase-encoding genes were found? (SQ1.5)

The CPE reported for samples taken in the EU/EFTA food chain originated from terrestrial food-producing animals and their environments (especially pigs, followed by bovines and poultry) and animal-derived products (e.g. pig and chicken meat) including those from aquatic animals, as well as food of non-animal origin (vegetables, herbs and spices) (Figures 2 and 3; Table B.1 in Appendix B and supplementary information in Annex C).

Most of the reported CPE were collected from pig samples (183 of 380 isolates, 257 when including also pig-associated environments), mostly originating from the EU/National AMR monitoring and/or trace back investigations performed by countries with positive findings (Table B.1).

The most common gene reported for isolates from pig production was $bla_{\text{VIM-1}}$, followed by $bla_{\text{OXA-48}}$, $bla_{\text{OXA-181}}$ and $bla_{\text{NDM-5}}$ ($bla_{\text{GES-5}}$, $bla_{\text{OXA-244}}$ and $bla_{\text{NDM-4}}$ were also reported), associated mainly to *E. coli*, as this is one of the main target species in the EU/National AMR monitoring. A diverse range of *E. coli* STs/ST Cplx were reported, as detailed in Table B.1 (Appendix B) and supplementary information in Annex C, with some, such as ST5229 and ST88 detected across farms (Carfora et al., 2022; Fischer et al., 2017). For bovine animals, the most common reported genes were $bla_{\text{OXA-181}}$ and $bla_{\text{NDM-5}}$ with also some reports of *E. coli* ST5229, whereas for broilers it was $bla_{\text{VIM-1}}$ in *E. coli*.

Raw meat samples from pig, chicken and bovines were occasionally contaminated with CPE indistinguishable from those described in the terrestrial animal species (e.g. ST32 *S.* Infantis carrying $bla_{\text{VIM-1}}$ in IncHI2/HI2A, pig production, Germany) (Table B.1 in Appendix B and and supplementary information in Annex C).

Additionally, CPE contamination in farm environments (eg. dust, waste) was also relatively frequent, and spread of carbapenemase-producing bacteria into the surrounding soil and water bodies could occur, making farms themselves reservoirs/sources for CPE in the wider environment (Borowiak et al., 2017; Carfora et al., 2022; EFSA BIOHAZ Panel, 2021). The presence of CPE (IMI-2 carrying *E. asburiae*) was also detected in livestock feed mills (Börjesson et al., 2022) and slaughterhouse environments (Panera-Martínez et al., 2024).

Reports on CPE from foods derived from aquatic animals and foods of non-animal origin (vegetables, herbs and spices) are more frequent than those from meat products, with a few documented cases collected from primary production, imported products at border control posts, processing plants and retail samples (Table B.1 and supplementary information in Annex C). CPE from these sources exhibited a greater diversity in carbapenemase genes and bacterial species (nine and five gene families, in seafood and vegetables, respectively). The $bla_{\text{IMI-1}}$ and bla_{IMP} gene were frequent in isolates from both seafood and vegetables. In addition, there were reports of $bla_{\text{NDM-1}}$ in seafood, KPC in vegetables, as well as a few single observations of other carbapenemase-types in both types of foods. Notably, those samples revealed the presence of a recently recognised carbapenemase gene, $bla_{\text{FLC-1}}$, in imported seafood, alongside genes more frequently associated with environmental samples, like $bla_{\text{IMI-2}}$ (Aubron et al., 2005). Moreover, there were more frequent combinations of different carbapenemase genes in one isolate, and the presence of bacterial species rarely associated with infections (e.g. *Pantoea* spp.). These findings suggest that methodological approaches differing from the monitoring programme, which prioritises *E. coli* and *Salmonella* may contribute to detecting this broader diversity.

As previously mentioned, there were also reports of carbapenemase-encoding genes ($bla_{\text{NDM-1}}$, $bla_{\text{OXA-48}}$) commonly associated with Enterobacterales in ready-to-eat insects[23] (mealworms and grasshoppers, considered as novel foods) (Milanović et al., 2018).

Overall, the complexity of the food production chain and the fact that CPE have been detected in virtually all steps of these chains makes it difficult to pinpoint specific reservoirs of carbapenemase-producing bacteria. This is complicated by the fact that official monitoring and reporting target only certain animals, food products and steps in the food production chain. Therefore, there is a large uncertainty on the relative contributions of different food products and processes in the dissemination of CPE. That said, the majority of observations of carbapenemase-producing isolates within the food chain are from pigs or pig production. Therefore, the food production chain associated with pigs warrants particular attention. Furthermore, there might also be additional sources and dissemination routes of CPE in the food production chain that are not included in the EU monitoring or targeted by existing research studies. Some settings that need to be considered, but where knowledge gaps exist, are foods of non-animal origin (e.g. fresh vegetables) – both imported and domestic, foods of aquatic- animal origin (e.g. aquaculture products), particularly imported goods and novel types of foods, such as edible insects, feed, as well as other livestock production (e.g. rabbits farming). There are indications that all of these might be important sources of CPE, but the current data is very limited.

3.2.4 | What is the geographical and temporal distribution of CPE? (SQ.1.6)

Since the first findings of CPE in the food chain in Germany in 2011–2012, CPE have been detected in 14 out of 30 EU/EFTA reporting countries: Austria, Belgium, Czechia, Germany, Greece, Hungary, Italy, Norway, the Netherlands, Portugal, Romania, Spain, Sweden and Switzerland (Figures 2–4, Table B.1 in Appendix B and supplementary information in Annex C).

[23]Data from positive-findings from ready-to-eat insects and fish indicate carbapenemase genes within the sampled microbiome but do not confirm their association with Enterobacterales, unlike culture-based data from other sources (Table 2, Annex C).

Data show a steady rise in CPE detections from 2015 to 2024 (Figures 5–6; Figure 2), driven particularly by pigs (257/380 isolates, Table B.1), which remain the most affected source across multiple countries including Czechia, Germany, Italy, Portugal, Romania and Spain (more details in Section 3.2.5).

Over time, CPE reports have extended beyond pigs, and include also bovines and poultry, though with fewer reports - e.g. $bla_{OXA-181}$ and bla_{NDM-5} in bovines (Italy) and bla_{VIM-1} in poultry (Germany, Austria) - and increasingly to animal-derived foods, (e.g. pig meat, chicken meat, seafood), foods of non-animal origin (e.g. vegetables, herbs, spices), novel foods (e.g. insects) and environmental reservoirs (e.g. farm dust, water bodies), (Figures 2 and 3).

Notably, detections in foods of aquatic animal origin and foods of non-animal origin, often linked to imported goods, have surpassed those in meat products in several years. Meanwhile, farm environments, including dust, have been identified as reservoirs of CPE, allowing the persistence of carbapenemases, as exemplified by the detection of bla_{VIM-1} in German pig farms since 2011 (Roschanski et al., 2019). Of concern, a 2022 report highlighted a Swedish feed mill contaminated with bla_{IMI-2} in *Enterobacter asburiae*, which could potentially contribute to the spread across livestock (Börjesson et al., 2022), although up to date, no CPE isolated food production animals or foods have been reported by this country (Table B.1; Figure 2).

New carbapenemase-encoding genes have emerged since 2015. Notably, bla_{NDM-5}, bla_{OXA-48}, $bla_{OXA-181}$ and bla_{VIM-1} persist across years and/or countries (e.g. bla_{VIM-1} in pigs in Germany, also in poultry in Austria, $bla_{OXA-181}$ in pigs in Italy – also bovines, Spain, emerging in Portugal in 2023, as well as bla_{NDM-5} in pigs from Czechia). Since 2015 there has been a significant increase in the number and diversity of *E. coli* STs, with over 50 new STs identified. However, uncertainty surrounds the true extent of CPE occurrence, as increased reports may reflect enhanced testing rather than prevalence rises.

Long-term systematic monitoring data offer clearer insights into pig, bovines and poultry production systems. Thus, a more detailed analysis of the EU monitoring data is presented in Section 3.2.5.

3.2.5 | EU wide analysis focusing on the isolates recovered within the harmonised EU monitoring (SQ1.6)

When considering only the isolates reported from the EU monitoring performed between 2015 and 2023 (Figures 5–7), the following findings can be highlighted:

- Evolving CPE epidemiology in the EU/EFTA food chain, with 11 countries reporting positive-findings and with increasing reports of carbapenemase genes in food-producing animals, particularly pigs.
- In 2015, carbapenemase-encoding genes were detected for the first time in food-producing animals within EU Monitoring. Single and multiple newly detected genes were seen in 2016 ($bla_{OXA-162}$), 2019 (bla_{OXA-48}, bla_{NDM-4}, bla_{GES-5}), 2021 ($bla_{OXA-181}$, bla_{NDM-5}) and 2023 ($bla_{OXA-244}$).
- Several genes were detected repeatedly in food-producing animals over a number of years after their first detection (bla_{NDM-5}, bla_{OXA-48}, $bla_{OXA-181}$, bla_{VIM-1}).
- Repeated detection of the same gene was also seen within the same animal reservoir and within the same country (e.g. bla_{NDM-5} in fattening pigs in Czechia, $bla_{OXA-181}$ in fattening pigs and bovines in Italy).
- Several genes have been found in food-producing animals in multiple EU/EFTA countries (bla_{NDM-5}, bla_{OXA-48}, $bla_{OXA-181}$, bla_{VIM-1}).
- Carbapenemase-encoding genes were detected more frequently in animals compared to animal-derived food, being detected more frequently in pigs. Lesser findings were seen in bovines followed by poultry, despite the fact that for bovines, fewer samples were tested compared to pigs and poultry.
- An increase in the number of positive-findings with regards to the previous years was seen in pigs in 2021/2023 for $bla_{OXA-181}$ and bla_{OXA-48} in Italy and Spain respectively. In Portugal, whereas in the previous years no detection had been reported, in 2023, different genes and gene combinations, including $bla_{NDM-5} + bla_{OXA-181}$, were detected for the first time.
- Some countries only reported positive findings for one single year (e.g. Belgium, Hungary, Portugal and Norway).

Some of these countries, such as Italy, Spain, Czechia, Austria, Germany, Norway and Portugal, have performed trace back investigations to identify potential epidemiological links as described in the previous sections.

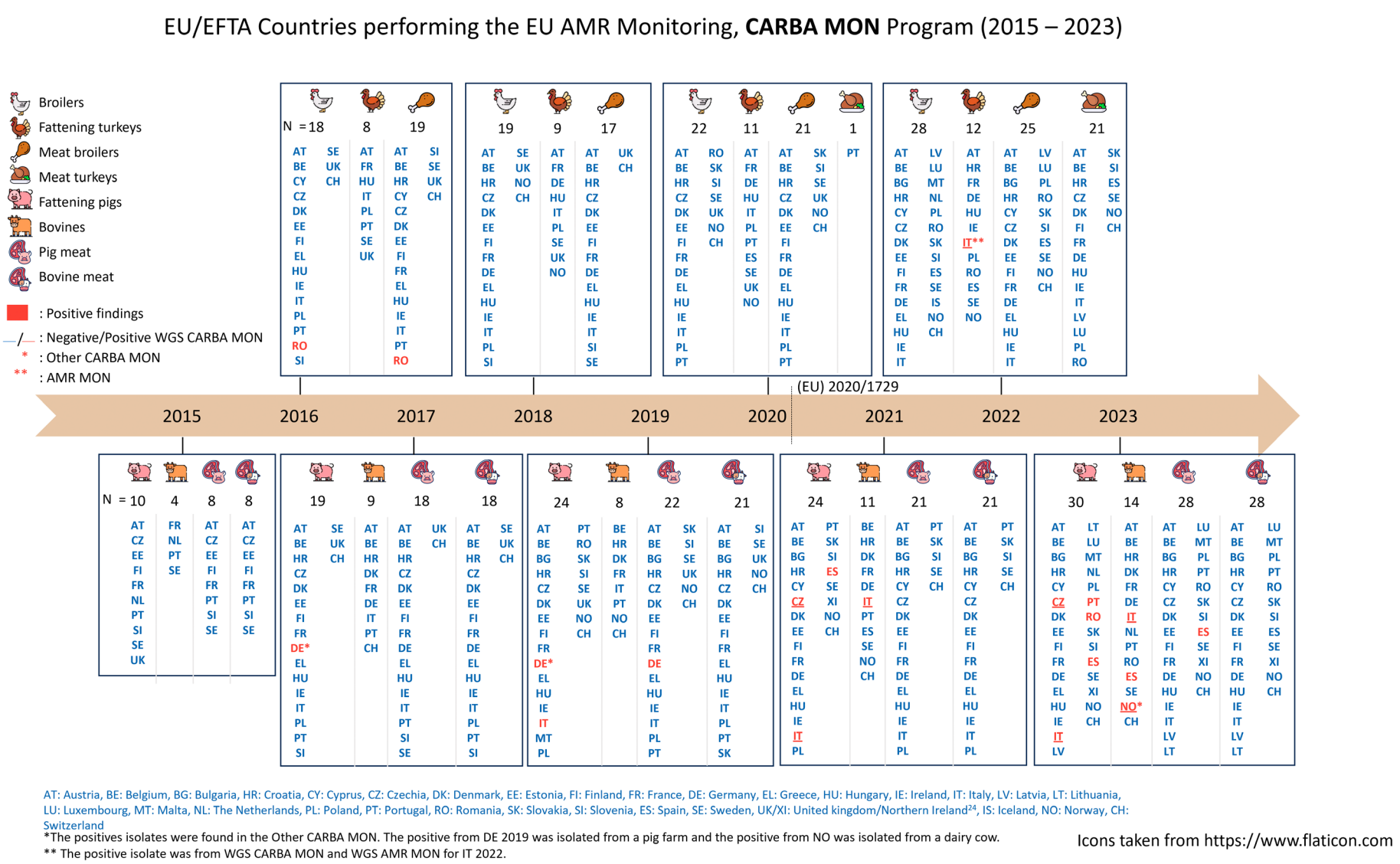

FIGURE 5 Progression of the number of countries testing (CARBA MON specific monitoring) over time in the EU/EFTA,[24] 2015–2023 (monitoring perfomed according to Commission Implementing Decision 2013/652/EU (in place 2014–2020) and (EU) 2020/1729 (2021-onwards)).

[24]Since 2021, the only United Kingdom data reported to EFSA were from Northern Ireland, in accordance with the agreement on the withdrawal of the United Kingdom of Great Britain and Northern Ireland from the European Union and the European Atomic Energy Community, and in particular Article 5(4) of the Windsor Framework (see Joint Declaration No 1/2023 of the Union and the United Kingdom in the Joint Committee established by the Agreement on the withdrawal of the United Kingdom of Great Britain and Northern Ireland from the European Union and the European Atomic Energy Community of 24 March 2023, OJ L 102, 17.4.2023, p. 87) in conjunction with section 24 of Annex 2 to that Framework.

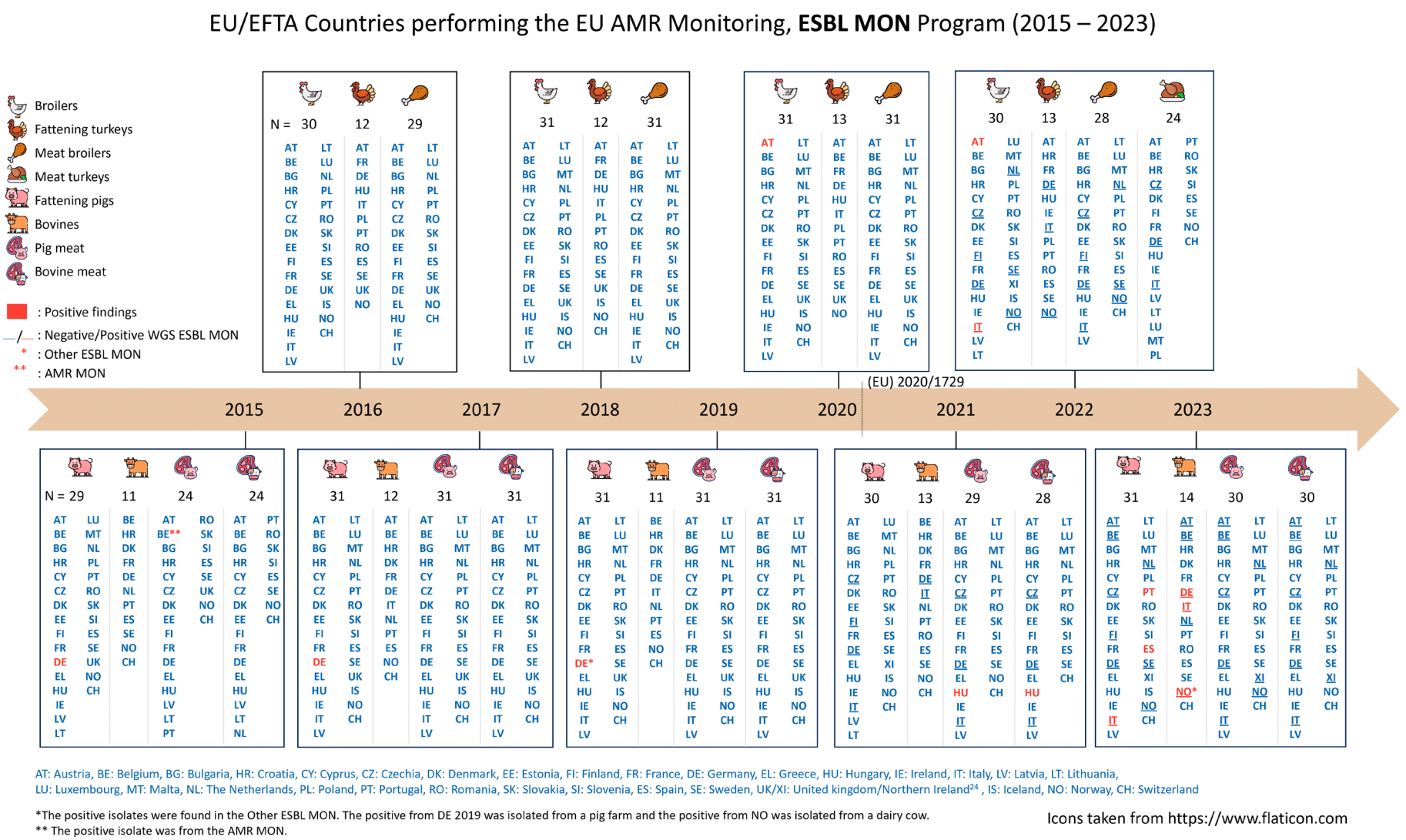

FIGURE 6 Progression of the number of countries testing (ESBL MON specific monitoring) over time in the EU/EFTA, 2015–2023 (monitoring perfomed according to Commission Implementing Decision 2013/652/EU (in place 2014–2020) and (EU) 2020/1729 (2021-onwards)).

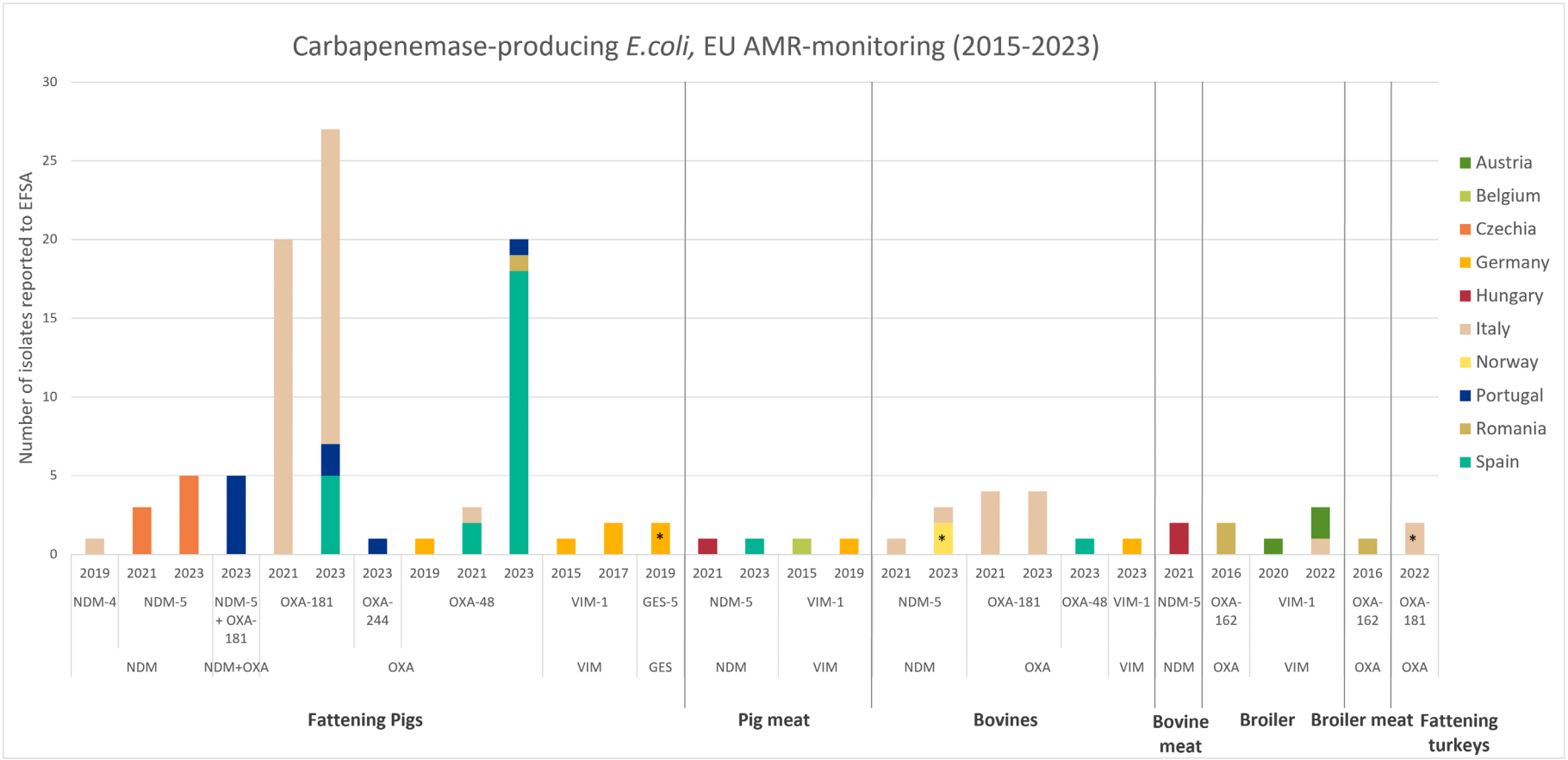

FIGURE 7 Carbapenemase-encoding genes in *E. coli* reported to EFSA by the EU/EFTA countries for different matrices within the EU AMR monitoring in the EU/EFTA, 2015–2023. *Identical isolates were collected from the same sample within both CARBA-MON and ESBL-MON, isolated with different selective media.

3.3 | What are the transmission dynamics of CPE in the food chain in the EU/EFTA? (AQ2)

Understanding how carbapenemase-producing Enterobacterales (CPE) spread within the food chain and their potential transmission between the food chain and humans is critical for assessing public health risks. This section examines the transmission dynamics of CPE within the food production system and their potential connections to human populations, aiming to better understand the mechanisms driving CPE dissemination and inform strategies to mitigate associated public health risks.

Transmission evidence relies on genetic similarity between isolates and/or plasmids and epidemiological connections between reservoirs (e.g. animals, food, humans). However, current literature lacks definitive proof of direct transmission, particularly between animals and humans, relying instead on molecular comparisons. Existing research primarily relies on comparative genetic molecular analyses, including STs and/or other clonal backgrounds, carbapenemase genes and plasmid type similarities across diverse ecological reservoirs. Molecular similarity based on other than full genome sequencing data (e.g. ST) should be interpreted with caution, especially in the absence of an epidemiologic link between reservoirs. In this section, findings based on molecular similarity between isolates and/or plasmids based on full sequence data and/or based on epidemiologically linked findings are emphasised. While direct transmission evidence remains scarce, preliminary hypotheses can be formulated based on substantive circumstantial evidence.

3.3.1 | Transmission within the food chain (SQ2.1)

3.3.1.1 | *Terrestrial food-producing animals and food thereof*

Transmission of CPE within terrestrial food-producing animals and derived foods in the EU/EFTA food chain involves multiple routes, primarily through animal movement and environmental contamination. Evidence of CPE transmission (based on information provided in Table B.1 and supplementary information in Annex C) is presented below.

Primary animal production and farm environments

A number of studies in different EU countries have documented the occurrence and transmission dynamics of CPE in different terrestrial animal production systems.

As already stated, Germany documented the first CPE detection in production animals and their farm environments worldwide in 2011, with sporadic but recurrent reports of bla_{VIM-1}-IncHI2-carrying *E. coli* ST88 and *S.* Infantis ST32 (non-motile) along the years in different animal production systems and foods (Falgenhauer et al., 2017; Fischer et al., 2012, 2013, 2017; Irrgang et al., 2019; Roschanski et al., 2018; Roschanski, Friese, et al., 2017). In 2015 and 2016 as part of the ESBL German monitoring programme and trace back investigations, highly related *E. coli* isolates, *S.* Infantis and *S.* Goldcoast harbouring bla_{VIM-1} pSE15-SA01028-like plasmid were identified in breeders and finisher pigs farms (Irrgang et al., 2017; Roschanski et al., 2019). Overall, those events demonstrate, according to the authors, the potential persistence of CPE over the years in pig production, highlighting their spread through both vertical transmission of CPE and horizontal transfer of mobile genetic elements (see Section 3.3.3.1).

Other recent studies have also revealed the transmission dynamics across production stages and beyond farm boundaries to other livestock and poultry species. Thus, an Italian study of Carfora et al. (2022) reported *E. coli* ST5229 ($bla_{OXA-181}$ on IncX3/IncX1 plasmids) detected as part of the AMR monitoring in pigs, bovines and turkeys (Table B.1 in Appendix B and supplementary information in Annex C). Trace back studies could link the positive CPE to the fattening farm supplying animals to the slaughterhouse and to the breeding farm supplying pigs to the fattening farm. The ST5229 with $bla_{OXA-181}$ -IncX1 was also isolated from a farm worker (see Section 3.3.2.1). In addition, the clone was also detected in a dairy herd with epidemiological connection to the pig farm. The same plasmids were also found in isolates belonging to additional STs. Altogether the study demonstrates the potential spread, as a combined effect of clonal spread and horizontal gene transfer, across production stages, but also to other production animals and humans when connections are established.

In line with the previous report, in Spain, between 2021 and 2023, several bla_{OXA-48}-positive isolates (the gene located on IncL plasmids) were identified in pigs from different farms and production stages and farms (from breeders to fattening pigs in farms and at slaughter). The detection of 13 different *E. coli* STs suggests a potential horizontal plasmid spread. Additionally, the presence of ST5229 presence in breeding and fattening farms also points clonal transmission likely via animal movement (piglets from the breeding unit to the fattening unit) (Table B.1 in Appendix B and supplementary information in Annex C).

Altogether these studies reveal that once CPE are introduced into primary production, especially at the top of the production pyramid (i.e. breeders), they could spread to other production stages or even to other farms by animal carriers or by the sources and transmission routes detailed in previous EFSA opinions (EFSA BIOHAZ Panel, 2021; EMA & EFSA, 2017).

Processing and handling (slaughter, processing plants and retail)

Transmission evidence at slaughter and processing stages is weaker, relying on findings of contamination with the hazards rather than proving direct links. CPE were recovered from slaughter settings, and this could enable cross-contamination

of carcasses, though no genomic or epidemiological data confirmed the transmission of CPE through slaughter and meat processing (Table B.1). Similarly, bla_{IMP}-positive *Serratia fonticola* found in fish samples in a processing plant (Ferri et al., 2023) hint at environmental reservoirs, as this species is primarily an environmental bacterium, however sequence data to support this are lacking.

3.3.1.2 | *Foods of aquatic animal origin, foods of non-animal origin and other novel foods*

CPE in foods of aquatic animal origin, often imported, include detections in Germany, Italy, the Netherlands, Portugal (Table B.1 in Appendix B and supplementary information in Annex C). Contaminated water (e.g. CPE were isolated from a natural fishery salted lake, Lazăr et al., 2021) and/or post-processing contamination likely drives this, especially in regions with high CPE circulation, but scarce data limits risk assessment. In Portugal, a bivalve production farm yielded a GES-5-producing *K. pneumoniae* strain with a novel ST not previously identified (Freire et al., 2023). This gene was detected earlier in Portugal in humans (Aires-de-Sousa et al., 2019), wild gulls (Aires-de-Sousa et al., 2020) and the aquatic environment (Manageiro et al., 2014), with consistent ColE plasmid types despite differing STs. This suggests potential plasmid-mediated transmission linking aquatic foods to environmental and human reservoirs, though epidemiological links remain unconfirmed. Data scarcity limits broader risk assessment for aquatic products.

Similarly, there have been observations of CPE in fresh vegetables and other foods of non-animal origin in several countries, including The Netherlands, Romania, Spain and Switzerland. These have been derived both from domestic and imported vegetables. While fresh vegetables and herbs have tested positive for CPE, the data to link these events is lacking. Imported products have shown a higher frequency of contamination, possibly due to waterborne exposure during cultivation or post-harvest handling (EFSA BIOHAZ Panel, 2021).

Novel foods (e.g. edible insects) have recently been reported as potential carbapenemase vectors, although the data remains very limited and the link to Enterobacterales was not confirmed. These new types of foods deserve more attention to establish their potential as vectors for antimicrobial resistant bacteria.

3.3.2 | Transmission between the food chain and humans (SQ2.1)

The transmission of CPE between the food chain and humans represents a critical public health concern, with potential spill over (animal-to-human) and spill back (human-to-animal) events amplifying antimicrobial resistance (AMR) spread.

3.3.2.1 | E. coli *transmission*

In a multicentric study in Italy, Carfora et al. (2022), reported that two farm workers were colonised in their gut with $bla_{OXA-181}$-positive *E. coli*. One isolate, identified as ST5229 carrying an IncX1-$bla_{OXA-181}$ plasmid, matched similar strains also colonising pigs on the same farm (see Section 3.3.1.1). These findings support the occurrence of spill over/spill back between farmed animals and farm workers. Although hardly reported for CPE, transmission between farm animals and farm workers is not unexpected, given the direct contact between them.

Broader surveys further highlight *E. coli* STs shared across human and food chain compartments, although of lower level of evidence due to lack of phylogenetic comparisons. This applies to most commonly STs/STcomplexes producing a given carbapenemase identified within the food chain with reports identifying them as sources of outbreaks or persistent AMR cases in human healthcare, including for:

- *E. coli* ST10, which represents a globally significant lineage producing NDM-5 in humans (ECDC, 2023). *E. coli* ST10 were isolated from pigs (with bla_{NDM-5} in Czechia, $bla_{OXA-181}$ in Italy and Spain, and bla_{OXA-48} in Spain), bovines ($bla_{OXA-181}$ in Italy), chicken meat ($bla_{OXA-162}$ in Romania) and seafood (bla_{VIM-1} in Germany, product imported from Italy);
- ST38, a lineage carrying the $bla_{OXA-244}$, which is commonly encountered as carbapenemase producer in European clinical settings (Poland, Norway, Netherlands, Germany and Switzerland) (Biedrzycka et al., 2024; Falgenhauer et al., 2020; Izdebski et al., 2024; Lindemann et al., 2023; Notermans et al., 2022). This same ST with this gene has been identified in poultry (chicken, turkey) in Egypt (Soliman et al., 2020) and with bla_{OXA-48} in a pig fom Italy. A phylogenetic study by Mo et al. (2023) found distinct monophyletic clades on human and Nordic broiler isolates, arguing against spill over from poultry. However, the study's focus on Nordic broiler production and exclusion of other regions/timeframes limit its generalisability, as broader poultry or pig reservoirs (e.g. Egypt, Portugal) could still contribute;
- ST48 multidrug-resistant NDM-5-producing strains, which are frequently found in humans. Therefore, the identification of ST48 from pigs (respectively carrying $bla_{OXA-181}$ from Italy and Spain, bla_{OXA-48} from Spain and bla_{VIM-1} from Germany) raises concern;
- Furthermore, ST101 was isolated from pigs (with bla_{NDM-5} in Czechia, bla$_{OXA-181}$ in Italy and bla_{OXA-48} in Spain) and broilers (bla_{VIM-1} in Austria). Again, this is a significant concern, given that human clinical ST101-NDM-5-producing strains have been reported in different countries, such as China or Pakistan (Qamar et al., 2019; Sun et al., 2019), but also Bulgaria (with ST6260 being an ST101-like background) (Markovska et al., 2024);
- Finally, ST410 has been isolated from pigs ($bla_{OXA-181}$ in Italy and Spain; bla_{OXA-48} in Spain) and bovine ($bla_{OXA-181}$ in Italy) and is another clonal type of concern in humans, being found as a common carrier reservoir of NDM-5.

3.3.2.2 | Salmonella enterica *transmission*

It is concerning that *S*. Infantis ST32 carrying VIM-1 in identical plasmids to the ones found in pig farms in Germany since 2011 has been observed in minced pork in the same country. Given the role of *Salmonella enterica* as a zoonotic pathogen with minimal natural human colonisation, its detection in minced pork consumed raw as 'Mett' (a popular German dish), may pose a risk of human infection with CPE through consumption of raw meat (Borowiak et al., 2017, 2018), and could allow a pig-to-human transmission through food ingestion.

Carbapenemase-producing *Salmonella enterica* isolates were not detected in EU harmonised surveillance of animals during 2022–2023. However, five human cases of carbapenemase-producing *Salmonella enterica* were reported in 2022, followed by six cases in 2023, with one of them harbouring bla_{NDM-1} and the rest bla_{OXA-48} genes (EFSA and ECDC, 2025). Given that *Salmonella enterica* is a zoonotic pathogen originating in animals, these findings suggest that the occurrence of acquired carbapenemases in *Salmonella enterica* from food-producing animals in the EU may be an emerging issue of public health relevance that current surveillance systems do not consistently detect in the animal reservoir.

3.3.2.3 | Klebsiella pneumoniae *transmission*

In Italy, in a study to investigate the role of cattle as carriers of carbapenem-resistant *K. pneumoniae*, a total of 258 milk filters collected by the Competent Authority in 150 dairy cattle farms in Parma province from 2019 to 2021 were screened (Bonardi et al., 2023). In the study, four carbapenem-resistant *K. pneumoniae* strains were identified, one producing the carbapenemase KPC-3. The KPC-3-positive *K. pneumoniae* was assigned to ST307 and WGS data was compared with those of 14 non replicate *K. pneumoniae* isolates collected in the 2017–2020 period from patients admitted at Parma University-Hospital. The ST307-KPC-3 positive strain from the milk filter shared several traits in common with a human clinical KPC-3-encoding ST307 isolate. Both encoded KPC-3, OXA-9, CTX-M-15 beta-lactamases and the intrinsic, chromosomally-encoded SHV-106, plus additional aminoglycosides, fluoroquinolones, sulfonamide, trimethoprim and tetracyclines resistance determinants. In the framework of the National Antibiotic-Resistance Surveillance (AR-ISS), a countrywide survey was conducted in 2016 and identified KPC-3-producing *K. pneumoniae* ST307 as the second most common carbapenem-resistant *K. pneumoniae* lineage circulating in Italy (Di Pilato et al., 2021). The identification of this high-risk clone in milk filters suggests a possible circulation of ST307 *K. pneumoniae* in an animal reservoir, suggesting the possibility of transmission between humans and cattle.

3.3.3 | Plasmids associated with the most common carbapenemase genes in the food chain and relationship with plasmid epidemiology in human cases (SQ2.1)

Here, the potential transmission of plasmids carrying the most common carbapenemase genes within the food chain and their epidemiological links to human cases, based on bacterial isolates from various sources and countries, is discussed.

3.3.3.1 | *Plasmids carrying the* bla_{VIM-1} *gene*

The bla_{VIM-1} gene was detected on IncHI2 plasmids in *E. coli* and *S*. Infantis from a livestock farm in Germany in 2011, and later also in swine and minced pork meat (Fischer et al., 2012, 2013, 2017; Roschanski et al., 2019; Irrgang et al., 2017). Plasmids from *E. coli* and *S*. Infantis carried the In*110* class 1 integron with the bla_{VIM-1} as a gene cassette (*aadA1-aacA4-*bla_{VIM-1}), as well as bla_{ACC-1}, *strA/strB*, *catA1* and *sul1* genes together with resistance to heavy metals (*ter-*, *mer-*, *sil-*, *ars-*, *rcn-* and *pco*) (Borowiak et al., 2017; Borowiak et al., 2018; Falgenhauer et al., 2017). The most relevant difference between the *E. coli* and *Salmonella enterica* plasmids (pRH-R27 from *Salmonella* and pRH-R178 from *E. coli*) was the presence in pRH-R27 of the two transfer regions of IncHI2 (Tra1, Tra2), while pH-R178 had only the locus Tra2, explaining why pRH-R178, unlike pRH-27, was non-transferable. A bla_{VIM-1}-I ncHI2 variant was identified by the German annual monitoring of ESBL/AmpC β-lactamase-producing *E. coli* in 2017–2018, in the caecal content of a fattening pig at slaughter. Overall, this plasmid showed similarity to the VIM-1-encoding plasmids previously identified from *Salmonella* and *E. coli*, but harboured three additional resistance gene-carrying segments, comprising bla_{SHV-12} and *qnrA1* genes, conferring beta-lactam and quinolone resistance and the *mph*(A)-*mrx-mphR* macrolide resistance operon (Pauly et al., 2021).

In 2021 in Norway, the emergence of IncHI2 plasmids carrying bla_{VIM-1} was described from environmental surveillance studies performed on *E. coli* isolates from raw and treated sewage collected from five sewage treatment plants also receiving hospital sewage (August, 2020 to February, 2022). Carbapenem resistance in Norway is low in clinical settings, with no bla_{VIM-1}-carrying *E. coli* detected in 2021. However, the emergence of bla_{VIM-1}-I ncHI2 plasmids in the treatment plant suggests a wider spread of this plasmid type also in other European countries (Marathe et al., 2023). The bla_{VIM-1}-IncHI2 plasmid confers resistance to heavy metals (silver, copper, mercury). This could be a factor positively favouring the success and persistence of this plasmid type within the food chain.

In recent years, there has been a growing interest in IncC-type plasmids, which are commonly identified among agricultural and clinical bacterial isolates in the USA, Europe and elsewhere. VIM-1 encoded by an IncC plasmid was identified in *K. pneumoniae* ST147 from a human patient in Greece and in an *E. coli* strain cultured from surface water bodies in Switzerland (p009_A-VIM-1). Plasmid p009_A-VIM-1 showed 99.9% nucleotide identity to pKP-Gr642, a bla_{VIM-19}-containing

plasmid from a *K. pneumoniae* isolate recovered in 2011 from a patient hospitalised in Greece (Bleichenbacher et al., 2020; Papagiannitsis et al., 2016). However, *E. coli* with bla_{VIM-1} on IncHI2 and IncC plasmids identified in the livestock and food chain sector cannot be certainly attributed to spill over from a human source.

Within the German national monitoring of zoonotic agents in 2019, *E. coli* 19-AB01133 was recovered from pork shoulder carried bla_{VIM-1} located on a self-transmissible IncC plasmid (formerly named IncA/C2 group). The plasmid was closely related to a previously described VIM-1-encoding plasmid from *E. coli* (S15FP06257_p) isolated from minced pig meat in Belgium. This study also demonstrated that besides the presence of the carbapenemase bla_{VIM-1} gene, other genes encoding β-lactam (bla_{SHV-5}, bla_{CMY-13}), aminoglycoside (*aadA1*, *aadA24*, *aac(6′)-Ib3*, *aac(6′)-II*, *aac(3)-I*), macrolide (*mph(B)*, sulphonamide (*sul1*) and trimethoprim (*dfrA1*)) resistance, were detected as well on the IncC plasmids (García-Graells et al., 2020; Pauly et al., 2020).

In summary, these findings highlight the evolution and persistence of bla_{VIM-1}-carrying plasmids in food-producing animals over time. However, plasmids identified in bacteria of animal and food origin are different from those described in bacteria of human origin. Therefore, it is difficult to identify a link between animal and human circulation for bacteria producing the VIM-1 carbapenemase.

3.3.3.2 | *Plasmids carrying the bla_{OXA-48}, $bla_{OXA-162}$ and $bla_{OXA-181}$ genes*

Surveillance studies in humans reviewed by Pitout and colleagues (Pitout et al., 2019), have shown that OXA-48, OXA-181, OXA-232, OXA-204, OXA-162 and OXA-244, in that order, are the most common OXA-48-like carbapenemases in Enterobacterales. OXA-48 has been associated with the Tn*1999* transposon located on the IncL plasmid and is endemic in North Africa and the Middle East. In a study from Europe on 684 carbapenemase-producing *K. pneumoniae*, isolated from patients in 244 hospitals in 32 European countries during the European Survey of Carbapenemase-producing Enterobacteriaceae, 36% were positive for $bla_{OXA-48-like}$ genes (240/284 were bla_{OXA-48}; David et al., 2019). OXA-48 has also been identified in bacteria of animal, environmental and food origin from Africa (Dossouvi & Ametepe, 2024). In both animal and human isolates characterised globally, the bla_{OXA-48} gene was mainly associated with one unique plasmid type of the IncL group (Dossouvi & Ametepe, 2024; Pitout et al., 2019). This plasmid did not carry further antimicrobial resistance determinants (Poirel et al., 2012).

The analysis of the available data showed that OXA-48-producing Enterobacterales were identified in 2018–2023 in Italy, Germany and Spain in porcine and bovine samples.

The fully sequenced *E. coli* isolate 19-AB01443 identified in Germany, belonging to ST295, harboured the bla_{OXA-48} gene on the IncL plasmid, which showed high degree of nucleotide identity (> 99%) and coverage (94%) with plasmids detected in *E. coli*, *K. pneumoniae*, *C. freundii*, *Raoultella planticola* and *E. cloacae* of human origin and in particular it showed highest concordance (identity: 99.96%, coverage: 94%) to the plasmid of *K. pneumoniae* that was isolated during a nosocomial outbreak in Germany, in 2016. These similarities support the hypothesis that the transmission of the IncL-bla_{OXA-48} plasmid among bacteria from humans to livestock and/or poultry has occurred (Irrgang, Pauly, et al., 2020).

The OXA-162, a derivative of OXA-48 by a single amino acid substitution (Thr213Ala) was described in *K. pneumoniae, E. coli*, *Raoultella ornithinolytica* and *C. freundii* from Turkey, Germany, Hungary and Greece (Pitout et al., 2019). The $bla_{OXA-162}$ gene mobilised by IS*6237* was located on an IncL-type plasmid (like bla_{OXA-48}).

In 2015, OXA-162-producing *E. coli* of chicken origin were identified in Romania. The plasmid encoding OXA-162 in chickens was not IncL but an IncHI2 type, also carrying the *mcr-1* gene, conferring colistin resistance. Previously, *mcr-1*-carrying IncHI2 plasmids have been widely observed among isolates from chickens, other production animals and food products from Europe and it is therefore possible that the acquisition of the Tn*6237* element with the $bla_{OXA-162}$ gene represents a recent acquisition on the *mcr-1*-carrying IncHI2 plasmid (Bortolaia et al., 2021).

OXA-181 is one of the most common global OXA-48-like derivatives. The $bla_{OXA-181}$ was localised on different plasmid types associated downstream of the insertion element IS*Ecp1* within Tn*2013*. This transposon was identified on an 84-kb mobile IncT-type plasmid in a *C. freundii* from Oman but also incorporated on a 7.6-kb ColE-type plasmid in *K. pneumoniae* and IncN in *Morganella morganii* (McGann et al., 2015; Potron et al., 2011; Villa et al., 2013). Currently in human surveillance, the most successful plasmid associated with the global spread of the $bla_{OXA-181}$ gene belongs to the IncX3 type. The $bla_{OXA-181}$-IncX3 plasmids have been described as endemic in the Indian subcontinent and sub-Saharan African countries (Pitout et al., 2019).

In the current literature available, the $bla_{OXA-181}$-IncX3 plasmid was initially reported in 2016 in *E. coli* associated to diarrhoea and oedema disease in two pigs sampled in Italy (Pulss et al., 2017). The $bla_{OXA-181}$-IncX3 plasmids were almost identical in nucleotide sequence and genetic organisation to plasmid pKS22-OXA-181 (accession number (acc. no.) KT005457) identified in a *Klebsiella variicola* strain isolated from fresh vegetables imported to Switzerland (Zurfluh et al., 2015).

As previously described, the EU Harmonised AMR Monitoring programme conducted in 2021 in Italy, identified $bla_{OXA-181}$ in *E. coli* isolated from caecal samples of pigs and bovines at slaughterhouses and in samples taken in animal-positive fattening pigs holdings (Carfora et al., 2022). This study highlighted the dissemination of the same *E. coli* strain (ST5229) in both breeding and fattening pigs, bovine beef and in a humans working in the farm. The $bla_{OXA-181}$ was in different types of plasmids, both IncX3 and IncX1, in isolates at slaughter and from tracing-back activities performed at farms of origin of the positive epidemiological units found at slaughter. Only in one case, the $bla_{OXA-181}$ gene was carried by a IncFII plasmid (in one isolate from tracing-back activities). In all the three plasmid types, $bla_{OXA-181}$ was part of a transposon with a similar general structure, which in all IncX1 plasmids resulted identical. The three resolved IncX3 plasmids harbouring $bla_{OXA-181}$

were very similar to each other (100% identity and 90%–91% coverage), the difference in the coverage included the resistance gene *qnrS1* that has been identified on the larger IncX3 plasmids (Carfora et al., 2022). The three plasmids showed 99% nucleotide identity but 89% coverage with IncX3 plasmids previously identified in Enterobacterales of human origin globally. The IncX1 novel and self-conjugative plasmids harboured $bla_{OXA-181}$ in an environment like that of Tn*2013* of the IncX3 plasmids. IncX1 also presented a type II RelE/RelB toxin/antitoxin system, contributing to the stabilisation of the plasmid. The study demonstrated that the same transposon containing $bla_{OXA-181}$ is mobilisable and can be introduced in different plasmid scaffolds. Additionally, tracing-back investigation in a breeding pigs holding demonstrated one *E. coli* isolate ST5229, harbouring a $bla_{OXA-181}$-positive IncX1 plasmid from a faecal sample provided from one of the farm workers. Most importantly, an almost identical $bla_{OXA-181}$-positive IncX1 plasmid (99.97–99.98% ID and 100% coverage) had been detected in *E. coli* belonging to the same ST (ST5229) in the same farm of breeding pigs.

In summary, plasmid similarities support the hypothesis that the transmission of the IncL-bla_{OXA-48} plasmid among bacteria from humans to livestock has occurred. Since this plasmid has been globally spread in human multifocal isolates over time, its presence in animal carriers poses a risk for its further expansion in bacteria from primary production. The IncX1-$bla_{OXA-181}$ plasmid identified in both human and animal ST5229 isolates from the same farm in Italy, suggested that a spill over and spill back between humans and animals can occur locally.

3.3.3.3 | *Plasmids carrying bla_{NDM} genes*

Several reports have demonstrated the dissemination of NDM among *E. coli* isolated not only from humans but also from animals and the environment. A systematic review based on 394 articles published in 2017–2021, mostly from European (49.7%) or Asian (31.7%) countries, and based on a genome meta-analysis (performed on 6167 *E. coli* isolates of swine origin downloaded from the Enterobase webserver on 24 July 2021) described 13 *E. coli* genomes carrying bla_{NDM-5} in China, but not in Europe (Hayer et al., 2022). In Greece, in 2020 the bla_{NDM-5} producing *E. coli* B103 ST361 was isolated from the faecal sample of a clinically healthy bovine in Thessaly (Tsilipounidaki et al., 2022). The *E. coli* B103 strain carried the bla_{NDM-5} gene located on an IncFII plasmid showing high similarity to the p52148_NDM-5 plasmid found in an *E. coli* isolate from Czechia (Chudejova et al., 2021). The bla_{NDM-5} was part of a gene array comprising IS26-ΔISAba125-bla_{NDM-5}-ble_{MBL}-IS91-*trpF-tat-sul1-qacEdelta1-aadA2* (BioProject ID: PRJNA746426).

Data from the EU AMR monitoring system 2021–2023 reported NDM-producing Enterobacterales in animals from different EU countries (Table 3, Table B.1 in Appendix B and supplementary information in Annex C).

The bla_{NDM-1} gene was detected on IncC in *E. coli* isolated from cattle in Spain (Tello et al., 2022), which was related to a bla_{NDM-1}-IncC-harbouring plasmid identified in *S. enterica* Corvallis in a wild bird in Germany (acc. no. CP027679). These bla_{NDM-1}-harbouring plasmids confer multidrug resistance, carrying genes for aminoglycoside, sulfonamide and trimethoprim resistance. The bla_{NDM-4} was identified on IncFII plasmids in *E. coli* of pig origin in Italy (Diaconu et al., 2020). In Czechia, bla_{NDM-5} was located on IncX3 plasmids in eight *E. coli* from three different STs isolated from pigs in surveillance studies performed in 2021, 2023 and 2024 (Table B.1, Supplementary information Annex C; EFSA and ECDC, 2023, 2024).

At a global level, in *E. coli* strains from faecal and environmental swabs obtained from seven pig farms in China (Peng et al., 2019), IncX3 was the predominant plasmid type associated with the bla_{NDM-5} variant.

In summary, further studies are needed to address if common NDM-encoding plasmids and clones are transmitted among animal and human bacteria. Locally, some successful plasmids like IncX3 promoted multiclonal spread and persistance of the bla_{NDM-5} carbapenemase gene variant in *E. coli* from food-producing animals over time.

3.3.4 | What are the risk factors identified for the emergence and spread? (SQ2.2)

In this section, the risk factors that could contribute to the emergence and spread of CPE both within the food chain and between the food chain and humans are presented.

Until now, the low detection rate of CPE in the food chain limits epidemiological studies. Therefore, risk factors for transmission of CPE are not widely documented.

Carbapenems are not used in animals, but other antimicrobials, particularly cephalosporins can positively select CPE of animal origin. Moreover, a wide variety of antibiotic resistance and metal-encoding genes have been co-located on carbapenemase-encoding plasmids (IncHI2 encoding VIM-1 or OXA-162, IncC encoding NDM-1) (Borowiak et al., 2017; Falgenhauer et al., 2017), conferring multidrug resistance phenotype to CPE. Co-resistance may be an important issue in the successful spread of the different CPE in bacteria of animal and environmental origin.

Animal carriers pose a risk for the introduction and spread of CPE in primary production. In a quantitative risk assessment study by mathematical modelling, the risk of CPE introduction from imported livestock, livestock feed, companion animals, hospital patients and returning travellers into livestock and poultry farms (broiler, hens, fattening pig, breeding pigs and veal calf farms) was assessed for the Netherlands. Livestock feed and imported livestock were found to be the most likely sources of CPE introduction into Dutch livestock farms particularly in swine and poultry production (Dankittipong et al., 2022). In a study in Greece, 213 faeces samples from healthy bovines from 25 different farms were tested. One isolate harboured a CPE gene (*E. coli* ST-361 bla_{NDM-5}). Additional bovine faeces or human samples collected from the farmer/farm workers tested negative for carbapenem resistance. The animal was imported from Czechia a month earlier and could have been already colonised (Tsilipounidaki et al., 2022). This suggests that import could pose a risk for the introduction of CPE into farms.

A recent study (Dankittipong et al., 2023) has evaluated the transmission of CPE in poultry chicks. In this trial where chicks were challenged in controlled biocontention facilities, a simulation model of potential transmission of *E. coli* harbouring $bla_{OXA-162}$ in a IncHI2 was evaluated. The transmission rates of CPE were 52%–68% lower compared to ESBL bla_{CTX-M2} and *catA1*, *E. coli* strains respectively. However, authors declared that it was not clear if these differences were caused by differences between the resistance genes or by other differences between the *E. coli* strains. In addition, the treatment with amoxicillin during 4 days increased the transmission rate more than three-fold in the three strains, highlighting the use of amoxicillin as a potential risk factor in this study.

As mentioned in Section 3.3.2, similarities were found regarding plasmid-gene combinations in isolates from pigs and a human worker on the same farm. It is likely that transmission did occur, although the direction remains unclear (Carfora et al., 2022). Human carriage of CPE may be a risk factor for the introduction of CPE in the primary production chain on a local scale.

3.4 | What are the methods in use for CPE detection and characterisation? (AQ3)

This section provides an update on the methods for detection and characterisation of CRE/CPE used in the official laboratories conducting the harmonised EU monitoring of antimicrobial resistance in zoonotic and commensal bacteria from food-producing animals and meat thereof in the EU/EFTA countries (see Section 3.1.4).

In the Scientific Opinion on carbapenem resistance in food animal ecosystems published in 2013 (EFSA BIOHAZ Panel, 2013), a critical analysis of the phenotypic and genotypic methods, as well as the interpretive criteria used for detection (isolation and identification) and characterisation of carbapenemase-producing bacteria was performed. A methodology including selective culture using meropenem, which offers a good balance between sensitivity and specificity, was proposed for the detection of carbapenemase-producing strains of Enterobacterales and *Acinetobacter* spp. However, it was specified that the proposed methodology was not validated, and any method proposed for CPE monitoring would need to undergo thorough experimental verification. Additionally, it was recommended that the identity of the genes responsible for the carbapenemase production should be determined by molecular methods, and that strain and plasmid typing should be performed to enhance understanding of the epidemiology of CPE in food-producing animal populations, foods and related food-producing environmental samples. The importance of ensuring that methods are sufficiently sensitive to detect low numbers of carbapenemase-producing bacteria in samples was emphasised.

In this context, the EURL-AR, with the support of its network, developed and validated a methodology for the surveillance of carbapenemase-producing *E. coli* (CARBA MON, Figure 5) from fresh meat and caecal samples (Hendriksen et al., 2023). The EURL-AR protocols[25] to be used for the EU specific monitoring of carbapenemase-producing *E. coli* (see Section 3.1.4) include a pre-enrichment step in which 1 g of caecal content or 25 g of meat are diluted 1:10 in buffered peptone water (BPW) and incubated at 37°C ± 1°C for 18–22 h. This is followed by culture of 10 µL of pre-enrichment broth onto commercially available chromogenic agars for isolation of carbapenemase-producing *E. coli* or other selective agars validated using the control strains provided by the EURL-AR, and incubation according to manufacturer's recommendations. One colony of presumptive carbapenemase-producing *E. coli* growing on the selective media should be subcultured onto MacConkey agar without antimicrobial supplements and incubated at 37°C ± 1°C for 18–22 h, and the resulting culture should be tested to confirm species identity. Confirmed *E. coli* should be tested for susceptibility to the antimicrobials described in Table 2 of Commission Implementing Decision 2020/1729/EU ('first panel of antimicrobials') by using the broth microdilution (BMD) reference method described in ISO 20776-1:2019. *E. coli* exhibiting a minimal inhibitory concentration (MIC) above the epidemiological cut-off value (ECOFF) for cefotaxime, ceftazidime and/or meropenem defined in 2020/1729/EU must be further tested either phenotypically, to confirm the carbapenemase phenotype, or genotypically, to detect presence of carbapenemase-encoding genes. The phenotypic test is done by testing susceptibility to the beta-lactam antimicrobials described in table 5 of 2020/1729/EU ('second panel of antimicrobials') using the BMD reference method (ISO 20776-1:2019) and interpreting the results according to the European Union Committee for Antimicrobial Susceptibility Testing (EUCAST) guidelines (EUCAST, 2017). The genotypic test is done by analysing WGS data using ResFinder according to the EURL-AR protocol for WGS.[26]

Notably, according to EUCAST guidelines (EUCAST, 2017), the isolates categorised as carbapenemase producers by the phenotypic test ('second panel of antimicrobials') require further analyses to unequivocally confirm carbapenemase presence. Carbapenemase presence can be confirmed using phenotypic tests, such as combination disk test methods, assays based on hydrolysis of carbapenems and lateral flow assays, and/or genotypic tests, such as polymerase chain reaction (PCR) and WGS. Details of the methods for carbapenemase confirmation, as well as criteria to interpret the results, are described by EUCAST (EUCAST, 2017). These tests to confirm carbapenemase presence are not mandatory within the European harmonised monitoring of AMR in food-producing animals and derived meat but are strongly recommended and also facilitated by the EURL-AR.

It is possible to detect carbapenemase-producing *E. coli* also using the protocols for the routine monitoring of AMR (AMR MON) in indicator *E. coli* and non-typhoidal *Salmonella enterica* and for the specific monitoring of ESBL-/AmpC-producing *E. coli* (ESBL MON, Figure 6) (see Section 3.1.4), as both protocols include antimicrobial susceptibility testing (AST) with the

[25] https://www.food.dtu.dk/english/topics/antimicrobial-resistance/eurl-ar/protocols.

[26] https://www.food.dtu.dk/english/-/media/institutter/foedevareinstituttet/temaer/antibiotikaresistens/eurl-ar/wgs/628_protocol-for-wgs-v2-2.pdf.

first panel of antimicrobials and allow detection of isolates with reduced susceptibility to cefotaxime, ceftazidime and/or meropenem, that would trigger AST with the second panel of antimicrobials. However, the routine monitoring (AMR MON) protocol has limited sensitivity for detection of carbapenemase-producing *E. coli*, which are expected to occur at low concentrations in animal and food samples. The protocol for the specific monitoring of ESBL-/AmpC-producing *E. coli* (ESBL MON, Figure 6) includes selective culturing on MacConkey agar containing 1 mg/L of cefotaxime with incubation at 44°C ± 0.5°C for 18–22 h, which also enables the detection of isolates with those carbapenemase variants hydrolysing cefotaxime (see Section 3.1.1). Indeed, several carbapenemase-producing *E. coli* detected in animals and food in EU/EFTA countries were detected using the ESBL/AmpC monitoring protocol (Figure 6, see Table B.1 in Appendix B and supplementary information in Annex C). However, *E. coli* producing OXA-48 and OXA-48-like enzymes, that hydrolyse cefotaxime poorly, are not detected by the ESBL/AmpC monitoring protocol unless they simultaneously co-produce an ESBL, an AmpC and/or an additional carbapenemase with hydrolytic activity toward cefotaxime. Furthermore, if a sample contains both an ESBL-/AmpC-producing *E. coli* and a carbapenemase-producing *E. coli*, the method will only detect one of the two (since only one colony is picked for downstream analysis from the selective agar). This is likely depending on the ratio between ESBL/AmpC- and carbapenemase-producing *E. coli* in a given sample.

The EURL-AR protocol for the CARBA MON has been developed to optimise sensitivity and specificity while limiting costs as, for example, the use of pre-enrichment in BPW allows the same culture to be used for different monitoring protocols (i.e. ESBL/AmpC-producing *E. coli*, *Salmonella* spp.).

Modifications of the EURL-AR protocol have been tested with the aim to reduce the microbiota present in faecal and food samples that may interfere with the detection of CPE. A study described improved detection of VIM-1-producing *E. coli* in pig faecal samples by adding a selective enrichment step with cefotaxime (1 mg/L)-containing broth between the pre-enrichment in BPW and the culture on selective agars (Irrgang et al., 2019). The same study also found that PCR on DNA from the selective enrichment broth culture followed by culture of positive samples on selective agars increased CPE detection (Irrgang et al., 2019). Another study showed that the sensitivity of the CARBA MON protocol increased when the pre-enrichment culture in BPW was cultured onto in-house produced agars (i.e. MacConkey agar supplemented with meropenem at concentrations corresponding to the ECOFF) instead of commercially available chromogenic agars, and this procedure had higher sensitivity compared to addition of a selective enrichment step in broth and PCR (Pauly et al., 2021). This study was validated with *E. coli* strains producing GES-5, KPC-2, NDM-1, OXA-48 and VIM-1 and using pig caecum as matrix (Pauly et al., 2021). Further evaluations are needed to ascertain to what extent the conclusions of these studies are applicable to additional CPE and to all the animal and food matrices monitored in the EU.

Once detected and confirmed, CPE should ideally be further characterised to identify clones and plasmids. This is key to understand the dynamics of transmission. There are several molecular methods for CPE characterisation as reviewed in EFSA BIOHAZ Panel (2013). Currently, WGS is the method of choice for unambiguous identification of clones and plasmids but other equivalent methods may become available. It is important to emphasise the usefulness of plasmid replicon types and carbapenemase genes as epidemiological markers to support investigation on possible presence of common plasmids in bacteria from different sources. Plasmid multilocus sequence typing (pMLST) classifying the replicon in Rep-alleles and the resistance gene environment are also useful traits for better identifying highly heterogeneous plasmids, such as the FII, FIA and FIB multi-replicon plasmids. The most accurate way to definitively demonstrate the transmission of indistinguishable plasmids among bacteria of different origins is based on the comparison of complete plasmid sequences. Partial plasmid information limits the possibility to prove transmission/dissemination routes among bacteria from animal and human sources.

From the above, it is clear that there are several methods to detect and characterise CPE from animal and food samples. The difficulties in issuing a standard protocol for CPE detection and characterisation arise from the following facts: (i) CPE occur at low concentrations and prevalence in animal and food samples (e.g. few positive animals within a farm and minimal presence in faecal/caecal samples), necessitating appropriate sampling strategies and highly sensitive detection approaches, like enrichment cultures and/or molecular methods to maximise detection probability; (ii) carbapenemases exhibit varying substrate profiles, with differences in both affinity and hydrolysis kinetics for different carbapenems and other beta-lactams which impacts the effectiveness of antibiotic-supplemented media used in enrichment protocols; and (iii) molecular methods for complete characterisation of clones and plasmids carrying carbapenemase-encoding genes are not used consistently across laboratories, limiting data comparability; (v) the continuous emergence of novel carbapenemase variants necessitates regular updates to detection methods to ensure comprehensive surveillance capability. To overcome these difficulties, EFSA launched the survey described in Sections 2.2.3 and 3.4.1, and signed the Framework Partnership Agreement (FPA) for data generation on CPE (see Section 1.2) in which further optimisations of the detection and characterisation methods will be covered.

3.4.1 | Information from EU/EFTA countries

In December 2024, EFSA launched a survey to obtain an overview of the methods currently used in the National Reference Laboratories in the EU/EFTA countries participating in the EU-monitoring for the isolation and characterisation of CRE, CPE and/or carbapenemases in monitoring and in research activities. The survey questions addressed the methods for detection of CRE/CPE in samples, verification of bacterial species identity, antimicrobial susceptibility testing, confirmation of

carbapenemase presence and further characterisation of isolates. Additionally, the survey included questions to detail the methods used for analysis of WGS data (Annex B2).

Answers were obtained from 32 laboratories from 30 EU/EFTA countries. Two countries, Romania and Spain, where animal and food samples are analysed in different laboratories, sent replies from two laboratories each. The information received is summarised in the following paragraphs. As the questions were specific to methods used for CRE/CPE monitoring and research, some of the laboratories that had not isolated any CRE/CPE at the time of the survey did not report any methods, even if they had the capacity to perform them.

All laboratories reported using the EURL-AR protocol for isolation of CRE/CPE from samples. Of note, this protocol is optimised for isolation of carbapenemase-producing *E. coli* from animal and food samples but, depending on the selective agar used by the laboratories, can also detect other CPE. Laboratories in Austria, Germany, Ireland, Luxembourg, the Netherlands, Slovenia and Spain reported the use of additional methods and/or variations of the EURL-AR protocol to increase sensitivity of CPE detection.

The modifications to the EURL-AR protocol for isolation of CRE/CPE from samples included: (i) use of PCR or metagenomics for carbapenemase gene detection in DNA extracted from enrichment cultures and/or growth material from agar plates; (ii) addition of selective enrichment steps with low concentrations of carbapenems; and/or (iii) use of additional selective agars. The detailed protocols will be collected and published in the context of the FPA described above.

All EU/EFTA countries except two reported conducting species identification on presumptive CRE/CPE isolates, with MALDI–TOF mass spectrometry being the method used in most laboratories ($n = 19$), followed by biochemical methods used in 11 laboratories, WGS used in seven laboratories and PCR used in two laboratories. All laboratories conducting species identification by WGS reported using a *k*-mer-based approach and, in addition, one laboratory reported the use of average nucleotide identity. Eight laboratories reported having the capacity to use more than one method for species identification.

Regarding AST to confirm the carbapenemase phenotype, all laboratories ($n = 32$) reported the use of BMD. One laboratory reported the use of disc diffusion besides BMD.

For the step to confirm carbapenemase presence, which is not compulsory according to the EURL-AR protocol but highly recommended also according to EUCAST, three laboratories reported experience with phenotypic methods, with two laboratories using the carbapenem inactivation method (CIM) (van der Zwaluw et al., 2015) and another laboratory using the Blue-Carba test (Pires et al., 2013). Twenty-two laboratories reported the capacity to use PCR and/or WGS to confirm carbapenemase presence. Classic and/or real-time PCR were conducted using in-house protocols. WGS was mainly available as short-read sequencing technology and only eight laboratories had long-read sequencing technology.

About a third of the survey focused on methods for analysing WGS data, and only 22 laboratories responded to these questions (Table 4). Of the laboratories that did not respond to this part of the survey, at least two had the capacity for WGS but had not yet applied it to CPE.

The bioinformatics set-up was different among the laboratories, with six laboratories using a commercial system and the remaining laboratories using in-house pipelines and open-source tools. The WGS-based methods for quality control, cluster analyses and genotypic characterisation of AMR and virulence determinants and mobile genetic elements are reported in Table 4. It is evident that different laboratories used different methods and although this is not necessarily a problem, it should be established whether the results obtained by the different methods are equivalent. Additionally, the implementation of the characterisation of mobile genetic elements, including plasmids, appeared to be inconsistent between laboratories, hampering the ability to elucidate the transmission and spread of carbapenemases.

TABLE 4 Methods for WGS data analysis used by the official laboratories conducting the harmonised EU monitoring of antimicrobial resistance in the EU/EFTA countries.

		Country																					
		AT	BE	CY	CZ	DE	DK	EE	ES	FI	IE	IS	IT	LU	LT	LV	MT[a]	NL	NO	PL	PT	RO	SE
Bioinformatics set-up	Commercial	■									■	■		■			■					■	
	In-house	■			■	■	■		■	■			■			■		■	■				■
	Open source		■					■			■		■		■	■				■	■	■	
	EFSA services									■													
Quality parameter	Phred score				■	■	■	■	■	■		■	■					■	■			■	■
	Number of reads	■	■	■	■	■	■		■	■		■	■	■	■			■	■	■	■		■
	Total base pairs		■		■	■	■	■	■		■	■	■	■				■	■	■	■		■
	Average read depth	■	■		■	■	■		■	■	■	■		■	■	■			■	■	■		■
	Contamination	■	■		■	■	■	■	■	■	■	■		■		■			■	■	■	■	■
	Total number of contigs	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		■	■	■	■	■	■
	Total length of contigs		■		■	■	■		■		■	■	■	■		■		■	■	■	■		■
	N50	■	■		■	■	■	■	■		■	■	■	■	■	■		■	■	■	■	■	■
	% Good Targets cgMLST	■																					
	Size of genome	■																					
	Genome completeness prediction				■																		
	GC content								■												■		
	L50								■														
	Read major fraction genus					■																	
	Contig major fraction genus					■																	
	MLST loci with multiple alleles					■																	
	Q30 base fraction					■																	
Cluster analyses[b]	MLST – *Escherichia coli*	■	■		■	■	■	■	■			■	■	■		■		■	■	■	■	■	■
	MLST – *Salmonella enterica*	■	■		■	■	■	■				■	■	■		■				■	■	■	■
	MLST – *Klebsiella pneumoniae*	■	■			■			■			■	■			■					■		■
	MLST – Other species					■			■			■	■								■		■
	cgMLST – *Escherichia coli*	■	■		■	■		■	■	■	■	■		■		■		■	■		■	■	
	cgMLST – *Salmonella enterica*	■	■		■	■		■		■	■	■		■		■					■	■	
	cgMLST – *Klebsiella pneumoniae*	■	■			■						■				■					■		
	cgMLST – Other species					■						■											

(Continues)

TABLE 4 (Continued)

		Country																					
		AT	BE	CY	CZ	DE	DK	EE	ES	FI	IE	IS	IT	LU	LT	LV	MT[a]	NL	NO	PL	PT	RO	SE
	Serotyping																						
	Phylogroup																						
AMR[b]	Abricate																						
	AbritAMR																						
	AMRFinderPlus																						
	Kleborate																						
	PointFinder																						
	ResFinder																						
	RGI/CARD																						
MGE[b]	IntegronFinder																						
	ISFinder (Insertion Sequence Finder)																						
	MGEFinder																						
	MOB-Suite																						
	MobileElementFinder																						
	PLACNET																						
	PlasmidFinder																						
	Platon																						
VF[b]	VFDB																						
	VirulenceFinder																						

Abbreviations: AMR, antimicrobial resistance; AT, Austria; BE, Belgium; CARD, comprehensive antimicrobial resistance database; cgMLST, core genome muli locus sequence typing; CY, Cyprus; CZ, Czechia; DE, Germany; DK, Denmark; EE, Estonia; ES, Spain; FI, Finland; IE, Ireland; IS, Iceland; IT, Italy; LT, Lithuania; LU, Luxembourg; LV, Latvia; MGE, mobile genetic element; MLST, multilocus sequence typing; MT, Malta; NL, the Netherlands; NO, Norway; PL, Poland; PT, Portugal; RGI, resistance gene identifier; RO, Romania; SE, Sweden; VF, virulence factor; VFDB, virulence factor database.

[a]The laboratory outsources WGS and provided information only for AMR analyses.

[b]Tools/databases for cluster analyses, AMR, MGE and VF were run from different set-ups in the different laboratories, which implies that laboratories used different versions of tools/databases depending on the frequency of updates.

3.5 | Control measures and contingency plans (AQ4)

In the CPE opinion released in 2013, the BIOHAZ Panel concluded that mitigation measures must be aimed firstly at preventing the introduction of CPE strains into food-producing animals, secondly, at reducing the prevalence and quantity of such organisms in food-producing animals and foods thereof, and thirdly, at reducing their transmission from contaminated animals/foods to humans. Accordingly, control measures were proposed (see EFSA BIOHAZ Panel, 2013, for further details). This section presents, for the EU/EFTA countries, what and where contingency plans are available for preparedness, what control and mitigation options are included in these plans or are being implemented, and in which circumstances these strategies are applied.

Briefly, the term contingency plans refer to plans that are prepared to respond effectively to unforeseen harmful events, for example the detection of CPE in a population. These plans are activated immediately upon detection, with the primary goal of limiting further spread. Control and/or mitigation actions, within or outside contingency plans, aim to reduce the rise, burden or spread of the hazard once it is already present in a population.

In line with the points raised in section 5 of the 2013 scientific opinion (EFSA BIOHAZ Panel, 2013), a survey was prepared for EU/EFTA countries focusing on questions related to contingency plans and control measures to mitigate the risk of CPE spread. The survey included 18 questions about legislation/regulations, contingency plans and control measures to mitigate the spread of CPE, detailed epidemiological investigations (e.g. trace back and/or trace-forward), inter-sectoral communication/actions between relevant departments, agencies or other stakeholders (human, food and/or veterinary) and coordinated actions among EU/EFTA or EU/EFTA-Non-EU countries in case of multi-country CPE detection (Annex B3). The survey was sent to the EU/EFTA countries (30 countries in total) asking for information on the existing contingency plans and mitigation/control measures against the spread of CPE in the food chain. All countries replied to the request, with 10 countries (Denmark, Finland, Germany, Italy, Lithuania, Malta, The Netherlands, Norway, Spain and Sweden) indicating to have some plans in place (Figures 8 and 9).

3.5.1 | What contingency plans, if any, are available for preparedness? (SQ4.1)

Of the 10 countries with specific plans to mitigate the spread of CPE, four have mandatory programmes included in national legislation (Denmark, Finland, Italy and Sweden). The remaining six countries (Germany, Lithuania, Malta, The Netherlands, Norway and Spain) have voluntary programmes. From these countries, Denmark, Finland, Lithuania and Malta have not yet detected, either through official monitoring or by other analyses, CPE so far and the Netherlands has not reported the detection of CPE through EC monitoring but CPE have been collected outside this monitoring (National monitoring/research).

Preparedness also involves rapid and efficient communication. In this sense, seven countries (Finland, Italy, Malta, Lithuania, The Netherlands, Norway and Sweden) reported to have organised inter-sectorial communications between agencies or departments in their plans (Figure 8). These vary depending on the organisation of government departments in each country but essentially aims to coordinate human and animal health actions from a One Health perspective. For instance, in Finland, if a CPE detected in humans would be attributable to an animal origin, the competent authority may take samples and analyse them. Each case idiosyncrasy determines the sampling strategy by decision of the competent authority in liaison with the human health care authorities according to the Finish questionnaire. Regarding potential control and mitigation measures in primary production, the legislation states that any control measures that would result from this investigation would be voluntary.

Communication could go beyond inter-sectorial communications at national level. As an example, Norway pointed out that they have established coordinated efforts which primarily align with EU/EFTA frameworks to ensure harmonised measures across MSs, and these comprise (i) regulatory alignment: actively implementing and complying EU directives and regulations, such as those related to animal health, food safety and antimicrobial resistance; (ii) collaboration in surveillance: participating in joint EU/EFTA monitoring programmes, such as those on AMR and zoonotic diseases, to ensure comparability of data and comprehensive risk assessment across borders.

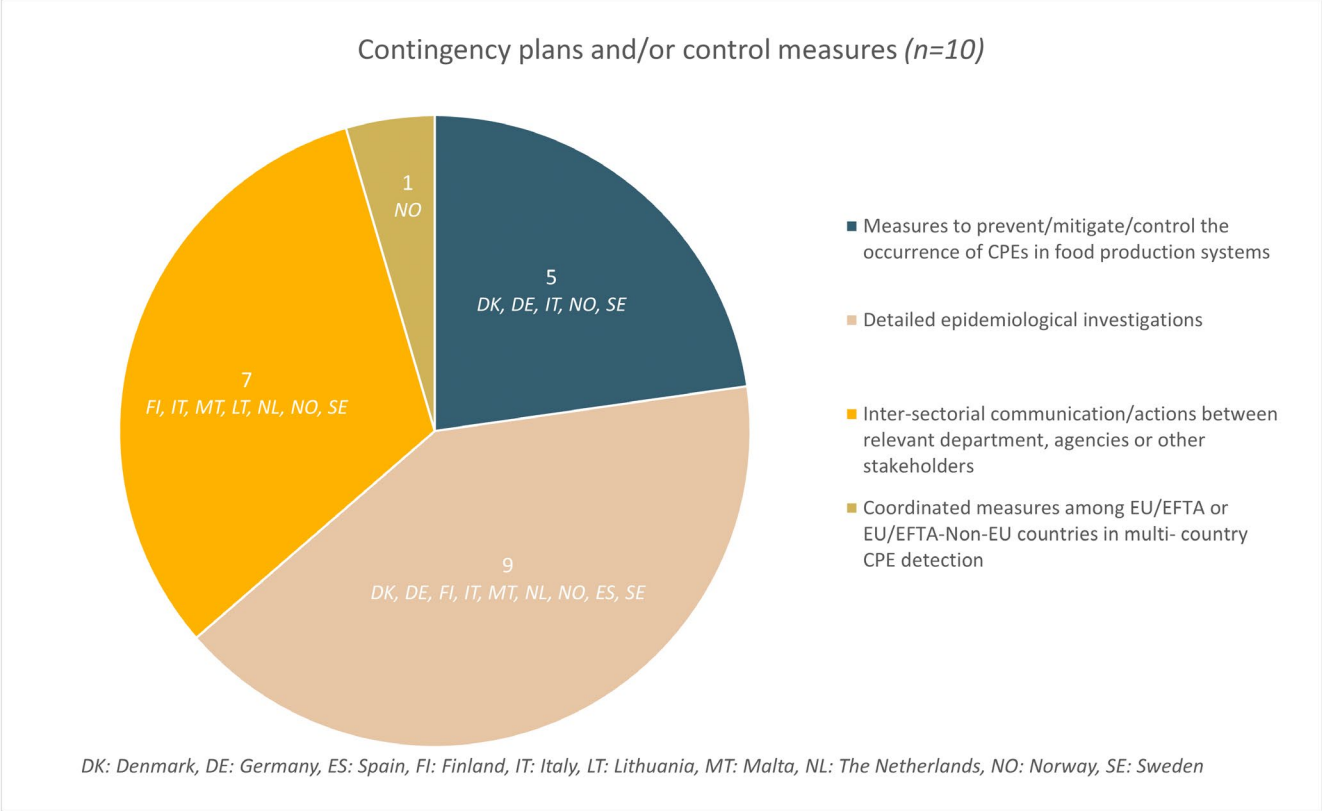

FIGURE 8 EU/EFTA countries with contingency plans and/or control measures against CPE in the food chain ($n = 10$). Numbers for each measure refers to the number of countries that reported to implement those measures.

3.5.2 | What mitigation/control measures (if any) are currently in place? (SQ4.2)

3.5.2.1 | *Prevention measures in place to avoid the introduction of CPE in the food chain*

A section of the questionnaire asked about measures in primary production and the food chain to reduce the likelihood of introducing CPE in these compartments (Figure 9). Reducing or restricting the use of antimicrobials in general, but with particular emphasis on broad-spectrum/extended-spectrum antimicrobials (polymyxins, quinolones and 3rd/4th generation cephalosporins), is a measure specifically included in the plans of countries that have already detected CPE (Italy, Norway and Sweden).

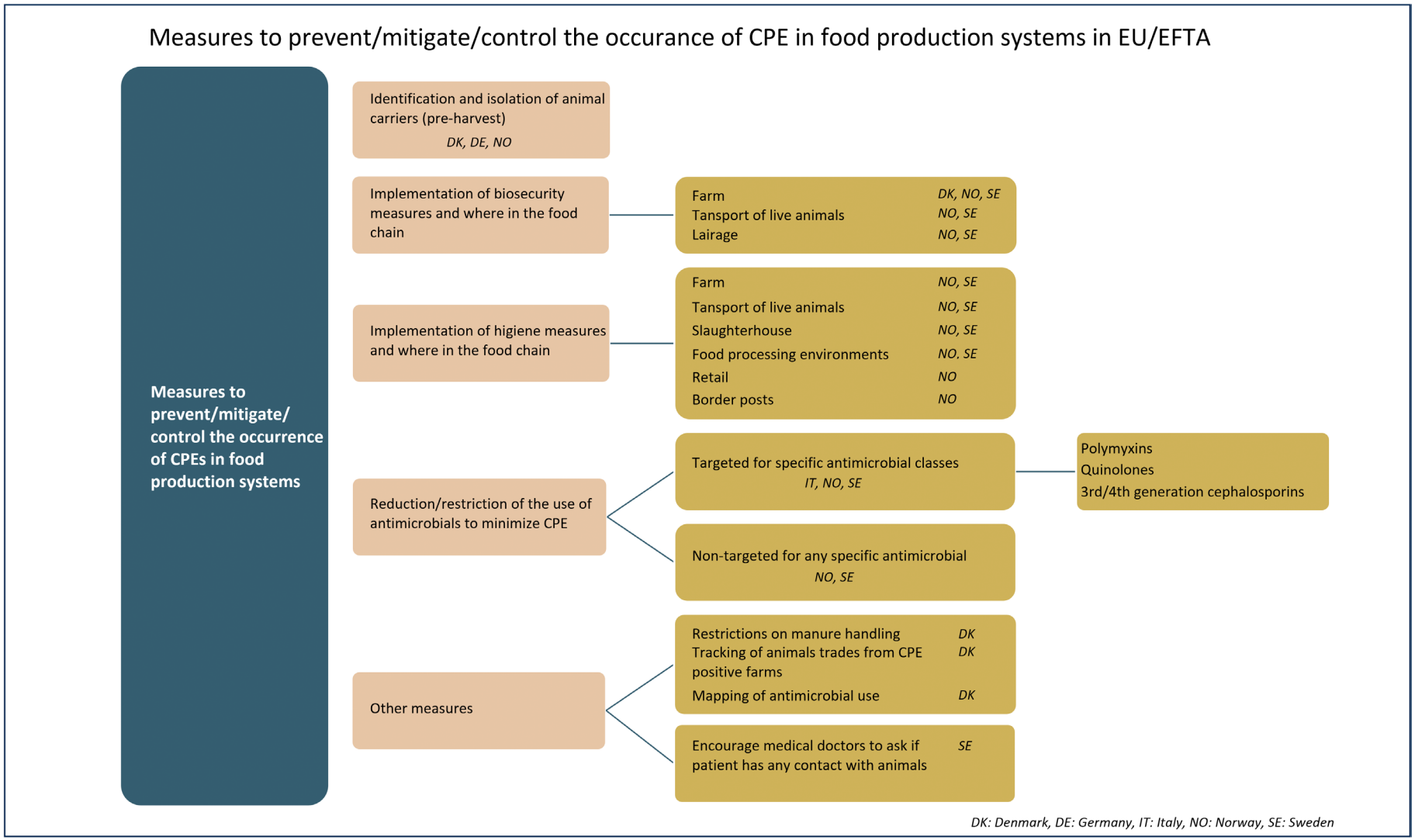

FIGURE 9 Measures reported to prevent/mitigate/control the occurrence of CPE in food production systems by 5 out of the 10 EU/EFTA countries with contingency plans and/or control measures against CPE in the food chain. Measures in the figure are structured by the mitigation strategies included in the questionnaire.

3.5.2.2 | *Contingency plans/strategies currently applied at the time of the first detection*

Epidemiological investigations are included in all plans except for one of the countries (Figure 8). The purpose of epidemiological investigations is to have an early response once CPE are detected to identify the source and halt its spread. These epidemiological investigations are based on trace back strategies in most countries. Trace back strategies identify and document the source of the detected CPE (Weiser et al., 2013). Three countries (Denmark, Malta and Norway) also reported trace-forward epidemiological investigations as part of their programmes. Trace-forward is performed in epidemiological investigations to identify yet unknown or potential clusters (Weiser et al., 2013).

Based on the information provided by Sweden, medical doctors are encouraged to ask patients whether they have been in contact with animals. This sort of measure, although not targeting directly animals or the food chain provides information on potential human-animal contacts, thus extending the investigation of the source or spread of CPE to non-human compartments. This information is particularly important for staff working with potential CPE sources such as animals or foods (either meat, fish or vegetables which may get contaminated).

According to the information provided in the questionnaire answers, as stated above, five countries (Denmark, Germany, Italy, Norway and Sweden) included measures to be implemented in case of detection of CPE in the primary production and/or the food chain (Figure 9).

In this sense the identification and isolation of CPE carriers is a measure included by several countries on only farm (Germany), or on farm, transport and at the lairage (Norway and Sweden).

Hygiene throughout the food production chain was also reported as a mitigation strategy in the programmes of Norway and Sweden. In Denmark, country which has not reported the detection of CPE to date, the CPE mitigation plan includes biosecurity measures related to (i) restrictions in manure handling, (ii) mapping of trade of animals from the targeted farm and (iii) mapping of antimicrobial use if the problem would be detected.

3.5.3 | In which circumstances are the contingency/mitigation/control strategies applied? (SQ4.3)

It is reasonable to assume that all countries with control plans in place activate the measures included in the plan if a CPE is detected. It should be mentioned too that some general measures such as biosecurity or antimicrobial use reduction are already in place on farms and are not exclusive of CPE mitigation.

In addition, Finland legislation covers the notification of CPE in animals to the authorities, but there is no legislation or operational instructions regarding the following measures for the control of further spread in the country.

Countries with control plans in place were also requested in the survey to submit data on studies that could be conducted to validate the interventions performed to mitigate or eradicate the CPE detected. None of the countries have conducted studies to date that validate the efficacy of the actions taken.

3.5.4 | Blockers and challenges faced by countries with contingency plans in place (SQ4.3)

Countries with plans in place were asked about the major challenges faced in the mitigation of CPE as this information is of relevance to detect weaknesses in CPE containment in primary production. Denmark, where the action plan places particular emphasis in the monitoring of *Salmonella*, reported that the occurrence of *Salmonella* resistant to critically important antibiotics (cephalosporins, carbapenems, fluoroquinolones and colistin) is fortunately very low. However, it was observed that farmers, veterinarians and slaughterhouse representatives are not always fully aware of the regulations necessitating reminders to conduct regular checks. This finding underscores the potential for underestimation of the problem by relevant actors who may perceive it as a minor problem.

Norway stressed the pivotal role of effective detection and management of isolated cases, crucial in prevention of CPE perpetuation and spread. Similar to Denmark, Norway pointed out that low prevalence limits epidemiological studies, which could contribute to a more comprehensive understanding of CPE transmission and spread.

A couple of countries have referred to the detection methods as part of the limitations or challenges encountered. Malta found challenges in lapse time for microbiological identification, a problem also highlighted by Spain, which has indicated difficulties monitoring the spread and adapting strategies in real-time. Furthermore, Spain has noted that rapid horizontal transfer of CPE hampers containment measures. The Netherlands approached the question from a different perspective, focusing on the risk assessment of the risks for public health of a CPE result in the animal sector and a decision-making framework. The overarching objective of these measures is to establish a framework for decision-making in the event of such an occurrence. They also consider that it would be helpful to have EU guidelines or a specific framework. In line with these concerns, Finland pinpointed the lack of analysis and shared understanding of the possible significance of CPE detection in animals for animal health, food safety and public health. Finally, Sweden identified 'resources' as their main bottleneck.

3.5.5 | Information provided by EU/EFTA countries with no containment and mitigation plans (SQ4.3)

Finally, information on the reasons for not implementing containment and mitigation strategies so far for CPE was collected from 18 out of the 20 countries which indicated the absence of contingency plans or control measures for CPE spread (Figure 10). Eight of those 20 countries have reported CPE-positive results so far (Austria, Belgium, Czechia, Greece, Hungary, Portugal, Romania and Switzerland). The main reasons indicated were lack of a legal basis for implementation (eight countries) and that the reduction of CPE was not a major concern (six countries), indicating that priority for this problem is lower relative to other hazards. In this sense, for instance, Croatia clarified that there were no reports of CPE in Enterobacterales in the food chain to date and Portugal detected the first CPE in 2023 and as a consequence is currently developing their legal plan. Other reasons cited included economic constraints (five countries) and prioritisation of other foodborne, zoonotic or AMR issues (three countries). Finally, the lack of specific measures for efficient control of CPE was a contributing factor for not carrying any programme (three countries).

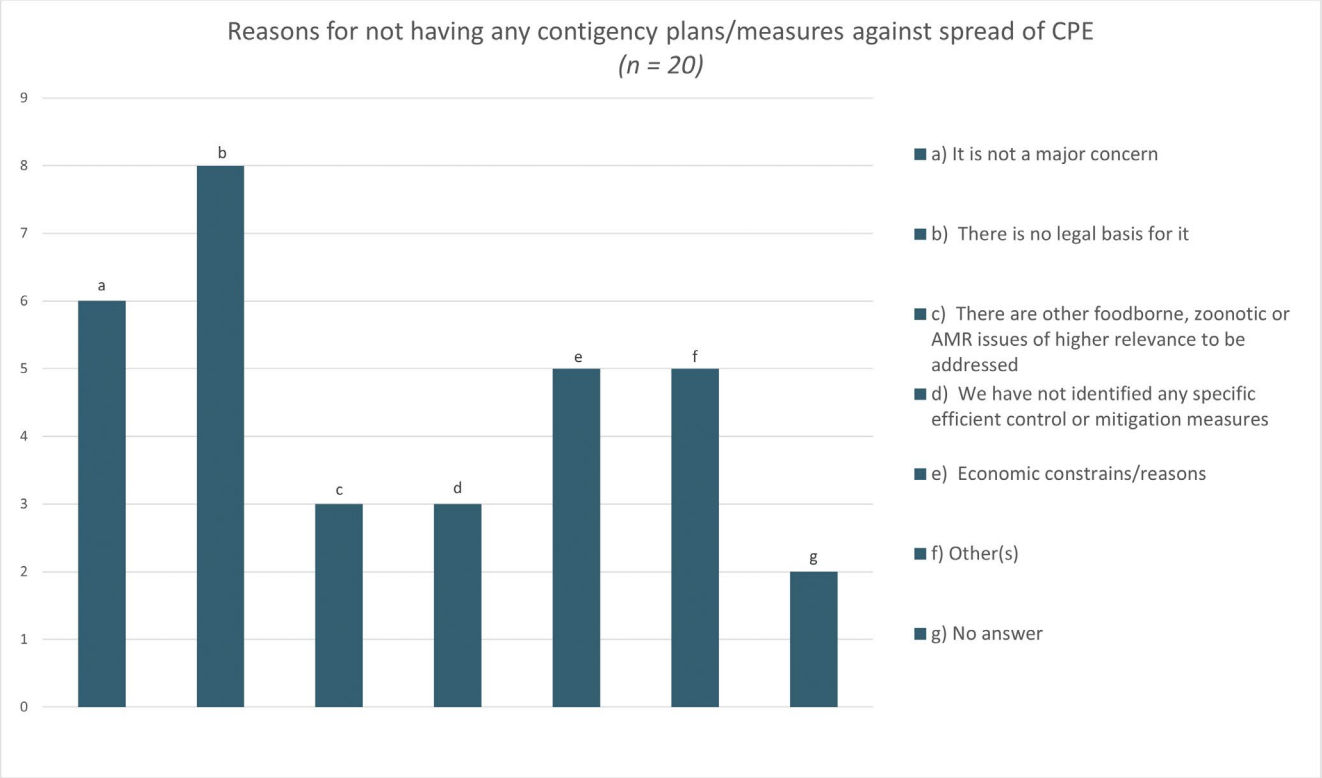

FIGURE 10 Reasons adduced by EU/EFTA countries for not having any contingency plans/measures against spread of CPE in the food chain ($n = 20$).

4 | CONCLUSIONS

AQ1. What is the current status of carbapenemase-producing Enterobacterales (CPE) in the food chain in the EU/EFTA since the last EFSA opinion?

SQ1.1 What carbapenemase-encoding genes have been found?

- Based on the scientific literature and the data from EU monitoring, at least 22 gene variants belonging to nine carbapenemase families have been detected. The most commonly reported genes are $bla_{\text{VIM-1}}$, $bla_{\text{OXA-48}}$ and $bla_{\text{OXA-181}}$, followed by $bla_{\text{NDM-5}}$ and $bla_{\text{IMI-1}}$.
- Less common genes include $bla_{\text{NDM-1}}$, $bla_{\text{OXA-162}}$, $bla_{\text{GES-5}}$, $bla_{\text{IMI-3}}$ and $bla_{\text{KPC-3}}$, with rare instances of other genes, such as $bla_{\text{OXA-244}}$, as well as gene combinations (e.g. $\text{bla}_{\text{NDM-5}} + bla_{\text{OXA-48}}$, $bla_{\text{NDM-5}} + \text{bla}_{\text{OXA-181}}$).

SQ1.2 What are the bacterial species in which they were found?

- The primary species reported is *E. coli*. However, this is also the species that is targeted in most of the research studies and the official EU monitoring.
- Other reported species are from the *Enterobacter* cloacae complex (*E. cloacae, E. asburiae* and *E. hormaechei*), the *K. pneumoniae* complex (*K. pneumoniae* and *K. variicola*) and *Salmonella* Infantis.

- Sporadic reports have also identified species from the *Klebsiella oxytoca* complex *(K. oxytoca* and *K. michiganensis)*, *E. von-holyi*, other *S. enterica* serovars (*S.* Goldcoast and *S.* Enteritidis), *Rahnella* spp., *Serratia fonticola, Pantoea* spp., *Raoultella* spp., *Citrobacter* spp., *Kluyvera cryocrescens*, *Morganella morganii* and *Proteus* spp.
- Limited data are available on bacterial species beyond *E. coli*, which is the primary focus of current systematic monitoring efforts.

SQ1.3 What are the CPE clones?

- *E. coli* shows the highest clonal diversity, with at least 66 different STs, 36 of which grouped into 13 ST complexes, followed by *Enterobacter* spp. (at least 10 STs), *Klebsiella* spp. (4 STs) and *Salmonella enterica* (2 STs), though most of these STs were represented by one to three isolates.
- Ubiquitous STs, detected across multiple food chain sources and countries, include *E. coli* ST23-Complex (ST88, ST410), ST101-Complex (ST5229, ST101), ST10-Complex (ST10, ST48, ST744) and ST542, alongside *Salmonella* Infantis ST32.
- Varying degrees of carbapenemase genes diversity is observed within these STs, with *E. coli* ST10 standing out for carrying the highest gene diversity ($bla_{\text{NDM-5}}$, $bla_{\text{OXA-181}}$, $bla_{\text{OXA-48}}$, $bla_{\text{OXA-162}}$ and $bla_{\text{VIM-1}}$) and matrix coverage (pigs, bovines, chicken meat and seafood).
- *K. pneumoniae* ST307 ($bla_{\text{KPC-3}}$ in bovine milk filters in Italy) and ST525 ($bla_{\text{OXA-48}}$ in pigs in Spain), have been reported and are also significantly associated with human infection cases.

SQ1.4. What are the CPE mobile genetic elements associated with the carbapenemase-encoding genes?

- The most frequently reported plasmid types are IncHI2 ($bla_{\text{VIM-1}}$ and $bla_{\text{OXA-162}}$), IncC ($bla_{\text{VIM-1}}$ and $bla_{\text{NDM-1}}$), IncX3 ($bla_{\text{NDM-5}}$ and $bla_{\text{OXA-181}}$), IncI and IncL ($bla_{\text{OXA-48}}$).

SQ1.5 What are the sources (animals, foods of animal and non-animal origin, and food production environments)?

- CPE have been detected in various sources/matrices:
    - Overall, most of the reports are from terrestrial food-producing animals and their environments, mainly from pigs, followed by bovines and poultry. Most of these isolates were collected from the EU and national AMR monitoring and/or trace back investigations which target these animals. Occasionally, CPE have been reported in raw meat from pigs, chicken and bovines. Identical CPE strains, such as S. Infantis ST32 ($bla_{\text{VIM-1}}$-IncHI2), were detected both in pig meat and pig production.
    - The distribution of carbapenemase-encoding genes varies by source, with pigs showing the greatest gene variety among livestock (e.g. predominantly $bla_{\text{VIM-1}}$, followed by $bla_{\text{OXA-48}}$, $bla_{\text{OXA-181}}$ and $bla_{\text{NDM-5}}$), bovines primarily harbouring $bla_{\text{OXA-181}}$ and $bla_{\text{NDM-5}}$, whereas in broilers $bla_{\text{VIM-1}}$ was predominant.
    - Compared to meat from terrestrial food-producing animals, CPE are more frequently detected in food derived from aquatic animals (including imported products). The aquatic-derived samples exhibited greater diversity in Enterobacterales species and carbapenemase genes. This included nine distinct gene families (e.g. bla_{IMP}, $bla_{\text{IMI-1}}$, $bla_{\text{NDM-1}}$) as well as recently characterised genes such as $bla_{\text{FLC-1}}$, with multiple genes occasionally detected within single isolates
    - Although only a few studies are available, CPE were also more frequently found in food of non-animal origin (including imported products), than in meat products. These reports show a high variety of Enterobacterales species and carbapenemase genes (including five gene families, with $bla_{\text{OXA-48}}$, bla_{VIM}, $bla_{\text{IMI-1}}$, bla_{IMP} and bla_{KPC}), often with detection of several genes within single isolates.
    - A few reports indicate the presence of carbapenemase-encoding genes in ready-to-eat insects, such as mealworms and grasshoppers, although these studies were targeting genes present in the microbiota and the association with the Enterobacterales could not be established.

- Limited data are available on sources beyond the systematically monitored food-producing animals e.g. foods of aquatic origin and of non-animal origin.

SQ1.6 What is the geographical and temporal distribution?

- Since CPE were first reported in Germany in 2011–2012 (VIM-1-producing *Salmonella* Infantis and *E. coli*), reports have emerged from 14 out of 30 EU/EFTA countries by 2024, namely Austria, Belgium, Czechia, Germany, Greece, Hungary, Italy, Norway, the Netherlands, Portugal, Romania, Spain, Sweden and Switzerland.
- A notable increase in the number of CPE reports has been observed, predominantly from pigs, with a surge in 2021 ($bla_{\text{OXA-181}}$, Italy) and 2023 ($bla_{\text{OXA-48}}$, Spain; $bla_{\text{OXA-181}}$, $bla_{\text{OXA-48}}$, $bla_{\text{OXA-244}}$ and $bla_{\text{NDM-5}}$, Portugal). This suggests that pig production serves as a primary source across multiple countries (e.g. Germany, Italy, Czechia, Spain and Portugal).
- CPE reports from food of non-animal origin, including imported products, have increased since 2015 surpassing the number of CPE detections from meat in several years.

- In the case of Sweden, the reported CPE were isolated from feed mills, but there have been no reports from food production animals or foods so far.
- From 2015 to 2024, several gene variants have been reported, with bla_{NDM-5}, bla_{OXA-48}, $bla_{OXA-181}$ and bla_{VIM-1} being repeatedly detected across years and/or detected in multiple countries (e.g. different years bla_{VIM-1} in pigs in Germany and poultry in Austria, and $bla_{OXA-181}$ in pigs in Italy, Spain, emerging in Portugal in 2023, as well as bla_{NDM-5} in pigs from Czechia).
- The number of detected *E. coli* STs also increased since 2015, with more than 50 different STs identified by 2024. Looking exclusively at the data from the harmonised EU monitoring, an increase in the number of reports was observed in 2021–2023. This was mostly explained by an increase of $bla_{OXA-181}$ and bla_{OXA-48} in pigs in Italy and Spain, respectively, together with the first CPE reports, with several genes and gene combinations, in Portugal in 2023.
- In general, when considering all available data (scientific literature, harmonised monitoring and research), an increase in CPE reports may partially reflect an increase in testing.

AQ2: What are the transmission dynamics of CPE in the food chain in the EU/EFTA?

SQ2.1. What are documented transmission/dissemination routes?

- Definitive evidence of CPE transmission is scarce. Evidence of transmission is inferred through analysis of genetic similarity in bacterial strains/ST/ST-complexes, carbapenemase and other resistance genes and plasmids across different reservoirs, with additional epidemiological data supporting these genetic connections only in some instances:
    - In Germany, CPE bla_{VIM-1}-IncHI2-carrying *E. coli* ST88 and *S.* Infantis ST32 have been recurrently found in the food chain along the years, with genomic and epidemiologic data supporting persistence and occasional spread within the pig production. Data suggest both vertical and horizontal gene amplification (*S.* Goalcoast, *Enterobacter* spp., other *E. coli* STs) contributing to their spread.
    - In Italy, *E. coli* ST5229, carrying $bla_{OXA-181}$ on IncX3/IncX1 plasmids, were reported in pigs, bovines and turkeys. Trace back analyses confirmed the transmission from breeding to fattening pigs and the epidemiological link to positive dairy calves, evidencing the transmission across farms and livestock species as a combined effect of clonal spread and horizontal gene transfer.
    - *E. coli* ST5229 carrying the IncX1-$bla_{OXA-181}$ plasmid was identified in a farm worker in one of the pig farms, suggesting that spill over and spill back between humans and animals can occur locally. Whatever the initial source might be, CPE have been amplified within intensive animal production systems, especially in pigs.
    - In Spain, IncL plasmids carrying bla_{OXA-48} contributed to the spread of this carbapenemase gene throughout the pig pyramid production system. Moreover, clonal transmission of bla_{OXA-48}-carrying *E. coli* ST5229, via animal movement, is also suggested due to its presence in breeding and fattening farms.
    - CPE have been recovered from slaughterhouses, and this could enable cross-contamination of carcasses, although no genomic or epidemiological data has confirmed so far the transmission of CPE through slaughter and meat processing.
    - bla_{IMP}-carrying *Serratia fonticola* was found in fish samples from a processing plant. This Enterobacterales species is primarily environmental, but there is no further data to identify the source.
    - The *E. coli* STs/ST complexes that are commonly found in the food chain (e.g. ST10, ST38, ST48, ST101 and ST410) have also been reported as the cause of human outbreaks, or as being frequently antimicrobial resistant *E. coli* STs/ST complexes in human healthcare. However, the scarcity of WGS data hinders phylogenetic resolution, leaving an open question as to whether these STs represent true food chain bridges or parallel clonal expansions.
    - *Salmonella* Infantis ST32 carrying bla_{VIM-1}, with plasmids identical to those reported in German pig farms since 2011, was isolated from minced pork in Germany. Given the established role of non-typhoidal *Salmonella* as a zoonotic pathogen with minimal natural human colonisation, its detection in 'Mett' – a raw pork dish widely consumed in Germany – suggests a potential risk of pig-to-human transmission through food.
    - Carbapenemase-producing *Salmonella* enterica isolates were not detected in EU harmonised surveillance of animals during 2022–2023. However, five human cases were reported in 2022, followed by six cases in 2023 (harbouring bla_{OXA-48} or bla_{NDM-1} genes). Given that *Salmonella* enterica is a zoonotic pathogen originating in animals, these findings suggest that the occurrence of acquired carbapenemases in *Salmonella enterica* from food-producing animals in the EU may be an underdetected emerging issue of public health relevance.
    - Current literature provides circumstantial evidence of plasmid transmission among bacteria from food-producing animals and humans. In a few cases, circulation of common plasmids between bacteria found in samples of animal and human origin was demonstrated. The best example is the bla_{OXA-48}-IncL plasmid that had been spreading for a long time in bacteria from humans and has been now identified in livestock.
    - The association of bla_{VIM-1} and $bla_{OXA-162}$ on IncHI2 plasmids was reported in different *E. coli* and *Salmonella enterica* isolates from animals, but these plasmids were not common in bacteria of human origin in Europe and globally. Therefore, based on the available evidence, it is difficult to identify a link between animal and human circulation for bla_{VIM-1}-carrying Enterobacterales.

SQ2.2: What are the risk factors identified for CPE emergence and spread?

- The low detection rate of CPE in the food chain thus far limits the possibilities to conclusively identify risk factors using observational studies.
- Co-resistance to different antimicrobials and/or metals is an important issue in the successful spread of the different plasmids carrying the carbapenemase genes in bacteria of animal and environmental origin.
- Movement and trade of CPE-positive animals and CPE-contaminated food products represent a risk factor for the introduction of CPE in the food chain.
- Human CPE carriers involved in animal or food production pose a risk for introducing CPE into the food chain.

AQ3: What are the methods in use for CPE detection and characterisation?

- Literature searches and a targeted survey show that laboratories in 30 EU/EFTA countries implement several methods for CPE detection, species identification and phenotypic and genotypic characterisation, including, among others, various selective media, PCR protocols and WGS analysis workflows.
- There is no single culture-based method that allows detection of all CPE in a sample, and no culture-independent method has been thoroughly evaluated to date.
- The methods used by the official laboratories for the detection of CPE in the framework of the harmonised EU monitoring of antimicrobial resistance in zoonotic and commensal bacteria from food-producing animals and meat thereof consist of a pre-enrichment culture, followed by isolation on selective media, which represents a compromise between sensitivity, specificity and costs.
- The methods used in the framework of the harmonised EU monitoring have proven useful to isolate CPE and detect an increase of CPE occurrence in food-producing animals in some EU/EFTA countries. However, some studies have shown that the sensitivity of the carbapenemase-producing *E. coli*-specific method can be improved. Additionally, the specific methods target only *E. coli* and do not target other clinically-relevant Enterobacterales.
- Protocols to improve the sensitivity of the methods to detect CPE in samples from food-producing animals and meat by using selective enrichment steps with low concentrations (i.e. close to the ECOFF) of carbapenems and/or PCR and metagenomic approaches to detect carbapenemase genes in enrichment cultures, followed by culture of PCR-positive enrichments, have been described and are used in some EU/EFTA countries, but have only been validated for specific epidemiological situations.
- With regards to the characterisation of the CPE, in at least 24 EU/EFTA countries, the official laboratories have capacity for WGS, although the capability and experience to identify and characterise clusters/clones and plasmids differ across laboratories.

AQ4: What contingency/mitigation/control plans to control the spread or potential spread of CPE in the food chain do currently exist in the EU/EFTA?

SQ4.1 What contingency plans, if any, are available for preparedness?

- Ten out of 30 EU/EFTA countries reported to have specific contingency plans for CPE control. From these 10 countries, Germany, Italy, The Netherlands, Norway, Sweden and Spain already had CPE findings, whereas Denmark, Finland, Lithuania and Maltahave not yet reported the occurrence of any CPE.
- These plans are part of mandatory programmes included in legislation in Denmark, Finland, Italy and Sweden, while the other six countries have voluntary programmes in place.

SQ4.2 What mitigation/control measures, if any, are currently in place?

- Epidemiological investigations, especially trace back investigations, are the most frequent actions reported by the countries implementing control plans (Denmark, Germany, Finland, Italy, Malta, the Netherlands, Norway, Spain and Sweden).
- Five countries (Denmark, Germany, Italy, Norway and Sweden) reported the current implementation of actions (or that they would implement actions) when CPE are detected. These are:
    - the identification and isolation of CPE carriers on farm only (Germany), or on farm, transport and lairage (Norway and Sweden),
    - the reduction of specified or or general antimicrobial use (Italy, Norway and Sweden),
    - the implementation of biosecurity-based strategies, such as hygiene (Denmark, Norway, Sweden), and restrictions on manure handling or animal trading from CPE-positive farms (Denmark).
- Inter-sectorial communication is useful to mitigate and control the spread of CPE among animals, humans and the environment. Seven countries (Finland, Italy, Malta, Lithuania, the Netherlands, Norway and Sweden) reported to include inter-sectorial communication between agencies or departments in their contingency plans.

SQ4.3 In which circumstances are the contingency/mitigation/control strategies applied?

- Besides measures such as biosecurity or antimicrobial use reduction, which are not specific for CPE, but applied routinely to protect animal health and mitigate AMR in general, all countries with control plans in place would activate the measures included in the plan if CPE are detected.
- Those countries with contingency plans in place, indicated that the main bottlenecks to monitor and control CPE were: lack of awareness, limitations in their detection (method sensitivity and diagnostic capacity) affecting the outcomes of epidemiological studies, rapid horizontal transfer of CPE, lack of resources, and finally lack of mandatory interventions and/or common EU guidelines for CPE control.
- Likewise, low prevalence of CPE, conflicting priorities and economic constraints are the main reasons for not implementing any mitigation or control plan in those countries that do not yet have specific measures related to CPE control.

5 | RECOMMENDATIONS

For a better understanding on how to prevent or minimise the occurrence and spread of CPE in food-producing animals, products derived thereof and food-producing environments, the following recommendations are made to fill the knowledge gaps identified in relation to the sources and dissemination pathways:

Sources of CPE

We recommend monitoring activities in food sources which are not targeted in current official monitoring, as well as their related environments:

- Fish and seafood products, e.g. from aquaculture (primary production and processing, retail), including imported foods.
- Foods of non-animal origin (pre/postharvest).
- Food production environments (manure, water, processing plants and other sources).
- Feed.
- Novel foods: e.g. insects.

Bacterial species carrying CPE genes

We recommend specific monitoring activities covering a larger set of bacterial species:

- Priority: Enterobacterales commonly associated with human infections, e.g. *Klebsiella* spp., *Enterobacter* spp. and *Salmonella enterica*.
- Other: additional Enterobacterales (e.g. *Providencia* spp., *Proteus* spp., *Citrobacter* spp., *Morganella* spp.), including aquatic/environmental Enterobacterales (e.g. *Serratia* spp.).

Transmission of CPE

We recommend performing:

- Trace back investigations to clarify transmission routes of positive findings within the food chain, including workers, feed, etc.
- Bacterial molecular typing (e.g. by WGS and plasmid characterisation) in combination with epidemiological studies to elucidate transmission events within the food chain and between the food chain and humans.
- Investigations to clarify the drivers that contribute to the selection and spread of CPE, genes and plasmids in the food chain (antimicrobials, metals, etc.).

Detection methods for CPE

We recommend:

- Comprehensive evaluation of protocols to increase sensitivity of methods for CPE detection.
- Complete and harmonised characterisation of mobile genetic elements, including plasmids, to elucidate the pathways of transmission and spread of carbapenemases.

Type of studies/research that could be conducted

Future research should address current limitations by designing targeted studies to elucidate transmission mechanisms. Emphasis should be placed on robust methodologies to clarify potential cross-reservoir transfer pathways, as existing evidence relies largely on genetic similarities across hosts without epidemiologically confirming transmission directionality.

Key considerations for immediate research are interdisciplinary collaboration, standardised protocols and advanced molecular typing techniques combined with epidemiological investigations. Elements to consider for designing such studies:

- Molecular epidemiology approach:
  - Detailed comparative genomic analysis of isolates from different reservoirs;
  - Complete sequencing of plasmids that carry carbapenemase genes;
  - Advanced phylogenetic analysis to track genetic similarities;
  - Molecular clock and evolutionary tree construction.
- Temporal and spatial correlation:
  - Longitudinal sampling across multiple reservoirs;
  - Geospatial mapping of genetic element distribution;
  - Time-series analysis of genetic element emergence;
  - Correlation of genetic variations with ecological/environmental factors.
- Pooled data analyses by combining all existing CPE data within the EU network for the purpose of e.g. comparative genomics analyses, risk factor analyses.

For the longer term, the following can be considered:

- Experimental validation:
  - In vitro transmission experiments;
  - Co-infection and mixed-culture studies;
  - Experimental infection models in controlled settings;
- Advanced computational modelling:
  - Develop transmission network models, for clones and plasmids;
  - Machine learning algorithms to predict transmission patterns;
  - Computational simulations of potential transmission routes;
- Metagenomic and microbiome analysis:
  - Comprehensive resistome profiling;
  - Network analysis of movement of resistance determinants and mobile elements.

A One Health approach, integrating human, animal and environmental health, is needed to address effectively the drivers of CPE spread in the food chain worldwide.

GLOSSARY

To harmonise the figures and tables shown in Sections 3.2.4 and 3.2.5, Appendix B and Supplemenatary information in Annex C, the different terms related to the sources were grouped as shown below.

Animals and environment
Terrestrial food-producing animals:

Pigs and/or their environment: samples from pigs at farms and slaughterhouse, environment samples connected to pig production (barns, gauze socks, boot socks, flies, manure, single or pooled faeces).
Bovines and/or their environment: samples from bovines at farms and slaughterhouse, environmental samples connected to bovine production (farm, milk filters).
Broilers and/or their environment: samples from broilers at farms and slaughterhouse, environmental samples connected to broiler production (dust and faeces at farms and equipment in slaughterhouse).
Turkeys and/or their environment: samples from turkeys at slaughterhouse.

Food

Pig meat: samples taken from pig meat at retail, diagnostic sample from minced pork meat.
Bovine meat: samples taken from bovine meat at retail.
Chicken meat: samples taken from broiler meat at retail.
Foods of aquatic animal origin: samples from seafood and different animal species from fresh and salt water (clams, bivalves, shrimps, common carp, codfish, tilapia (fish raw frozen) and other fishery products), from primary production (wild or aquaculture) collected at production site, processing plant, retail and/or border control posts.
Food of non-animal origin: samples taken from different vegetables (seasonal vegetables, fresh organic vegetables, glassworts/samphire, mixed salads), herbs and spices (coriander, basil) including retail and/or border control post samples.
Ready-to-eat insects samples from grasshoppers and mealworms.

General environment:

Natural water sources: samples from natural fishery salted lakes.

Humans

Human: samples from pig farm workers.

Other

Feed mills: livestock feed mills environmental samples.

ABBREVIATIONS

acc. no.	Accession number
AMR	antimicrobial resistance
AQ	assessment question
AST	antimicrobial susceptibility testing
ATC	anatomical therapeutic chemical
AWaRE	access, watch, reserve
BIOHAZ	Biological Hazards (EFSA Panel on)
BMD	broth microdilution
BPW	buffered peptone water
CARD	comprehensive antimicrobial resistance database
cgMLST	core genome multilocus sequence typing
CHDL	carbapenem-hydrolysing class D (β)-lactamase
CIM	carbapenem inactivation method
CPE	carbapenemase-producing Enterobacterales
CRE	carbapenem-resistant Enterobacterales
DDD	defined daily doses
EARS-Net	European Antimicrobial Resistance Surveillance Network
ECDC	European Centre for Disease Prevention and Control
ECOFF	Epidemiological cut-off value
EEA	European Economic Area
EFTA	European Free Trade Association
EMA	European Medicines Agency
ESAC-Net	European Surveillance of Antimicrobial Consumption Network
ESBL	Extended-spectrum β-lactamase
EUCAST	European Union Committee on Antimicrobial Susceptibility Testing
EURGen-Net	European Antimicrobial Resistance Genes Surveillance Network
EURL-AR	European Reference Laboratory for Antimicrobial Resistance
EuSCAPE	European Survey of Carbapenemase-producing Enterobacteriaceae
EUSR-AMR	European Summary Report on Antimicrobial Resistance
ExPEC	extraintestinal pathogenic *Escherichia coli*
HPCIA	highest priority critically important antimicrobials
hvKp	hypervirulent *Klebsiella pneumoniae*
Inc	incompatibility group
KPC	*Klebsiella pneumonia*e carbapenemase
MALDI-TOF	matrix-assisted laser desorption/ionisation (MALDI)–time-of-flight mass spectrometry (TOF)
MBL	metallo-β-lactamase
MDR	multidrug-resistant

MDRO	multidrug-resistant organism
MGE	mobile genetic element
MIC	minimal inhibitory concentration
MLST	multilocus sequence typing
NRL-AR	National Reference Laboratories for Antimicrobial Resistance
OXA	oxacillinase
PBP	penicillin-binding protein
PCR	polymerase chain reaction
pMLST	plasmid multi-locus sequence typing
RGI	resistance gene identifier
RRA	rapid risk assessment
ST	sequence type
ST-Cplx	sequence type complex
ToR	Terms of reference
VF	virulence factor
VFDB	Virulence factor database
WG	Working group
WGS	whole-genome sequencing
WHO	World Health Organization

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SPECIFIC MAP DISCLAIMER

Any designation of Kosovo is without prejudice to positions on status and is in line with United Nations Security Council Resolution 1244 and the International Court of Justice Opinion on the Kosovo Declaration of Independence.

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SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

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APPENDIX A

Literature searches performed

Generic searches were carried out in Web of Science and Pubmed, using the combination of the term "carbapenemase" with the keywords "food" or "animal".

Specific targeted searches were performed in Web of Science combining keywords related to carbapenemases (including most common enzymes)/carbapenem resistance) together with terms related to the food-prodution (food-producing animals, foods thereof, foods of non-animal origin) and with terms related to Enterobacterales (including those bacteria of clinical relevance present in the food chain).

The terms and hits obtained are shown in Table A.1. Duplicates among all searches were eliminated, titles of 2015 references were revised and not relevant ones were discarded. A total of 846 were further considered for abstract reading. Those focusing on the EU/EFTA were used for data extraction. Examples of references with information on CPE in the food chain in other parts of the world were considered to contextualise the EU/EFTA data.

TABLE A.1 Search strings used to recover information on CPE in the food chain.

Period[a]	Topic genes, enzymes, resistance:		Topic matrices		Topic bacteria	Results
1/1/2011–19/12/2024 (Web of Science)	Carbapenemase	AND	Food		–	632
			Animal		–	774
	(ndm OR vim OR oxa OR kpc OR "New Delhi Metallo*" OR GES OR IMI OR IMP OR blandm OR blavim OR blaoxa OR blakpc OR blaGES OR blaIMI OR blaIMP OR carbapenemase OR "carbapenem resistan*" OR "carbapenem-resistan*")	AND	**Animals related:** (ruminant OR cattle OR dairy OR veal OR beef OR cow OR bull OR calf OR ox OR heifer OR bovine OR goat OR sheep OR lamb OR pig OR swine OR sow OR boar OR pork OR piglet OR poultry OR chicken OR "Gallus gallus" OR turkey OR broiler OR chick OR duck OR hen OR geese OR ostriche OR quail OR fowl OR pheasant OR hatchery OR aquaculture OR fish OR finfish OR seafood OR shellfish OR bivalve* OR mussel* OR crustacean OR cephalopod OR mollusc OR lobster OR oyster* OR salmon OR shrimp* OR prawn*)	AND	**Topic Bacteria:** (Enterobacterales OR Enterobacteriales OR Enterobacteria OR Klebsiella OR Escherichia OR Salmonella OR Citrobacter OR Enterobacter OR "K. pneumoniae" OR "E. coli")	1626
		AND	**Foods of non-animal origin related:** (crop OR vegetable OR cereal OR fruit OR salad OR herbs OR spice OR manure OR slurry OR irrigation)	AND		179

[a]Further searches were done to cover the period December to end of February 2025, with only two additional references relevant for the current opinion.

APPENDIX B

Occurrence of CPE in the food chain in the EU/EFTA

TABLE B.1 Overview of carbapenemase-producing Enterobacterales (CPE) in the food chain and human interface, EU/EFTA countries, 2011–2024.

Year	Country	Carbapenemase type	CPE (n)[a]	Matrix (sample type) level 3	Matrix (sample type) combined categories	Type of study (EU monitoring programme)	Strain species[b]	ST- complex or eBG[c]	MLST[b]	Plasmids[b,e]	References/source of information[d]
2011	DE	VIM-1	2	Fattening pigs farm (gauze socks)	Pigs and/or their environment	Research	*Escherichia coli*	ST23-Cplx	ST88	IncHI2; 220 kb	Fischer et al. (2012, 2017)
2011	DE	VIM-1	35	Fattening pigs farm (faeces, manure, flies, boot socks)	Pigs and/or their environment	Research	*Escherichia coli*	ST23-Cplx	ST88	IncHI2; 220 kb	Fischer et al. (2017), Roschanski, Friese, et al. (2017)
2011–2012	DE	VIM-1	1	Broilers farm, dust	Broilers and/or their environment	Research	*Escherichia coli*	ST131-Cplx	ST131	IncHI2 (St-1)	Roschanski et al. (2018)
2011	DE	VIM-1	2	Broilers farm, dust	Broilers and/or their environment	Research	*Salmonella* Infantis	eBG 31	ST32	IncHI2; 300 kb	Fischer et al. (2013)
2011	DE	VIM-1	1	Fattening pigs farm (boot socks)	Pigs and/or their environment	Research	*Salmonella* Infantis	eBG 31	ST32	IncHI2; 300 kb	Fischer et al. (2013, 2017)
2011	DE	VIM-1	1	Fattening pigs farm (pooled faeces)	Pigs and/or their environment	Research	*Salmonella* Infantis	eBG 31	ST32	IncHI2; 300 kb	Fischer et al. (2013, 2017)
2012	DE	VIM-1	1	Fattening pigs farm	Pigs and/or their environment	Research	*Salmonella* Infantis	eBG 31	ST32	IncHI2; 300 kb	Fischer et al. (2017)
2015	CH	OXA-181	1	Herbs and spices (imported)	Foods of non-animal origin	Research	*Klebsiella variicola*	NA	NA	IncX3-type; 51 kb	Zurfluh et al. (2015)
2015	BE	VIM-1	1	Pig meat	Pig meat	EU monitoring (AMR MON)	*Escherichia coli*	NA	ST5869	IncA/C2 (S15FP06257_p)	García-Graells et al. (2020), EFSA and ECDC (2017), Survey
2015	DE	VIM-1	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (ESBL MON)	*Escherichia coli*	ST23-Cplx	ST88	Chromosomal	Irrgang et al. (2017), EFSA and ECDC (2017), Survey
2015	DE	VIM-1	1	Pig meat	Pig meat	Passive surveillance	*Salmonella* Infantis	eBG 31	ST32	IncHI2/HI2A (ST1); 300 kb	Borowiak et al. (2017), EFSA and ECDC (2019), Survey
2016	RO	NDM-like	2	Natural fishery salted lakes	Natural water sources	Research	*Escherichia coli*	NA	NA	NA	Lazăr et al. (2021)
2016	RO	OXA-162	1	Broilers (caecal samples at slaughter)	Broilers and/or their environment	EU monitoring (CARBA MON)	*Escherichia coli*	NA	ST4980	IncHI2/pST4	Bortolaia et al. (2021), EFSA and ECDC (2018), Survey
2016	RO	OXA-162	1	Broilers (caecal samples at slaughter)	Broilers and/or their environment	EU monitoring (CARBA MON)	*Escherichia coli*	ST155-Cplx	ST155	IncHI2/pST4	Bortolaia et al. (2021), EFSA and ECDC (2018), Survey

(Continues)

TABLE B.1 (Continued)

Year	Country	Carbapenemase type	CPE (n)[a]	Matrix (sample type) level 3	Matrix (sample type) combined categories	Type of study (EU monitoring programme)	Strain species[b]	ST- complex or eBG[c]	MLST[b]	Plasmids[b,e]	References/source of information[d]
2016	RO	OXA-162	1	Chicken meat	Chicken meat	EU monitoring (CARBA MON)	*Escherichia coli*	ST10-Cplx	ST10	IncHI2/pST4	Bortolaia et al. (2021), EFSA and ECDC (2018)
2016	IT	OXA-181	1	Pigs farm (faecal sample)	Pigs and/or their environment	Research	*Escherichia coli*	ST101-Cplx	ST359	IncX3; 51.5 kb	Pulss et al. (2017)
2016	IT	OXA-181	1	Pigs farm (faecal sample)	Pigs and/or their environment	Research	*Escherichia coli*	ST86-Cplx	ST641	IncX3; 51.5 kb	Pulss et al. (2017)
2016	DE	VIM-1	1	Diagnostic sample (sick piglet)	Pigs and/or their environment	Passive surveillance	*Salmonella* Infantis	eBG 31	ST32	IncHI2/HI2A (ST1); 300 kb	Borowiak et al. (2017), Survey
2016	DE	VIM-1	32	Fattening pigs farm (faeces, boot swabs)	Pigs and/or their environment	Research (trace back investigation)	*Escherichia coli*	ST23-Cplx	ST88	Chromosomal (23 isolates), IncHI2 (210 kb, 250 kb, 375kb) (9 isolates)	Irrgang et al. (2019), Survey
2016	DE	VIM-1	4	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	Research (trace back investigation)	*Escherichia coli*	ST23-Cplx	ST88	IncHI2 (ST1)	Irrgang et al. (2017), Survey
2016	DE	VIM-1	1	Seafood, clams (imported)	Foods of aquatic animal origin	Research	*Escherichia coli*	ST10-Cplx	ST10	IncY	Roschanski et al. (2017)
2017	NL	IMI-1	1	Seafood, shrimps (imported)	Foods of aquatic animal origin	National monitoring	*Enterobacter cloacae* complex	NA	ST411	No plasmid found (present in EcloIMEX elements), potentially in the chromosome	Brouwer et al. (2018), Survey
2017	NL	FLC-1 + IMI-2	1	Seafood, shrimps (imported)	Foods of aquatic animal origin	National monitoring	*Enterobacter cloacae*	NA	ST813	p3442-FLC-1; 93 kb, IncFII-Y-9, p3442-IMI-2; 78 kb, IncFII-Y-10	Brouwer et al. (2019), Survey
2017	DE	VIM-1	1	Breeding pigs farm (faecal samples)	Pigs and/or their environment	Research	*Enterobacter cloacae*	NA	NA	IncHI2 (ST1); 290 kb	Roschanski et al. (2019)
2017	DE	VIM-1	1	Pigs farm (boot swabs)	Pigs and/or their environment	Research	*Salmonella* Goldcoast	eBG 251	ST358	IncHI2; 300 kb	Roschanski et al. (2019)
2017	DE	VIM-1	1	Breeding pigs farm (faecal samples)	Pigs and/or their environment	Research	*Salmonella* Infantis	eBG 31	ST32	IncHI2; 300 kb	Roschanski et al. (2019)
2017	DE	VIM-1	1	Fattening pigs farm (faecal samples)	Pigs and/or their environment	EU/National monitoring (OTHER CARBA MON)	*Escherichia coli*	ST10-Cplx	ST48	450kb, IncHI2A_1, RepA_1_pKPC-CAV1321, IncHI2_1, IncFIB(AP001918)_1, IncFII_1	EURL-AR WorkshopMeeting_2024_Irrgang, EFSA and ECDC (2019), Survey

TABLE B.1 (Continued)

Year	Country	Carbapenemase type	CPE (n)[a]	Matrix (sample type) level 3	Matrix (sample type) combined categories	Type of study (EU monitoring programme)	Strain species[b]	ST- complex or eBG[c]	MLST[b]	Plasmids[b,e]	References/source of information[d]
2017	DE	VIM-1	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (ESBL MON)	*Escherichia coli*	NA	ST7593	IncHI2; 306 kb	Pauly et al. (2021), EFSA and ECDC (2019), Survey
2018	NL	NDM-5 + OXA-48	1	Seafood, shrimps (imported)	Foods of aquatic animal origin	National monitoring	*Enterobacter cloacae*	NA	NA	NA	Bruggemana et al. (2024), Survey
2018	BE	NDM-1	NA	Grasshoppers	Ready-to-eat insects	Research	NA	NA	NA	NA	Milanović et al. (2018)
2018	NL	NDM-1	NA	Mealworms	Ready-to-eat insects	Research	NA	NA	NA	NA	Milanović et al. (2018)
2018	NL	NDM-1	NA	Grasshoppers	Ready-to-eat insects	Research	NA	NA	NA	NA	Milanović et al. (2018)
2018	NL	OXA-48	NA	Grasshoppers	Ready-to-eat insects	Research	NA	NA	NA	NA	Milanović et al. (2018)
2018	BE	OXA-48	NA	Mealworms	Ready-to-eat insects	Research	NA	NA	NA	NA	Milanović et al. (2018)
2019	DE	GES-5	1	Fattening pigs farm (faecal samples)	Pigs and/or their environment	EU/National monitoring (OTHER CARBA MON)	*Escherichia coli*	NA	ST1084	pEC19-AB02908; 12 kb	Irrgang, Tausch, et al. (2020), EFSA and ECDC (2021)
2019	DE	GES-5	1	Fattening pigs farm (faecal samples)	Pigs and/or their environment	EU/National monitoring (OTHER ESBL MON)	*Escherichia coli*	NA	NA	NA	Irrgang, Tausch, et al. (2020), EFSA and ECDC (2021)
2019	NL	IMI-1	2	Seafood, shrimps (imported)	Foods of aquatic animal origin	National monitoring	*Enterobacter cloacae*	NA	NA	NA	Bruggemana et al. (2024), Survey
2019	SE	IMI-2	1	Livestock feed mill	Environment	Research	*Enterobacter cloacae*	NA	ST657	IncFII, IncFIB, IncFII(Yp)-group	Börjesson et al. (2022)
2019	RO	KPC	1	Vegetables	Foods of non-animal origin	Research	*Morganella morganii*	NA	NA	NA	Colosi et al. (2020)
2019	RO	KPC	1	Vegetables	Foods of non-animal origin	Research	*Klebsiella oxytoca*	NA	NA	NA	Colosi et al. (2020)
2019	IT	KPC-3	1	Seafood, clams	Foods of aquatic animal origin	National monitoring	*Klebsiella michiganensis*	NA	ST382	IncFII	Simoni et al. (2022)
2019	IT	NDM-4	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (CARBA MON)	*Escherichia coli*	ST86-Cplx	ST641	IncFII; 53,043 bp	Diaconu et al. (2020), EFSA and ECDC (2021), Survey
2019	DE	OXA-48	1	Fattening pigs farm (faecal samples)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	ST23-Cplx	ST295	IncL/M; 63 kb	Irrgang, Pauly, et al. (2020), EFSA and ECDC (2021)
2019	RO	OXA-48	1	Vegetables	Foods of non-animal origin	Research	*Enterobacter cloacae*	NA	NA	NA	Colosi et al. (2020)

(Continues)

TABLE B.1 (Continued)

Year	Country	Carbapenemase type	CPE (n)[a]	Matrix (sample type) level 3	Matrix (sample type) combined categories	Type of study (EU monitoring programme)	Strain species[b]	ST- complex or eBG[c]	MLST[b]	Plasmids[b,e]	References/source of information[d]
2019	HU	OXA-48-like	NA	Freshwater fish, carp	Foods of aquatic animal origin	Research	NA	NA	NA	NA	Libisch et al. (2022)
2019	DE	VIM-1	1	Pig meat	Pig meat	EU monitoring (CARBA MON)	*Escherichia coli*	NA	ST5869	IncA/C2; 190 kb	Pauly et al. (2021), EFSA and ECDC (2021), Survey
2020	NL	IMI-1	2	Seafood, shrimps (imported)	Foods of aquatic animal origin	National monitoring	*Enterobacter cloacae*	NA	NA	NA	Bruggemana et al. (2024), Survey
2020	NL	IMI-2	1	Seafood, frozen tilapia (imported)	Foods of aquatic animal origin	National monitoring (OTHER CARBA MON)	*Enterobacter cloacae*	NA	NA	NA	Bruggemana et al. (2024), EFSA and ECDC (2022), Survey
2020	NL	IMI-3	1	Seafood, frozen tilapia (imported)	Foods of aquatic animal origin	National monitoring (OTHER CARBA MON)	*Enterobacter cloacae*	NA	NA	NA	Bruggemana et al. (2024), EFSA and ECDC (2022), Survey
2020	NL	IMI-3	1	Vegetables (imported)	Foods of non-animal origin	National monitoring (OTHER CARBA MON)	*Enterobacter cloacae*	NA	NA	NA	Bruggemana et al. (2024), EFSA and ECDC (2022), Survey
2020	ES	IMP	1	Vegetables	Foods of non-animal origin	Research	*Proteus* sp.	NA	NA	NA	Jiménez-Belenguer et al. (2023)
2020	ES	IMP + OXA-48	1	Vegetables	Foods of non-animal origin	Research	*Rahnella* sp.	NA	NA	NA	Jiménez-Belenguer et al. (2023)
2020	IT	KPC-3	1	Milk filter	Bovines and/or their environment	Research	*Klebsiella pneumoniae*	NA	ST307	NA	Bonardi et al. (2023)
2020	ES	NDM-1	1	Dairy cattle	Bovines and/or their environment	Research	*Escherichia coli*	NA	ST11626	IncC; 145,165 bp, pEC1110_NDM-1	Tello et al. (2022)
2020	EL	NDM-5	1	Bovine farm (faecal samples)	Bovines and/or their environment	Research	*Escherichia coli*	NA	ST361	IncFII; 100 kb	Tsilipounidaki et al. (2022)
2020	AT	VIM-1	1	Broilers (caecal samples at slaughter)	Broilers and/or their environment	EU monitoring (ESBL MON)	*Escherichia coli*	NA	ST1196	IncFIB(AP001918), IncFII(pRSB107), IncN, IncR	EFSA and ECDC (2022), Survey
2020	ES	VIM	1	Vegetables	Foods of non-animal origin	Research	*Serratia* sp.	NA	NA	NA	Jiménez-Belenguer et al. (2023)
2021	NL	IMI-3	1	Herbs and spices (imported)	Foods of non-animal origin	National monitoring	*Enterobacter asburiae*	NA	NA	NA	Bruggemana et al. (2024), EFSA and ECDC (2023), Survey

TABLE B.1 (Continued)

Year	Country	Carbapenemase type	CPE (n)[a]	Matrix (sample type) level 3	Matrix (sample type) combined categories	Type of study (EU monitoring programme)	Strain species[b]	ST- complex or eBG[c]	MLST[b]	Plasmids[b,e]	References/source of information[d]
2021	ES	IMP + VIM	2	Vegetables	Foods of non-animal origin	Research	*Rahnella* sp.	NA	NA	NA	Jiménez-Belenguer et al. (2023)
2021	HU	NDM-5	2	Bovine meat	Bovine meat	EU monitoring (ESBL MON)	*Escherichia coli*	ST405-Cplx	ST405	NA	EFSA and ECDC (2023), EURL-AR WorkshopMeeting_ 2023_Ivanova
2021	HU	NDM-5	1	Pig meat	Pig meat	EU monitoring (ESBL MON)	*Escherichia coli*	ST405-Cplx	ST405	NA	EFSA and ECDC (2023), EURL-AR WorkshopMeeting_ 2023_Ivanova
2021	CZ	NDM-5	2	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	NA	ST898	IncX3; 46 kb	EFSA and ECDC (2023), Survey
2021	CZ	NDM-5	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	ST10-Cplx	ST10	IncX3; 46 kb	EFSA and ECDC (2023), Survey
2021	IT	NDM-5	1	Bovine animals < 1 year of age (caecal samples at slaughter)	Bovines and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	ST10-Cplx	ST617	ColpVC Col(BS512) IncX4 Col(MG828) Col156 Col(MG828)	EFSA and ECDC (2023), Survey
2021	IT	OXA-48	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	ST38-Cplx	ST38	No plasmid found	Carfora et al. (2022), EFSA and ECDC (2023), Survey
2021	ES	OXA-48	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	ST23-Cplx	ST410	IncL/M(pOXA48)	EFSA and ECDC (2023), Survey
2021	ES	OXA-48	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	NA	ST457	IncL/M(pOXA48)	EFSA and ECDC (2023), Survey
2021	ES	OXA-48	1	Fattening pigs farm	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	ST10-Cplx	ST34	IncL/M(pOXA-48)	Survey
2021	ES	OXA-48	2	Fattening pigs farm	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	ST10-Cplx	ST48	IncL/M(pOXA-48)	Survey

(Continues)

TABLE B.1 (Continued)

Year	Country	Carbapenemase type	CPE (n)[a]	Matrix (sample type) level 3	Matrix (sample type) combined categories	Type of study (EU monitoring programme)	Strain species[b]	ST- complex or eBG[c]	MLST[b]	Plasmids[b,e]	References/source of information[d]
2021	ES	OXA-48	1	Fattening pigs farm	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	ST155-Cplx	ST58	IncL/M(pOXA-48)	Survey
2021	ES	OXA-48	3	Fattening pigs farm	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	ST101-Cplx	ST101	IncL/M(pOXA-48)	Survey
2021	ES	OXA-48	6	Fattening pigs farm	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	ST23-Cplx	ST410	IncI1 (4 isolates), IncL/M(pOXA-48) (2 isolates)	Survey
2021	ES	OXA-48	1	Fattening pigs farm	Pigs and/or their environment	National monitoring	*Escherichia coli*	ST448-Cplx	ST448	IncI1	Survey
2021	ES	OXA-48	1	Breeding pigs farm (sow)	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	NA	ST525	IncL/M(pOXA-48)	Survey
2021	ES	OXA-48	2	Fattening pigs farm	Pigs and/or their environment	Research (trace back investigation)	*Escherichia coli*	ST86-Cplx	ST877	IncI1 (1 isolate), IncL/M(pOXA-48) (1 isolate)	Survey
2021	ES	OXA-48	1	Fattening pigs farm	Pigs and/or their environment	Research (trace back investigation)	*Escherichia coli*	ST10-Cplx	ST1303	IncI1	Survey
2021	ES	OXA-48	3	Fattening pigs farm	Pigs and/or their environment	Research (trace back investigation)	*Escherichia coli*	ST23-Cplx	ST1998	IncL/M(pOXA-48) (2 isolate), IncI1 (1 isolate)	Survey
2021	ES	OXA-48	1	Fattening pigs farm	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	NA	ST3014	IncL/M(pOXA-48)	Survey
2021	ES	OXA-48	7	Fattening and breeding pigs farm (sow)	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	ST101-Cplx	ST5229	IncL/M(pOXA-48) (6 isolates), IncI1 (1 isolate)	Survey
2021	ES	OXA-48	3	Vegetables	Foods of non-animal origin	Research	*Enterobacter* sp.	NA	NA	NA	Jiménez-Belenguer et al. (2023)

TABLE B.1 (Continued)

Year	Country	Carbapenemase type	CPE (n)[a]	Matrix (sample type) level 3	Matrix (sample type) combined categories	Type of study (EU monitoring programme)	Strain species[b]	ST- complex or eBG[c]	MLST[b]	Plasmids[b,e]	References/source of information[d]
2021	ES	OXA-48	2	Vegetables	Foods of non-animal origin	Research	*Pantoea* sp.	NA	NA	NA	Jiménez-Belenguer et al. (2023)
2021	ES	OXA-48	3	Vegetables	Foods of non-animal origin	Research	*Raoutella* sp.	NA	NA	NA	Jiménez-Belenguer et al. (2023)
2021	ES	OXA-48 + VIM	1	Vegetables	Foods of non-animal origin	Research	*Enterobacter* sp.	NA	NA	NA	Jiménez-Belenguer et al. (2023)
2021	IT	OXA-181	7	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	ST101-Cplx	ST5229	IncX1(2 isolates), IncX3 (2 isolates), (IncFIB, IncFIC(FII), IncX1) (2 isolates), (IncFIB, IncFIC(FII), IncFII(pCoo), IncI1-I(Alpha), IncX1) (1 isolate)	Carfora et al. (2022), EFSA and ECDC (2023), Survey
2021	IT	OXA-181	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	ST101-Cplx	ST101	IncB/O/K/Z_2, IncFIA, IncFIB, IncFIC(FII), IncFII(pCTU2), IncX3	Carfora et al. (2022), EFSA and ECDC (2023), Survey
2021	IT	OXA-181	2	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	ST23-Cplx	ST410	(IncFIA(HI1), IncI1-I(Alpha), IncR, IncX1, IncY) (1 isolate), (IncFIB; IncFIC(FII), IncI1-I(Alpha), IncX3) (2 isolates)	Carfora et al. (2022), EFSA and ECDC (2023), Survey
2021	IT	OXA-181	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	NA	ST117	IncX3	Carfora et al. (2022), EFSA and ECDC (2023), Survey
2021	IT	OXA-181	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	ST10-Cplx	ST3489	IncX3	Carfora et al. (2022), EFSA and ECDC (2023), Survey
2021	IT	OXA-181	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	NA	ST7461	IncX3	Carfora et al. (2022), EFSA and ECDC (2023), Survey
2021	IT	OXA-181	2	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	NA	ST542	IncFII (1 isolate), IncX3 (1 isolate)	Carfora et al. (2022), EFSA and ECDC (2023), Survey
2021	IT	OXA-181	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	ST10-Cplx	ST218	IncX3	Carfora et al. (2022), EFSA and ECDC (2023), Survey

(Continues)

TABLE B.1 (Continued)

Year	Country	Carbapenemase type	CPE (n)[a]	Matrix (sample type) level 3	Matrix (sample type) combined categories	Type of study (EU monitoring programme)	Strain species[b]	ST- complex or eBG[c]	MLST[b]	Plasmids[b,e]	References/source of information[d]
2021	IT	OXA-181	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	ST10-Cplx	ST10	IncX3	Carfora et al. (2022), EFSA and ECDC (2023), Survey
2021	IT	OXA-181	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	NA	NA	IncFII, IncX3, IncY	Carfora et al. (2022), EFSA and ECDC (2023), Survey
2021	IT	OXA-181	2	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	ST10-Cplx	ST48	IncX3 (1 isolate), IncX3, IncFIB, IncFIC(FII), IncX1 (1 isolate)	Carfora et al. (2022), EFSA and ECDC (2023), Survey
2021	IT	OXA-181	6	Fattening and breeding pigs farm (farrowing, weaner, finisher units)	Pigs and/or their environment	Research (trace back investigation)	*Escherichia coli*	ST101-Cplx	ST5229	IncX1	Carfora et al. (2022)
2021	IT	OXA-181	1	Breeding pigs farm (gestation unit)	Pigs and/or their environment	Research (trace back investigation)	*Escherichia coli*	NA	ST244	IncX1	Carfora et al. (2022)
2021	IT	OXA-181	1	Breeding pigs farm (weaner unit)	Pigs and/or their environment	Research (trace back investigation)	*Escherichia coli*	NA	ST1494	IncFII	Carfora et al. (2022)
2021	IT	OXA-181	2	Bovine animals <1 year of age (caecal samples at slaughter)	Bovines and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	ST101-Cplx	ST5229	IncFIB, IncFIC(FII), IncX3 (1 isolate), IncFIC(FII) IncX1 (1 isolate)	Carfora et al. (2022), EFSA and ECDC (2023), Survey
2021	IT	OXA-181	1	Bovine animals <1 year of age (caecal samples at slaughter)	Bovines and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	NA	ST542	IncFIB, IncFIC(FII), IncX3, IncY	Carfora et al. (2022), EFSA and ECDC (2023), Survey
2021	IT	OXA-181	1	Bovine animals <1 year of age (caecal samples at slaughter)	Bovines and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	ST10-Cplx	ST10	IncFIA(HI1), IncFIB, IncFIC(FII), IncHI1A, IncHI1B(R27), IncX3	Carfora et al. (2022), EFSA and ECDC (2023), Survey
2021	IT	OXA-181	1	Dairy cattle	Bovines and/or their environment	Research (trace back investigation)	*Escherichia coli*	ST101-Cplx	ST5229	IncX1	Carfora et al. (2022)
2021	IT	OXA-181	1	Farm workers	Human	Research (trace back investigation)	*Escherichia coli*	ST101-Cplx	ST5229	IncX1	Carfora et al. (2022)

TABLE B.1 (Continued)

Year	Country	Carbapenemase type	CPE (n)[a]	Matrix (sample type) level 3	Matrix (sample type) combined categories	Type of study (EU monitoring programme)	Strain species[b]	ST- complex or eBG[c]	MLST[b]	Plasmids[b,e]	References/source of information[d]
2021	IT	OXA-181	1	Farm workers	Human	Research (trace back investigation)	*Escherichia coli*	ST10-Cplx	ST744	IncX1	Carfora et al. (2022)
2021	ES	VIM	2	Vegetables	Foods of non-animal origin	Research	*Pantoea* sp.	NA	NA	NA	Jiménez-Belenguer et al. (2023)
2021	ES	VIM	2	Vegetables	Foods of non-animal origin	Research	*Rahnella* sp.	NA	NA	NA	Jiménez-Belenguer et al. (2023)
2022	PT	GES-5	1	Seafood, bivalves	Foods of aquatic animal origin	Research	*Klebsiella pneumoniae*	NA	DLV644	ColE	Freire et al. (2023)
2022	IT	IMP	7	Seafood, Codfish at processing plant	Foods of aquatic animal origin	Research	*Serratia fonticola*	NA	NA	NA	Ferri et al. (2023)
2022	ES	KPC	1	Poultry slaughterhouses, equipment	Broilers and/or their environment	Research	*Citrobacter freundii*	NA	NA	NA	Panera-Martínez et al. (2024)
2022	ES	NDM	9	Poultry slaughterhouses, equipment	Broilers and/or their environment	Research	*Escherichia coli*	NA	NA	NA	Panera-Martínez et al. (2024)
2022	ES	NDM	9	Poultry slaughterhouses, equipment	Broilers and/or their environment	Research	*Serratia fonticola*	NA	NA	NA	Panera-Martínez et al. (2024)
2022	IT	OXA-48-like	1	Seafood, Codfish at processing plant	Foods of aquatic animal origin	Research	*Salmonella* Enteritidis	NA	NA	NA	Ferri et al. (2023)
2022	ES	OXA-48	2	Breeding pigs farm (sow)	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	ST46-Cplx	ST46	IncL/M(pOXA-48)	Survey
2022	ES	OXA-48	1	Breeding pigs farm (sow)	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	ST101-Cplx	ST101	IncL/M(pOXA-48)	Survey
2022	ES	OXA-48	1	Breeding pigs farm (sow)	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	ST23-Cplx	ST410	IncL/M(pOXA-48)	Survey
2022	ES	OXA-48	2	Breeding pigs farm (sow)	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	ST10-Cplx	ST744	IncL/M(pOXA-48)	Survey

(Continues)

TABLE B.1 (Continued)

Year	Country	Carbapenemase type	CPE (n)[a]	Matrix (sample type) level 3	Matrix (sample type) combined categories	Type of study (EU monitoring programme)	Strain species[b]	ST- complex or eBG[c]	MLST[b]	Plasmids[b,e]	References/source of information[d]
2022	ES	OXA-48	1	Breeding pigs farm (sow)	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	NA	ST8432	IncL/M(pOXA-48)	Survey
2022	ES	OXA-48	1	Breeding pigs farm (sow)	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	NA	NA	IncL/M(pOXA-48)	Survey
2022	IT	OXA-181	2	Fattening turkeys (caecal samples at slaughter)	Turkeys and/or their environment	EU monitoring (WGS AMR MON, WGS CARBA MON)	*Escherichia coli*	ST101-Cplx	ST5229	IncFIB, IncX1	EFSA and ECDC (2024), Survey
2022	AT	VIM-1	1	Broilers (caecal samples at slaughter)	Broilers and/or their environment	EU monitoring (ESBL MON)	*Escherichia coli*	ST101-Cplx	ST101	Col(pHAD28) IncFIB(AP001918), IncFII, IncI1-I(Alpha), IncN	EFSA and ECDC (2024), Survey
2022	AT	VIM-1	1	Broilers (caecal samples at slaughter)	Broilers and/or their environment	EU monitoring (ESBL MON)	*Escherichia coli*	NA	ST154	IncFIB(AP001918), IncFIC(FII), IncI1-I(Alpha), IncN	EFSA and ECDC (2024), Survey
2022	IT	VIM-1	1	Broilers (caecal samples at slaughter)	Broilers and/or their environment	EU monitoring (WGS ESBL MON)	*Escherichia coli*	NA	ST216	IncY, IncX1, Col8282, ColpVC, IncI1-I(Alpha), IncR, IncX1	EFSA and ECDC (2024), Survey
2023	NL	FRI	1	Seafood, frozen tilapia (imported)	Foods of aquatic animal origin	National monitoring	*Enterobacter cloacae*	NA	NA	NA	Bruggemana et al. (2024), Survey
2023	CH	IMI-1	1	Herbs and spices (imported)	Foods of non-animal origin	Research	*Enterobacter cloacae*	NA	ST411	Chromosomal	Tresch et al. (2024)
2023	CH	IMI-1	1	Herbs and spices (imported)	Foods of non-animal origin	Research	*Enterobacter cloacae*	NA	ST1516	Chromosomal	Tresch et al. (2024)
2023	CH	IMI-1	1	Herbs and spices (imported)	Foods of non-animal origin	Research	*Enterobacter cloacae*	NA	ST820	Chromosomal	Tresch et al. (2024)
2023	CH	IMI-1	1	Herbs and spices (imported)	Foods of non-animal origin	Research	*Enterobacter cloacae*	NA	ST412	Chromosomal	Tresch et al. (2024)
2023	CH	IMI-1	1	Herbs and spices (imported)	Foods of non-animal origin	Research	*Enterobacter cloacae*	NA	ST3044	Chromosomal	Tresch et al. (2024)
2023	CH	IMI-1	1	Herbs and spices (imported)	Foods of non-animal origin	Research	*Enterobacter vonholyi*	NA	ST3052	Chromosomal	Tresch et al. (2024)
2023	CH	IMI-1	1	Herbs and spices (imported)	Foods of non-animal origin	Research	*Enterobacter cloacae*	NA	ST477	Chromosomal	Tresch et al. (2024)

TABLE B.1 (Continued)

Year	Country	Carbapenemase type	CPE (n)[a]	Matrix (sample type) level 3	Matrix (sample type) combined categories	Type of study (EU monitoring programme)	Strain species[b]	ST- complex or eBG[c]	MLST[b]	Plasmids[b,e]	References/source of information[d]
2023	CH	IMI-6	1	Vegetables	Foods of non-animal origin	Research	*Enterobacter asburiae*	NA	ST657	IncFII(Yp); 168 kb	Tresch et al. (2024)
2023	NL	NDM-1	1	Seafood, shrimps (imported)	Foods of aquatic animal origin	National monitoring (OTHER WGS MON)	*Escherichia coli*	NA	NA	NA	Bruggemana et al. (2024), EFSA and ECDC (2025), Survey
2023	NL	NDM-1	1	Seafood, shrimps (imported)	Foods of aquatic animal origin	National monitoring	*Enterobacter cloacae*	NA	NA	NA	Bruggemana et al. (2024), Survey
2023	NL	NDM-1	1	Seafood, frozen tilapia (imported)	Foods of aquatic animal origin	National monitoring	*Enterobacter cloacae*	NA	NA	NA	Bruggemana et al. (2024), Survey
2023	CZ	NDM-5	4	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	ST10-Cplx	ST10	IncX3; 46 kb	EFSA and ECDC (2025), Survey
2023	CZ	NDM-5	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	NA	ST75	IncX3; 46 kb	EFSA and ECDC (2025), Survey
2023	IT	NDM-5	1	Bovine animals <1 year of age (caecal samples at slaughter)	Bovines and/or their environment	EU monitoring (WGS ESBL MON)	*Escherichia coli*	ST10-Cplx	ST15578	IncFIB(AP001918), IncFII(pAMA1167-NDM-5), IncFIA, IncY	EFSA and ECDC (2025), Survey
2023	ES	NDM-5	1	Pig meat	Pig meat	EU monitoring (CARBA MON)	*Escherichia coli*	NA	NA	NA	EFSA and ECDC (2025), Survey
2023	NO	NDM-5	2	Bovine animals (caecal samples at slaughter)	Bovines and/or their environment	EU/National monitoring (WGS OTHER CARBA MON, WGS OTHER ESBL MON)	*Escherichia coli*	NA	NA	NA	EFSA and ECDC (2025), Survey
2023	PT	NDM-5 + OXA-181	5	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (CARBA MON, ESBL MON)	*Escherichia coli*	NA	NA	NA	EFSA and ECDC (2025), Survey
2023	PT	OXA-48	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (CARBA MON)	*Escherichia coli*	NA	NA	NA	EFSA and ECDC (2025), Survey
2023	RO	OXA-48	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (CARBA MON)	*Escherichia coli*	NA	NA	NA	EFSA and ECDC (2025), Survey

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TABLE B.1 (Continued)

Year	Country	Carbapenemase type	CPE (n)[a]	Matrix (sample type) level 3	Matrix (sample type) combined categories	Type of study (EU monitoring programme)	Strain species[b]	ST- complex or eBG[c]	MLST[b]	Plasmids[b,e]	References/source of information[d]
2023	ES	OXA-48	1	Bovine animals <1 year of age (caecal samples at slaughter)	Bovines and/or their environment	EU monitoring (CARBA MON)	*Escherichia coli*	ST23-Cplx	ST1725	IncL/M(pOXA-48)	EFSA and ECDC (2025), Survey
2023	ES	OXA-48	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (CARBA MON)	*Escherichia coli*	ST10-Cplx	ST34	IncI1	EFSA and ECDC (2025), Survey
2023	ES	OXA-48	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (CARBA MON)	*Escherichia coli*	ST23-Cplx	ST88	IncL/M(pOXA-48)	EFSA and ECDC (2025), Survey
2023	ES	OXA-48	2	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (CARBA MON)	*Escherichia coli*	ST101-Cplx	ST101	IncL/M(pOXA-48)	EFSA and ECDC (2025), Survey
2023	ES	OXA-48	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (CARBA MON)	*Escherichia coli*	NA	ST117	IncL/M(pOXA-48)	EFSA and ECDC (2025), Survey
2023	ES	OXA-48	3	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (CARBA MON)	*Escherichia coli*	ST23-Cplx	ST410	IncI1 (1 isolate), IncL/M(pOXA-48) (1 isolate), NA (1 isolate)	EFSA and ECDC (2025), Survey
2023	ES	OXA-48	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (CARBA MON)	*Escherichia coli*	ST448-Cplx	ST448	IncL/M(pOXA-48)	EFSA and ECDC (2025), Survey
2023	ES	OXA-48	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (CARBA MON)	*Escherichia coli*	ST86-Cplx	ST453	IncL/M(pOXA-48)	EFSA and ECDC (2025), Survey
2023	ES	OXA-48	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (CARBA MON)	*Escherichia coli*	ST86-Cplx	ST641	IncL/M(pOXA-48)	EFSA and ECDC (2025), Survey
2023	ES	OXA-48	2	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (CARBA MON)	*Escherichia coli*	ST10-Cplx	ST744	IncL/M(pOXA-48)	EFSA and ECDC (2025), Survey
2023	ES	OXA-48	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (CARBA MON)	*Enterobacter cloacae*	NA	ST1011	IncL/M(pOXA-48)	EFSA and ECDC (2025), Survey
2023	ES	OXA-48	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (CARBA MON)	*Escherichia coli*	ST23-Cplx	ST1725	IncL/M(pOXA-48)	EFSA and ECDC (2025), Survey

TABLE B.1 (Continued)

Year	Country	Carbapenemase type	CPE (n)[a]	Matrix (sample type) level 3	Matrix (sample type) combined categories	Type of study (EU monitoring programme)	Strain species[b]	ST- complex or eBG[c]	MLST[b]	Plasmids[b,e]	References/source of information[d]
2023	ES	OXA-48	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU/National monitoring (OTHER CARBA MON)	*Escherichia coli*	ST101-Cplx	ST5229	IncL/M(pOXA-48)	EFSA and ECDC (2025), Survey
2023	ES	OXA-48	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	NA	ST5759	NA	EFSA and ECDC (2025), Survey
2023	ES	OXA-48	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (CARBA MON)	*Escherichia coli*	ST10-Cplx	ST10170	NA	EFSA and ECDC (2025), Survey
2023	ES	OXA-48	1	Breeding pigs farm (sow)	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	ST10-Cplx	ST34	IncI1	Survey
2023	ES	OXA-48	1	Fattening pigs farm	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	ST23-Cplx	ST360	IncL/M(pOXA-48)	Survey
2023	ES	OXA-48	1	Fattening pigs farm	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	NA	ST542	IncL/M(pOXA-48)	Survey
2023	ES	OXA-48	1	Breeding pigs farm (sow)	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	ST86-Cplx	ST641	IncI1	Survey
2023	ES	OXA-48	1	Fattening pigs farm	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	ST10-Cplx	ST744	IncL/M(pOXA-48)	Survey
2023	ES	OXA-48	1	Multiplier pigs farm	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	NA	ST1196	IncI1	Survey
2023	ES	OXA-48	1	Fattening pigs farm	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	NA	ST4429	IncL/M(pOXA-48)	Survey

(Continues)

TABLE B.1 (Continued)

Year	Country	Carbapenemase type	CPE (n)[a]	Matrix (sample type) level 3	Matrix (sample type) combined categories	Type of study (EU monitoring programme)	Strain species[b]	ST- complex or eBG[c]	MLST[b]	Plasmids[b,e]	References/source of information[d]
2023	ES	OXA-48	2	Multiplier pigs farm	Pigs and/or their environment	National monitoring (trace back investigation)	*Klebsiella pneumoniae*	NA	ST4682	IncI1 (1 isolate), Chromosome (1 isolate)	Survey
2023	ES	OXA-48	7	Fattening, breeding (sow) and multiplier pigs farm	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	ST101-Cplx	ST5229	IncL/M(pOXA-48) (6 isolates), IncI1 (1 isolate)	Survey
2023	IT	OXA-181	1	Bovine animals <1 year of age (caecal samples at slaughter)	Bovines and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	NA	ST1152	IncX3, IncFII(pAR0022), IncFIC(FII), ColKP3, IncFIB(AP001918), ColRNAI, Col(MG828)	EFSA and ECDC (2025), Survey
2023	IT	OXA-181	1	Bovine animals <1 year of age (caecal samples at slaughter)	Bovines and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	ST23-Cplx	ST410	ColRNAI, IncFII(pAR0022), IncFII(pRSB107), IncX3, IncFIB(AP001918), IncFII(pECLA), IncI1-I(Alpha), IncFIA, ColKP3, Col(pHAD28), Col440II, IncQ1, ColpVC, Col(BS512), Col(MG828)	EFSA and ECDC (2025), Survey
2023	IT	OXA-181	1	Bovine animals <1 year of age (caecal samples at slaughter)	Bovines and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	NA	ST540	NA	EFSA and ECDC (2025), Survey
2023	IT	OXA-181	1	Bovine animals <1 year of age (caecal samples at slaughter)	Bovines and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	ST101-Cplx	ST5229	Col440II, IncX1, IncX9, IncFII(pCoo), IncFII(pAR0022), ColKP3, ColRNAI, IncFIB(AP001918), IncFIC(FII), Col156, Col(MG828)	EFSA and ECDC (2025), Survey
2023	IT	OXA-181	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS ESBL MON)	*Escherichia coli*	NA	NA	NA	EFSA and ECDC (2025), Survey

TABLE B.1 (Continued)

Year	Country	Carbapenemase type	CPE (n)[a]	Matrix (sample type) level 3	Matrix (sample type) combined categories	Type of study (EU monitoring programme)	Strain species[b]	ST- complex or eBG[c]	MLST[b]	Plasmids[b,e]	References/source of information[d]
2023	IT	OXA-181	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	NA	NA	Col(pHAD28) Col(MG828), IncFII(pAR0022), IncFII(pCoo), IncX3, ColKP3, Col(pHAD28)	EFSA and ECDC (2025), Survey
2023	IT	OXA-181	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	ST101-Cplx	ST101	ColRNAI, IncFII(pECLA), IncB/O/K/Z, IncX3, IncFII(pAR0022), IncFIB(AP001918), ColpEC648, Col(MG828), Col(pHAD28)	EFSA and ECDC (2025), Survey
2023	IT	OXA-181	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	ST165-Cplx	ST165	IncFII(pAR0022), IncFIC(FII), Col(MG828), IncB/O/K/Z, IncFII(pECLA), IncX3, IncFII(29), ColKP3, Col440II, Col(pHAD28), Col(MG828), Col156	EFSA and ECDC (2025), Survey
2023	IT	OXA-181	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	NA	ST3014	ColRNAI, Col(MG828), IncFIA(HI1), IncX9, IncX1, ColKP3, IncFII(pECLA), IncI1-I(Alpha), IncFIB(K)	EFSA and ECDC (2025), Survey
2023	IT	OXA-181	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	ST10-Cplx	ST34	Col440I, Col(MG828), IncFII(pHN7A8), IncFII(pAR0022), IncX3, ColKP3, Col(pHAD28)	EFSA and ECDC (2025), Survey
2023	IT	OXA-181	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	ST156-Cplx	ST348	Col(pHAD28), IncB/O/K/Z, IncFII(pECLA), IncFII(pAR0022), IncFIC(FII), IncX3, IncFIB(AP001918), ColKP3, Col440II, ColRNAI	EFSA and ECDC (2025), Survey

(Continues)

TABLE B.1 (Continued)

Year	Country	Carbapenemase type	CPE (n)[a]	Matrix (sample type) level 3	Matrix (sample type) combined categories	Type of study (EU monitoring programme)	Strain species[b]	ST- complex or eBG[c]	MLST[b]	Plasmids[b,e]	References/source of information[d]
2023	IT	OXA-181	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	ST23-Cplx	ST410	IncFIC(FII), IncFII(pAR0022), IncX3, IncFIB(AP001918), Col(MG828), ColKP3, Col3M	EFSA and ECDC (2025), Survey
2023	IT	OXA-181	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	ST23-Cplx	ST410	IncY, IncX1, IncX9, IncFII(pECLA), IncI1-I(Alpha), ColKP3, ColRNAI, Col440II, ColpEC648, Col156, Col(MG828)	EFSA and ECDC (2025), Survey
2023	IT	OXA-181	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Kluyvera cryocrescens*	ST23-Cplx	ST410	Col(MG828), Col(BS512), IncX3, IncFIC(FII), IncFII(pAR0022), IncFII(pECLA), IncI1-I(Alpha), Col440II, Col(pHAD28), IncQ1, IncFIB(AP001918)	EFSA and ECDC (2025), Survey
2023	IT	OXA-181	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	NA	ST4450	IncFII(pAR0022), IncFIC(FII), pENTAS02, ColRNAI, IncX3, IncX1, Col(pHAD28), ColKP3, Col156, Col440II, Col440I, IncFIB(AP001918), Col(MG828)	EFSA and ECDC (2025), Survey
2023	IT	OXA-181	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	ST101-Cplx	ST5229	Col(MG828), Col(pHAD28), IncX3, IncX8, IncX4, IncI1-I(Alpha), IncFII(pECLA), ColKP3, Col(CriePir75), Col440II, ColRNAI, Col156, IncFIB(AP001918)	EFSA and ECDC (2025), Survey

TABLE B.1 (Continued)

Year	Country	Carbapenemase type	CPE (n)[a]	Matrix (sample type) level 3	Matrix (sample type) combined categories	Type of study (EU monitoring programme)	Strain species[b]	ST- complex or eBG[c]	MLST[b]	Plasmids[b,e]	References/source of information[d]
2023	IT	OXA-181	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	ST101-Cplx	ST5229	Col(pHAD28), Col440II, ColRNAI, IncX1, IncFIB(AP001918), Col(Ye4449), Col(CriePir75), Col(pHAD28), Col156, ColKP3, IncFIC(FII), IncFII(pAR0022)	EFSA and ECDC (2025), Survey
2023	IT	OXA-181	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	ST101-Cplx	ST5229	Col156, ColRNAI, p0111, Col(MG828), ColKP3, IncX3, IncX8, IncX4, IncFII(pAR0022), IncFIC(FII), IncFIB(AP001918), Col(pHAD28)	EFSA and ECDC (2025), Survey
2023	IT	OXA-181	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	ST101-Cplx	ST5229	Col(MG828), Col(VCM04), ColRNAI, Col(pHAD28), IncX4, IncX8, IncFIC(FII), IncFII(pAR0022), IncX1, IncX3, ColKP3, Col156, Col440II, IncFIB(AP001918), Col440I	EFSA and ECDC (2025), Survey
2023	IT	OXA-181	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	NA	ST542	Col(MG828), IncX9, IncX1, IncR, ColKP3, Col(pHAD28), Col440II, ColpVC	EFSA and ECDC (2025), Survey
2023	IT	OXA-181	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	NA	ST5752	Col(MG828), Col(pHAD28), IncFIC(FII), ColKP3, ColRNAI, IncFIB(pB171), Col440I, IncX3, IncFII(pAR0022), IncFII(pECLA), IncI1-I(Alpha), Col156	EFSA and ECDC (2025), Survey

(Continues)

TABLE B.1 (Continued)

Year	Country	Carbapenemase type	CPE (n)[a]	Matrix (sample type) level 3	Matrix (sample type) combined categories	Type of study (EU monitoring programme)	Strain species[b]	ST- complex or eBG[c]	MLST[b]	Plasmids[b,e]	References/source of information[d]
2023	IT	OXA-181	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	NA	ST5752	IncFII(pAR0022), Col(pHAD28), Col(MG828), ColKP3, IncX1, IncFIB(pB171), IncX3, Col(pHAD28), ColRNAI, Col440II, Col440I, IncI1-I(Alpha)_1, IncFII(pECLA)_1	EFSA and ECDC (2025), Survey
2023	IT	OXA-181	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	ST155-Cplx	ST58	IncFII, IncFII(pAR0022), IncFIB(AP001918), IncX9, IncR, IncI1-I(Alpha), IncFII(pECLA), ColKP3, IncX1, IncQ1	EFSA and ECDC (2025), Survey
2023	IT	OXA-181	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (WGS CARBA MON)	*Escherichia coli*	ST10-Cplx	ST761	IncQ1, Col440II, Col(pHAD28), Col156, Col(MG828), ColpVC, ColRNAI, IncL	EFSA and ECDC (2025), Survey
2023	PT	OXA-181	2	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (CARBA MON, ESBL MON)	*Escherichia coli*	NA	NA	NA	EFSA and ECDC (2025), Survey
2023	ES	OXA-181	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (CARBA MON)	*Escherichia coli*	ST10-Cplx	ST10	ColKP3	EFSA and ECDC (2025), Survey
2023	ES	OXA-181	3	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (CARBA MON)	*Escherichia coli*	ST23-Cplx	ST410	ColKP3 (2 isolates), NA (1 isolate)	EFSA and ECDC (2025), Survey
2023	ES	OXA-181	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (ESBL MON)	*Escherichia coli*	NA	NA	ColKP3	EFSA and ECDC (2025), Survey
2023	PT	OXA-244	1	Fattening pigs (caecal samples at slaughter)	Pigs and/or their environment	EU monitoring (CARBA MON)	*Escherichia coli*	NA	NA	NA	EFSA and ECDC (2025), Survey
2023	DE	VIM-1	1	Bovine animals <1 year of age (caecal samples at slaughter)	Bovines and/or their environment	EU monitoring (WGS ESBL MON)	*Escherichia coli*	NA	ST847	Untypable; 16.7kb	Irrgang et al. (2025), EFSA and ECDC (2025), Survey

TABLE B.1 (Continued)

Year	Country	Carbapenemase type	CPE (n)[a]	Matrix (sample type) level 3	Matrix (sample type) combined categories	Type of study (EU monitoring programme)	Strain species[b]	ST- complex or eBG[c]	MLST[b]	Plasmids[b,e]	References/source of information[d]
2023	AT	VIM-1	1	Chicks	Broilers and/or their environment	Research (trace back investigation)	*Escherichia coli*	NA	ST1196	NA	Survey
2023	AT	VIM-1	1	Chicks	Broilers and/or their environment	Research (trace back investigation)	*Escherichia coli*	ST155-Cplx	ST155	NA	Survey
2023	AT	VIM-1	1	Chicks	Broilers and/or their environment	Research (trace back investigation)	*Klebsiella pneumoniae*	NA	NA	NA	Survey
2023	AT	VIM-1	1	Broilers farm, swabs	Broilers and/or their environment	Research (trace back investigation)	*Enterobacter hormaechei*	NA	NA	NA	Survey
2023	AT	VIM-1	1	Broilers farm, swabs	Broilers and/or their environment	Research (trace back investigation)	*Citrobacter* sp.	NA	NA	NA	Survey
2024	CZ	NDM-5	2	Fattening pigs farm	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	NA	ST75	IncX3	Survey
2024	CZ	NDM-5	2	Fattening pigs farm	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	ST10-Cplx	ST10	IncX3	Survey
2024	CZ	NDM-5	1	Fattening pigs farm	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	ST10-Cplx	ST3489	IncX3	Survey
2024	CZ	NDM-5	1	Fattening pigs farm	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	ST155-Cplx	ST58	IncX3	Survey
2024	CZ	NDM-5	1	Fattening pigs farm	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	ST101-Cplx	ST101	IncX3	Survey
2024	CZ	NDM-5	1	Fattening pigs farm	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	NA	ST1147	IncX3	Survey

(Continues)

TABLE B.1 (Continued)

Year	Country	Carbapenemase type	CPE (n)[a]	Matrix (sample type) level 3	Matrix (sample type) combined categories	Type of study (EU monitoring programme)	Strain species[b]	ST- complex or eBG[c]	MLST[b]	Plasmids[b,e]	References/source of information[d]
2024	CZ	NDM-5	1	Fattening pigs farm	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	ST46-Cplx	ST46	IncX3	Survey
2024	ES	OXA-48	1	Multiplier pigs farm	Pigs and/or their environment	EU monitoring (CARBA MON)	*Escherichia coli*	ST10-Cplx	ST10	IncI1	Survey
2024	ES	OXA-181	1	Multiplier pigs farm	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	ST10-Cplx	ST10	ColKP3-IncX3	Survey
2024	ES	OXA-181	1	Fattening pigs farm	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	ST10-Cplx	ST48	ColKP3-IncX3	Survey
2024	ES	OXA-181	4	Multiplier pigs farm	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	ST23-Cplx	ST410	ColKP3-IncX3	Survey
2024	ES	OXA-181	1	Multiplier pigs farm	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	NA	ST542	ColKP3-IncX3	Survey
2024	ES	OXA-181	1	Multiplier pigs farm	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	ST155-Cplx	ST1015	ColKP3-IncX3	Survey
2024	ES	OXA-181	1	Fattening pigs farm	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	NA	ST4038	IncX3	Survey
2024	ES	OXA-181	1	Multiplier pigs farm	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	ST469-Cplx	ST4623	ColKP3-IncX3	Survey
2024	ES	OXA-181	1	Multiplier pigs farm	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	ST101-Cplx	ST5229	ColKP3-IncX3	Survey

TABLE B.1 (Continued)

Year	Country	Carbapenemase type	CPE (n)[a]	Matrix (sample type) level 3	Matrix (sample type) combined categories	Type of study (EU monitoring programme)	Strain species[b]	ST- complex or eBG[c]	MLST[b]	Plasmids[b,e]	References/source of information[d]
2024	ES	OXA-181	1	Multiplier pigs farm	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	ST10-Cplx	ST5708	ColKP3-IncX3	Survey
2024	ES	OXA-181	1	Multiplier pigs farm	Pigs and/or their environment	National monitoring (trace back investigation)	*Escherichia coli*	NA	ST134	ColKP3-IncX3	Survey
2024	AT	VIM-1	1	Broilers (caecal samples at slaughter)	Broilers and/or their environment	EU monitoring (ESBL MON)	*Escherichia coli*	ST469-Cplx	ST679	IncI2(Delta), IncN, p0111	Survey

Abbreviations: AT, Austria; BE, Belgium; CH, Switzerland; CZ, Czechia; DE, Germany; eBG, e-burst group; EL, Greece; ES, Spain; HU, Hungary; Inc., Plasmid incompatibility group; IT, Italy; MLST, multilocus sequence typing; NA, not available; NL, The Netherlands; NO, Norway; PT, Portugal; RO, Romania; ST, multilocus sequence type; ST-Cplx, multilocus sequence type complex.

[a]The isolates with 'NA' for number of CPE are reports from microbiome analyses (qPCR and/or metagenomics), without linking genes to the specific species samples.

[b]As reported by the authors/laboratories.

[c]ST-Cplx for *E. coli* and e-BG for *Salmonella* spp. obtained from Enterobase (https://enterobase.warwick.ac.uk/).

[d]Survey: Information directly communicated by the EU/EFTA countries with positive findings, further information is provided in supplementary information included in Annex C. Presentations provided at the EURL-AR Network Workshop meetings can be accessed at: https://www.food.dtu.dk/english/topics/antimicrobial-resistance/eurl-ar/presentations/workshop-2024 and https://www.food.dtu.dk/english/topics/antimicrobial-resistance/eurl-ar/presentations/workshop-2023).

[e]Plasmids formerly designated as IncL/M, are currently designated as IncL (A. Carattoli, personal communication).

APPENDIX C

Flaticon icons used in the figures included in the scientific opinion

Figures in Section 3.2 include several icons taken from Flaticon.com (https://www.flaticon.com/). As requested by Flaticon, the links to the icons used are listed below.

- Pig icon (href = "https://www.flaticon.com/free-icons/pig" title = "pig icons" > Pig icons created by Freepik - Flaticon),
- Pork icon (href = "https://www.flaticon.com/free-icons/pork" title = "pork icons" > Pork icons created by SetitikPixelStudio - Flaticon),
- Cow icon (href = "https://www.flaticon.com/free-icons/cow" title = "cow icons" > Cow icons created by Freepik - Flaticon),
- Meat icon (href = "https://www.flaticon.com/free-icons/meat" title = "meat icons" > Meat icons created by SetitikPixelStudio - Flaticon),
- Chicken icons (href = "https://www.flaticon.com/free-icons/chicken" title = "chicken icons" > Chicken icons created by Freepik - Flaticon),
- Chicken leg icon(href = "https://www.flaticon.com/free-icons/chicken-leg" title="chicken leg icons">Chicken leg icons created by Freepik - Flaticon),
- Turkey icon (href = "https://www.flaticon.com/free-icons/turkey" title = "turkey icons" > Turkey icons created by Freepik - Flaticon),
- Roasted turkey icon (href = "https://www.flaticon.com/free-icons/roasted-turkey" title="roasted turkey icons" > Roasted turkey icons created by Mihimihi - Flaticon),
- Shrimp icon (href = "https://www.flaticon.com/free-icons/shrimp" title = "Shrimp icons" > Shrimp icons created by Freepik - Flaticon),
- Cabbage icon (href = "https://www.flaticon.com/free-icons/cabbage" title = "cabbage icons" > Cabbage icons created by Freepik - Flaticon)
- Grasshopper icon (href = "https://www.flaticon.com/free-icons/grasshopper" title = "grasshopper icons" > Grasshopper icons created by Freepik - Flaticon).

ANNEXES

ANNEX A

Protocol for the assessment of 'Occurrence and spread of carbapenemase-producing Enterobacterales (CPE) in the food chain in the EU/EFTA. Part 1: 2025 update'

Annex A can be found in the online version of this output ('Supporting information' section).

ANNEX B

Surveys shared with the MSs through the EU-survey platform

Annex B (B1–B3) can be found in the online version of this output ('Supporting information' section).

ANNEX C

Supplementary information - Comprehensive overview of CPE in the food chain in the EU/EFTA countries: time of detection, countries of isolation, carbapenemases, sources, bacterial species, sequence types, plasmid types and references

Annex C can be found in the EFSA Knowledge Junction community on https://zenodo.org/uploads/15025629