DTU Fødevareinstituttet
DTU National Food Institute

The 11th EURL-AMR Proficiency Test

Selective isolation of E. coli with presumptive ESBL, AmpC or carbapenemase phenotypes from meat or caecal samples 2025

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1. Introduction

This report describes and summarises the results from the eleventh matrix-based proficiency test (Matrix PT), conducted by The National Food Institute (DTU Food) in its capacity as the EU Reference Laboratory for Antimicrobial Resistance in Food, Feed & Animal Health (EURL-AMR), for the purposes of External Quality Assessment (EQA). The PT focused on the selective isolation of extended-spectrum beta-lactamase (ESBL)-, AmpC- and carbapenemase (CP)-producing *Escherichia coli* from meat and caecal samples of animal origin as well as on antimicrobial susceptibility testing (AST) of the isolated *E. coli*.

In the European Union (EU), the mandatory, harmonized AMR monitoring includes ESBL-, AmpC- and CP-producing indicator *E. coli* in food-producing animals. To support EU Member States (MS) and affiliated countries in their capacity to selectively isolate and characterize ESBL-, AmpC- and CP-producing *E. coli*, the EURL-AMR offers matrix-based PT schemes on an annual basis. These schemes were initiated in 2015 and originally targeted only ESBL- and AmpC-producing *E. coli* but were later expanded to also include CP-producing *E. coli*. The PT schemes consist of screening of either meat or caecal matrix samples of animal origin, according to common protocols defined by the European Commission (EC) and validated by the EURL-AMR.

Similar to previous EURL-AMR Matrix PT rounds, the aim of this specific PT was to: i) monitor the capacity of the National Reference Laboratories (NRL-ARs) for the isolation, identification, and AST of ESBL-, AmpC- and CP-producing *E. coli*; ii) identify laboratories that may require assistance to improve their performance in the isolation and AST of *E. coli* from meat and caecal matrices; and iii) identify potential problems or focus areas for future training and research.

When reading this report, the following should be taken under consideration:

1) The selection of test strains was based on phenotypes determined through Minimum Inhibitory Concentration (MIC) results obtained at the EURL-AMR lab at the Technical University of Denmark, National Food Institute (DTU Food). After strain selection, the MIC testing was repeated to confirm the MIC values and generate the table of expected AST results. The genetic basis for resistance was known, as all the selected test strains had been whole-genome sequenced (WGS). After preparation of the matrix meat and caecal samples, the MIC values were re-confirmed by isolating the test strains from the samples and performing another round of AST.

2) No thresholds were set in advance for the evaluation of the performance of the participating laboratories. Therefore, results were not classified as above or below a certain threshold but were, instead, evaluated case by case.

3) When receiving results 'deviating from the expected interpretation', participants should carefully analyse those in a self-evaluation, including considerations for corrective actions. Note that since the methods used for MIC determination have limitations, it is not considered an error to obtain a one-level two-fold dilution difference in the MIC of a specific antimicrobial when testing the same strain. In some cases, if the expected MIC is close to the breakpoint value for categorising the strain as susceptible or resistant, such a two-fold dilution difference (which is acceptable) may result in two different, yet both valid, phenotypic interpretations. This means that the same strain may correctly be categorized as both susceptible and resistant for a certain antimicrobial, depending on the MIC value obtained. When organizing PTs, the PT organizers try to avoid such so-called *"breakpoint issues"*

by selecting test strains with MIC values well removed from the cut-offs for resistance. However, that is not always feasible for all strain-antimicrobial combinations. Therefore, the EURL-AMR network unanimously agreed in 2008 that if there is a high proportion of incorrect results received for a specific strain-antimicrobial combination (equal to or above 25% of submitted results), then the reasons behind this discordance must be further examined and, on selected occasions, explained in detail case by case, these results may subsequently be omitted from the evaluation report.

For reasons of anonymity, in this report laboratory names have been replaced with laboratory codes. Each laboratory code is only known to the corresponding laboratory, and the entire list of laboratories and their codes is confidential and known only to relevant representatives of the EURL-AMR and the EU Commission. All conclusions are public.

The draft of the report was sent out to the network for commenting in May 2026, and the network was invited to a webinar with presentations of the PT results in June 2026. The draft report was hereafter edited accordingly, and then approved.

2. Materials and Methods

2.1 Participants in PT 2025

A pre-notification (Appendix 1), announcing the Matrix PT 2025, was distributed by e-mail on 6 October 2025 to the designated National Reference Laboratories (NRLs) of all EU Member States, as well as Iceland, Norway, Serbia, Switzerland, Ukraine and the United Kingdom. In total, 36 laboratories participated in the Matrix PT, and results from 34 laboratories from 32 countries are included in the present report. Two countries (Romania and Spain) enrolled two NRLs each, as they have separate laboratories designated for the analyses of meat and caecal samples. Participation was free of charge for EU member-states; however, participants were responsible for covering all costs associated with analyses. Participants from non-EU countries were charged a participation fee.

2.2 Preparation of samples

Eight samples were prepared and dispatched for isolation of ESBL-, AmpC- and CP-producing *E. coli*, as well as identification and antimicrobial susceptibility testing (AST) of the obtained isolates. The samples included either beef meat or cattle caecal content and were either spiked with test strains or left unmodified.

The meat used for the ***meat samples*** was minced beef of Danish origin (raised, slaughtered and packed in Denmark) acquired in local supermarkets on 20 October 2025. The meat came from four different batches (based on production date and slaughterhouse), each bought in sufficient amount to cover both the pre-testing and preparation of the samples. The meat was pretested using the official method for selective isolation of *E. coli* producing ESBL, AmpC or carbapenemases from meat (https://www.food.dtu.dk/english/topics/antimicrobial-resistance/eurl-ar/protocols). The aim of pretesting was to ensure the absence of ESBL-, AmpC- or CP-producing *E. coli* in the batch of meat selected for sample preparation, as well as to ascertain the level of background bacteria present in the meat matrix. A batch fulfilling pretesting requirements was chosen for preparation of aliquots of 25 g of meat, which were then spiked with the test isolates, as described below.

The test isolates selected for the Matrix PT 2025 were prepared in advance of spiking and sub-cultured the day before sample preparation. For sample preparation and standardization of the spiking, suspensions of the relevant isolates equal to McFarland 0.5 were prepared in saline tubes. This corresponded to approximately 10^8 CFU/mL, as confirmed by viable counts of serial dilutions on Luria Bertani (LB) agar plates. The standardized suspensions were further diluted to obtain the desired concentration per test isolate, selected in advance based on the results of previous Matrix PTs. 25 µl of each test isolate at the appropriate dilution was used to spike 25 g of meat sample, thus yielding the final matrix samples for the PT. Sample EURL-M-11.3 was spiked in the same way as the test samples but with a susceptible *E. coli* strain (ATCC 25922), and was, therefore, expected to be negative for ESBL-, AmpC- and CP-producing *E. coli*. The final inoculum in samples EURL-M-11.1, M-11.2, M-11.3 and M-11.4 of this PT was expected to be approx. 10^3 CFU/g meat.

One slaughterhouse provided on 22 October 2025, 15 ***cattle caecal samples*** from different farms. The caecal samples were tested using the official selective isolation protocol for ESBL-, AmpC- and CP-producing *E. coli* from caeca (https://www.food.dtu.dk/english/topics/antimicrobial-resistance/eurl-ar/protocols). One caeca batch that had tested negative for ESBL-, AmpC- and CP-producing *E. coli* was chosen for preparation of the caecal matrix of the samples. 1 g aliquots of caecal content were either used directly as blank sample (sample EURL-M-11.7) or spiked with 10 µl of a dilution containing approx. 10^6 CFU/ml, corresponding to an expected spiking level of 10^4 CFU/g for samples EURL-M-11.5, M-11.6 and M-11.8. The inoculum strains were selected based on having been initially isolated from cattle caecal samples, as this approach has previously been shown to enhance the survival of the inoculum. Otherwise, the caecal matrix samples provide poor support for the *E. coli* inoculum.

The minimal inhibitory concentrations (MIC) for the targeted antimicrobials were determined using the broth microdilution method both when testing the strains used for spiking in the preparatory phase as well as when testing the isolates after sample preparation to generate the expected results (Appendix 2).

To follow up on the stability of the inoculum in the matrix samples after shipping, sets of the eight samples were tested at four time points after shipment (over the course of two weeks) using the official selective *E. coli* isolation protocols. During this period, the meat and caecal samples were kept at 4°C, to mimic the conditions in the shipment parcel.

2.3 Isolation and identification of ESBL-, AmpC- or carbapenemase-producing *E. coli* from meat and caecal samples

The official protocols for the selective isolation and identification of ESBL-, AmpC- and/or CP-producing *E. coli* were available on the EURL website (https://www.food.dtu.dk/english/topics/antimicrobial-resistance/eurl-ar/). For species confirmation of presumptive *E. coli* isolates, various methods were permitted, as these are not specified in the legislation (EU Commission implementing decision on the monitoring and reporting of antimicrobial resistance in zoonotic and commensal bacteria, 2020/1729/EU). Laboratories were requested to describe the methods they used for the selective isolation and identification of presumptive ESBL-, AmpC- or CP-producing *E. coli* using a dedicated methods sheet to be completed in the database upload system.

2.4 Antimicrobial susceptibility testing

The panels of antimicrobials recommended for AST in this PT are derived from the 2020/1729/EU Commission implementing decision on the monitoring and reporting of antimicrobial resistance in zoonotic and commensal bacteria (Table 1).

The guidelines for performing AST using dilution methods were in accordance with ISO 20776-1:2019 and whenever commercial methods were used, the guidelines of the manufacturer were followed. MIC determination was performed using the Sensititre (Trek Diagnostic Systems Ltd, UK) panels EUVSEC3 (Panel 1) and EUVSEC2 (Panel 2).

MIC results were interpreted using the EUCAST epidemiological cut-off values (www.eucast.org), as per the regulation referred to above, or as recommended by EFSA and described in the PT protocol (Appendix 3). The results of the ESBL confirmatory testing were interpreted according to the recommendations by EFSA and as described in the regulation, based on MIC testing of the second panel of antimicrobials, which is intended to be used every time a strain is found resistant to either cefotaxime, ceftazidime and/or meropenem.

2.5 Distribution

The meat samples were frozen at -80°C and kept at this temperature after preparation and until the time for shipment. The caecal samples were sent shortly after preparation and therefore kept at 4°C until the time for shipment. On the day of shipment, the samples were tightly packed in thermos boxes with cooling elements frozen at -80°C. The parcels contained the eight samples in tubes, and an additional tube containing a temperature logger to register the temperature at 15 min intervals during transport. Furthermore, the parcel contained a welcome letter with the laboratory ID number and a labelled envelope for returning the temperature logger to the EURL-AMR.

The protocol and test forms for the PT were made available online on the EURL-AMR website before launching the PT.

The thermos boxes used for the shipment of the samples were enclosed in double-pack containers and sent to the selected laboratories as “Biological Substance category B (UN3373)”, in accordance with the International Air Transport Association (IATA) regulations. The parcels were dispatched from DTU Food on November 3, 2025.

2.6 Procedure

Participants were instructed to download the protocol and test forms (Appendices 3 and 4) from the EURL-AMR website and to process the samples according to the EU protocol for the selective isolation of presumptive ESBL-, AmpC- and CP-producing *E. coli* from meat or caecal samples, following the same procedures as for the EFSA monitoring.

Upon arrival of the parcels, the participants were requested to fill in a small introductory questionnaire available in the database, which included details on sample reception (measured temperature and date/time), the laboratory’s monitoring activities, and the methods used in the laboratory. The registration of the temperature was extracted and read from the returned temperature loggers to provide the temperature ranges along the shipment and at sample reception/opening.

After completion of the tests, laboratories were requested to enter the obtained results into an electronic sheet in the EURL-AMR web-based database through a secure individual login. The PT

webtool for data submission was activated on December 19, 2025, and the deadline for data entry was January 26, 2026. All participating laboratories submitted results on time.

The results from the selective isolation of ESBL-, AmpC- and CP-producing *E. coli* were evaluated separately from the AST results. In terms of the isolation results, samples were defined as positive if an isolate was obtained and positively identified as *E. coli*. In terms of AST, the results of susceptibility testing of the obtained isolates using the two MIC panels (Table 1) were analysed separately in a similar way as for the *E. coli* AST PTs. This included both the read values of MIC and their corresponding resistant/susceptible (R/S) interpretations. Based on the results of the susceptibility testing, participants were asked to classify the isolates obtained according to the defined EFSA criteria for interpretation of ESBL-, AmpC- and/or CP-producing isolates.

After the deadline, the qualitative results indicating if the samples were positive or negative for ESBL-, AmpC-, or CP-producing *E. coli*, as well as the interpretations of the AST results, and the conclusion on the observed *E. coli* phenotypes were evaluated against the expected results and scored as correct or incorrect. Submitted MIC values were not scored. Non-submission of results was not penalized. As no threshold for acceptable performance has been agreed, the performance was evaluated case by case and was not characterized as acceptable or unacceptable based on the deviation percentage.

Table 1. Panel of antimicrobials recommended for susceptibility testing of bacteria included in the 2025 Matrix PT

Escherichia coli **Panel 1**	***Escherichia coli*** **Panel 2**
Ampicillin, AMP	Cefepime, FEP
Amikacin, AMK	Cefotaxime + clavulanic acid (F/C)
Azithromycin, AZI	Cefotaxime, FOT
Cefotaxime, FOT	Cefoxitin, FOX
Ceftazidime, TAZ	Ceftazidime, TAZ
Chloramphenicol, CHL	Ceftazidime+ clavulanic acid (T/C)
Ciprofloxacin, CIP	Ertapenem, ETP
Colistin, COL	Imipenem, IMI
Gentamicin, GEN	Meropenem, MERO
Meropenem, MERO	Temocillin, TRM
Nalidixic acid, NAL	
Sulfamethoxazole, SMX	
Tetracycline, TET	
Tigecycline, TGC	
Trimethoprim, TMP	

3. Results

Sample shipment and delivery took place within the expected timeframe and all temperature measurements recorded by the loggers during parcel shipment and by the participants at the time of parcel opening were considered acceptable for sample integrity. All samples received have thus been considered acceptable for testing in this PT round.

All 34 participating laboratories processed and tested the samples as instructed and submitted results, corresponding to a total of 32 submitted sets or results per sample. For the eight PT samples (four meat and four caecal), laboratories were expected to enter on the webtool a total of 6400 MIC results together with the respective R/S phenotype interpretation. Those correspond to 4800 results for the six test strains, if the susceptible (M-11.3) and blank sample (M-11.7) are excluded. Furthermore, participants were expected to report 1600 MIC results for the two reference/QC strains *E. coli* ATCC 25922 and *Acinetobacter baumannii* 2012-70-100-69.

Besides the MIC results, participants were asked to submit resistance phenotype classifications (susceptible, ESBL, AmpC, ESBL+AmpC, carbapenemase, or Other phenotype) for each of the eight PT samples, corresponding to 256 interpretation results evaluated in this report. It should be noted that the two laboratories that test only meat and the two laboratories that test only caeca were evaluated only on the results they submitted for the four meat samples or the four caecal samples, respectively.

3.1 Overall results of the qualitative, selective isolation

All laboratories successfully isolated the test strains from samples M-11.1, M-11.2, M-11.4, and M-11.6, whereas all but one laboratory (#016) successfully isolated the test strain from sample M-11.5. In contrast, only two laboratories (i.e. 6%) were successful in isolating the test strain from M-11.8, with the rest of the laboratories not having retrieved any isolate from this sample. The challenge in the isolation and/or viability of this test strain was also observed during stability testing at the EURL-AMR laboratory, where the test strain was only recovered from the sample M-11.8 when testing was performed during the first week after shipment, but not during repeat testing afterwards. Due to the apparent challenge in the isolation and/or viability of this test strain, there was no penalty in the score for not obtaining an isolate from sample M-11.8.

Two laboratories (#056 and #026) reported positive findings of an ESBL+AmpC-producing and a carbapenemase-producing *E. coli* isolate, respectively, from sample M-11.3, which had been inoculated with a susceptible strain only. Except for these two instances, no other laboratory reported any results for the two negative control samples M-11.3 and M-11.7 (blank control).

3.2 Methods used by participants

Information on the methods used for the selective isolation and identification was collected from the participants through the webtool. All 34 participating laboratories reported that the selective isolation procedure was performed as described in the EURL-recommended protocols.

Eighteen laboratories provided information on the type of plates used for the selective isolation of carbapenemase producers. The reported brand/plates used were CHROMID CARBA SMART Agar

(n=7), CHROMID CARBA Agar (n=7), CHROMID OXA-48 (n=8), CHROMagar mSuperCARBA (n=7) and MacConkey supplemented with meropenem (n=2).

Given that only two laboratories were successful in isolating the test strain from sample M-11.8, consideration was given to whether the type of plates employed by these laboratories may have contributed to their success in the isolation of the test strain. The two laboratories reported having used CHROMagar mSuperCARBA and CHROMID CARBA/OXA-48 agar, respectively. These types of plates were used by several other laboratories as well, so their usage is unlikely to explain the success in the isolation.

Species identification (ID) of the isolates was performed using MALDI ToF (n=17 when considering MALDI-ToF as the sole method of identification and n=20 when considering all laboratories using this method, both exclusively and in-tandem with other identification methods), biochemical tests (n=8, out of which two used MALDI-ToF as well), chromogenic media (n=5, out of which one used MALDI-ToF as well) or PCR using published methods (n=4, out of which one reported using the AUTOMIC-i-600 system).

All laboratories performed the broth microdilution testing using panel 1, with the antimicrobials and ranges defined for *E. coli* isolates under the EU Commission regulation 1729/2020. All laboratories reported that they applied the broth microdilution method using panel 2 to test presumptive ESBL-, AmpC- and/or carbapenemase-producing isolates, when relevant. One laboratory reported not using MacConkey medium for subcultivation of presumptive ESBL-, and CP-producing isolates, in order to not lose any potential resistance determinants. A second laboratory reported using an enrichment broth for the negative samples, which was screened for ESBL and carbapenemase genes.

All results were interpreted according to the EFSA criteria for ESBL, AmpC and carbapenemase phenotype classification.

3.3 Antimicrobial susceptibility testing

Out of the expected 4800 AST results, laboratories submitted on the webtool a total of 4025 MIC results with corresponding phenotype interpretations (susceptible vs resistant). Almost all the non-submitted results (96%) were related to failure in the isolation of the test strain from sample M-11.8 which affected 30 out of the 32 laboratories reporting AST results for that sample.

A first overview of the submitted results revealed a high level of concordance for most strain-antimicrobial combinations. For the combinations of M-11.4 cefepime and M-11.6 cefoxitin, over 25% of the laboratories submitted an unexpected phenotype interpretation, associated mostly with a one-fold dilution difference around the breakpoint (i.e. breakpoint issue). Thus, these strain-antimicrobial combinations were not scored (Table 2).

Table 2. List of strain-antimicrobial combinations for which the results were blanked (excluded from evaluation) in the Matrix PT 2025 due to high discordance (submitted results were correct for ≤ 75% of participating laboratories).

Strain	Antibiotic	% correct results
M-11.4	Cefepime	67 %
M-11.6	Cefoxitin	45 %

Figure 1 shows the proportion of deviations among the evaluated results (i.e. submitted results after excluding the blanked strain-antimicrobial combinations of Table 2) per laboratory. As can be seen in Figure 1, there is variation in the proportion of deviations between the laboratories, with most laboratories (26 out of 34 laboratories, i.e. 76%) having a deviation proportion below 2,5%, and the rest ranging between 3,3 - 15,3%.

There was a high number of deviations (15 deviations) recorded for laboratory #016; however, 14 of these deviations were associated with AST of M-11.6. It is likely that the isolate the laboratory identified as M-11.6 was not the expected one, but another strain with a different antimicrobial resistance profile. This would explain the high discordance in the MIC values obtained for this sample as well as its unexpected identification as carbapenemase-producing. Barring the deviations related to this sample, the laboratory only had one additional deviation in the submitted AST phenotypic interpretations.

Similarly, for laboratory #026 all deviations were associated with the AST of sample M-11.2. These deviations may also be due to having tested an isolate different from the expected one for this sample.

In the case of laboratory #040, there appeared to be no systematic error associated with the nine deviations recorded. The laboratory should perform a self-assessment to identify possible reasons behind these deviations.

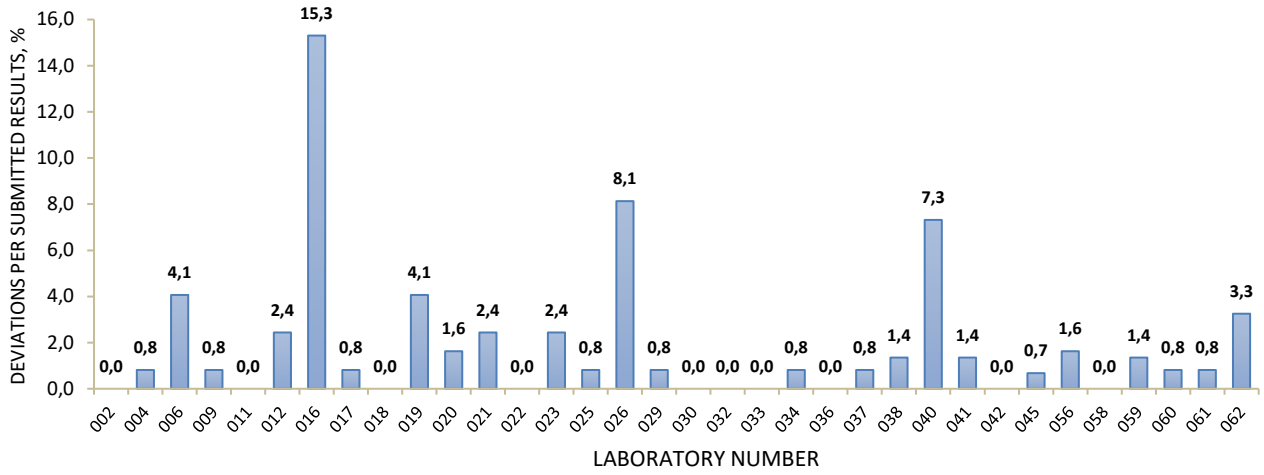

Figure 1. Proportion of deviations among evaluated (i.e. submitted and not blanked) AST R/S interpretation results per participating laboratory, Matrix PT, 2025.

The full list of deviations can be found in Appendix 6.

As the results of AST depend on the isolation and identification procedures, no threshold was set for acceptance of the performance of laboratories participating in this PT. The capacity of the laboratories to perform AST of *E. coli* is evaluated in more detail in the annual *E. coli* AST PT schemes organized by the EURL-AMR (https://www.food.dtu.dk/english/Topics/Antimicrobial-resistance/EURL-AR/EQAS).

Figure 2 shows the percentage of scored deviations per tested antimicrobial. Overall, the number of deviations was low for most antimicrobials. However, in this year's iteration of the matrix PT a higher number of deviations was observed compared to the previous year. The highest percentage of deviations was recorded for imipenem (5,6%) and temocillin (5,6%), followed by ertapenem (5,0%). These results should, however, be interpreted with caution, as some of these deviations may be due to the isolation of unexpected isolates rather than AST discrepancies (e.g. laboratory #016 having isolated an unexpected strain from sample M-11.6)

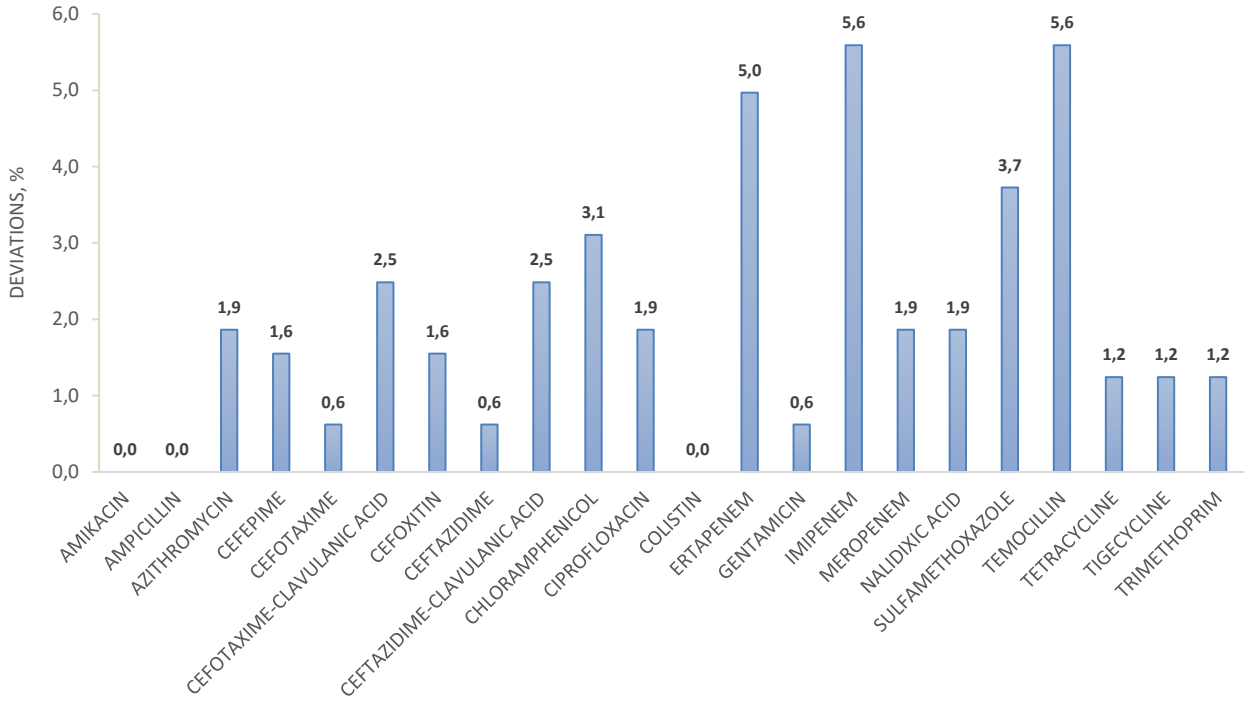

Figure 2. Proportion of deviations among evaluated AST interpretation results per antimicrobial, Matrix PT, 2025

Figure 3 shows the deviation percentage per strain-antimicrobial combination, for those combinations where the deviation percentage exceeded 5%. The two combinations with deviation percentage over 25% (Table 2) were blanked, and are, therefore, not shown in the Figure. Besides these two combinations, in this PT round there was particularly high discordance in the case of ertapenem for strain M-11.4 as well as for temocillin for strain M-11.1, for which 22% of the R/S interpretation results were incorrect (Fig. 3). Most of these deviations were related to breakpoint issues.

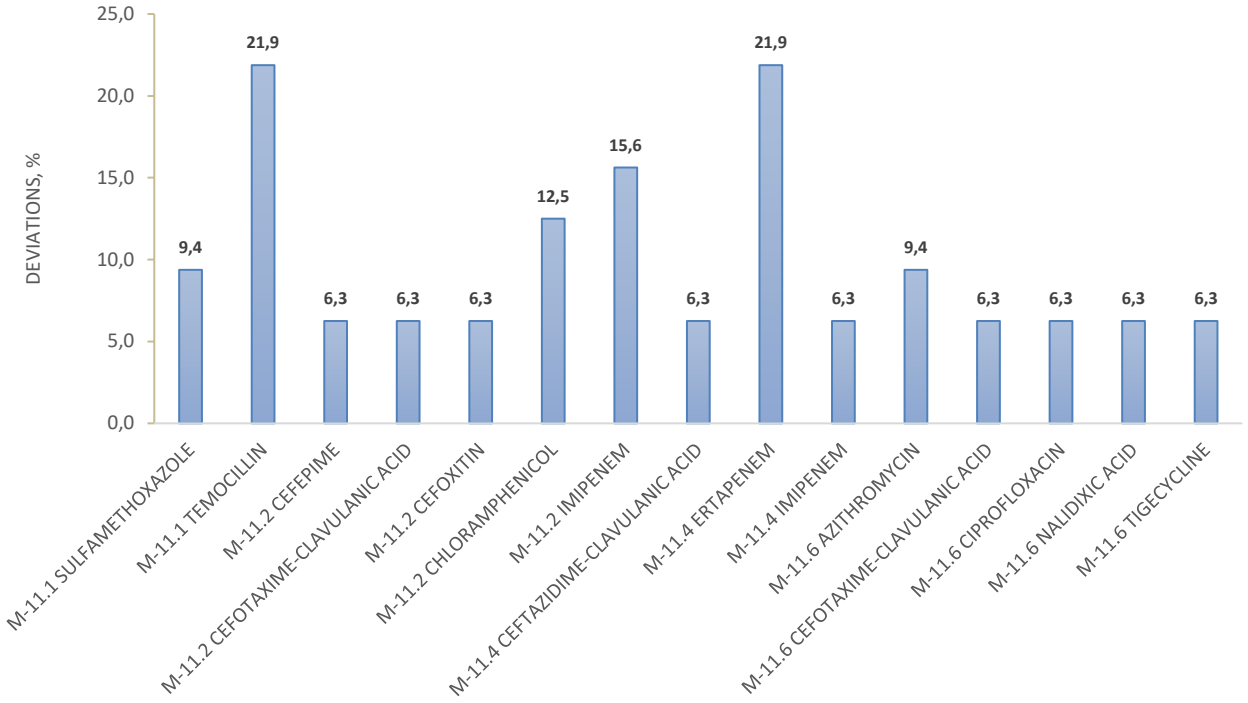

Figure 3. Proportion of deviations among submitted AST interpretation results per strain-antimicrobial combination, Matrix PT, 2025. Only deviations with a proportion between 5-25 % are shown.

The level of deviations per sample was higher than in the previous year, although it did not exceed 5% for any of the samples (Fig. 4). Most deviations were recorded, in decreasing order, for samples M-11.2 and M-11.6.

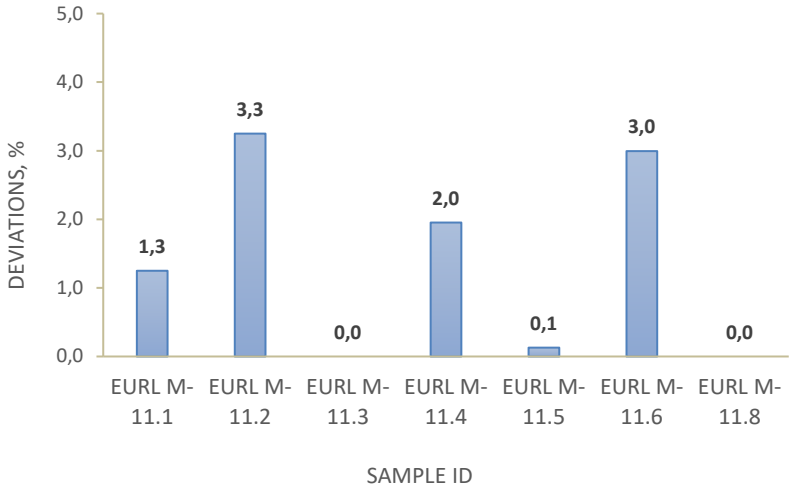

Figure 4. Proportion of deviations among submitted AST interpretation results per sample, Matrix PT, 2025

3.4 Classification of *E. coli* test strains into ESBL, AmpC, ESBL+AmpC, carbapenemase and Other phenotypes

In total, laboratories were expected to submit 256 phenotype interpretation results, including 64 interpretation results for the negative control samples M-11.3 and 11.7. As expected, laboratories did not submit any interpretation results for the negative control samples, except for two laboratories which, as previously mentioned, reported positive findings for sample M-11.3, which had been inoculated with a susceptible strain only.

Excluding the negative control samples, the total amount of phenotype interpretation qualitative test results received for the test strains was 163. Most of the non-submissions were associated with failure in the isolation of the strain from sample M-11.8, which was not penalized. Of the 165 evaluated phenotype submissions, 161 (98 %) were in concordance with the expected phenotype (Table 3).

Six deviations were observed in total, including:

- two deviations for the negative control sample M-11.3 (reported by one laboratory as ESBL+AmpC and by another as carbapenemase-producing);
- one deviation for sample M-11.2, reported by one laboratory as of Other phenotype instead of carbapenemase-producing. The discrepancy resulted from unexpected AST results leading to susceptible phenotype interpretations for imipenem (breakpoint-related deviation) and meropenem (non-breakpoint-related deviation);
- two deviations for M-11.4, which was expected to be reported as of AmpC phenotype. The first deviation was related to discordance in the AST results for all carbapenems, which led to the classification of the strain as carbapenemase-producing. The discrepancies in the AST results were not related to breakpoint issues, and it is unclear whether they were related to technical issues or due to the testing of a strain different than the expected one for this sample. In the case of the second deviation, one laboratory reported M-11.4 as of Other phenotype, due to a non-breakpoint-related deviation in the AST of ertapenem.
- one deviation for M-11.6, which was reported as of CP phenotype instead of ESBL or ESBL+AmpC phenotype, as expected. This deviation, recorded for laboratory #016, was likely due to the testing of an unexpected isolate from sample M-11.6, which differed in its AMR profile from the test strain that was expected to be isolated from this sample, as discussed previously.

Table 3. Overview of expected phenotypes, Matrix PT 2025.

Strain ID	Expected phenotype	Genotype	Additional phenotype approved	No of Deviations (%)
M-11.1	Carbapenemase	NDM-5	None	0 (0%)
M-11.2	Carbapenemase	OXA-48	None	1 (3%)
M-11.3	Susceptible			2 (6%)
M-11.4	AmpC	AmpC C-42T	None	2 (6%)
M-11.5	Carbapenemase	NDM-5, CTX-M-15	None	0 (0%)
M-11.6	ESBL	CTX-M-55	ESBL+AmpC	1 (3%)
M-11.7	Blank			0 (0%)
M-11.8	Carbapenemase	OXA-181	None	0 (0%)

4. Discussion

4.1 ESBL-, AmpC- and carbapenemase-producing *E. coli* isolation and identification

In the 2025 round of the Matrix PT, the isolation of test strains was in general successful for both the meat and caecal samples, with the exception of the carbapenemase-producing strain spiked in sample M-11.8, which was only retrieved by two out of 32 laboratories. The strain was originally isolated from a calf caecal sample, which would typically make it well-adapted to survive in the same type of matrix. However, it is not uncommon for test strain inocula to become markedly reduced after spiking into caecal matrix. Furthermore, this strain carries $bla_{\text{OXA-181}}$ and its successful isolation may be influenced by the type of agar and conditions used for selection and isolation. In general, previous Matrix PTs have consistently identified challenges when isolating CP-producing strains from animal matrices, especially in the case of strains of low-level carbapenem resistance, even when using selective agars that should target both ESBL- and CP- producing *E. coli*.

Exempting the difficulties in the isolation of M-11.8, there was only one additional instance of failed isolation, from sample M-11.5.

4.2 Antimicrobial susceptibility testing

In the 2025 iteration of the Matrix PT there was a higher number of deviations observed compared to the past two years. However, most of the deviations were associated with breakpoint issues that fall within the acceptable method variation, as well as with deviations resulting from the isolation and testing of strain(s) different than the expected ones (isolate from M-11.6 for laboratory #016 and possibly isolate from M-11.2 for laboratory #026).

There was high variation in the results reported for M-11.4 cefepime and M-11.6 cefoxitin, and as a result these two strain-antimicrobial combinations were blanked in the scoring. In addition, there were only few results reported and scored for M-11.8, as the respective strain was successfully isolated by only two laboratories.

Three laboratories reported for M-11.1 an MIC for sulfamethoxazole that was much higher than expected (MIC of 128 and > 512 instead of ≤ 8), and a corresponding resistant phenotype for that antimicrobial. The reason behind this is unclear but can be caused by misreading of the sulfamethoxazole MIC by disregarding the specific guidelines for this compound, i.e. that MIC should be read at the lowest concentration that inhibits ≥80 % of growth as compared to the growth control (see EUCAST reading guide for broth microdilution).

Excluding M-11.6, for which most of the deviations were likely due to the testing of an unexpected isolate from laboratory #016, most non-breakpoint-related deviations were observed for M-11.2 and M-11.4. For M-11.4, these deviations were mostly associated with AST of carbapenems and observed across different laboratories, whereas for M-11.2 the deviations were linked to different antimicrobials. Although several laboratories reported deviations for M-11.2, most non-breakpoint-related deviations for this sample were reported from one laboratory (#026), likely due to the testing of an unexpected strain for this sample. There was only one deviation recorded for M-11.5. A small number of the deviations recorded in this PT may have been caused by natural variation in the phenotype of some of the strains.

In five cases, compared to two cases in 2024 and eight cases in 2023, participants reported correct MIC values but with incorrect R/S interpretations. It is unclear whether this was due to technical errors or because the participants used different guidelines for the interpretation.

4.3 Conclusions on the identification of ESBL, AmpC and carbapenemase phenotypes

In this year's PT, a total of six deviations in ESBL/AmpC/CP phenotype classifications were observed, including two deviations for the negative control sample M-11.3 (reported by one laboratory as ESBL+AmpC and by another as carbapenemase-producing), and four deviations for the test strains. Specifically, sample M-11.2 was reported by one laboratory as of Other phenotype instead of carbapenemase-producing, sample M-11.4 was classified by two laboratories as carbapenemase-producing and of Other phenotype instead of the expected AmpC-phenotype, and M-11.6 was reported by one laboratory as of carbapenemase instead of ESBL phenotype; however, the latter is likely attributed to the laboratory having isolated a strain different from the expected one.

The reasons behind the rest of the deviations are unclear, but phenotype classification discrepancies in the Matrix PTs are not uncommon, given that the samples of Matrix PTs include naturally contaminated matrices, and thus there is always a risk of exchange of gene(s) from the background bacteria in the matrix.

In general, with matrix PTs it is expected to see occasional deviations in the resistance phenotypes, and possibly even in the ESBL categorisations, due to interactions with bacteria and/or mobile genetic elements from the microbiota of the matrix samples, and these cannot be accounted for as they are not necessarily detected in the tests performed by the EURL-AMR. In general, it is practically impossible to avoid having generic Enterobacterales or *E. coli*, and sometimes even other ESBL bacteria, in some parts of the meat and caecal matrix. The screening performed when preparing the samples to assess the level of background bacteria in the matrix material only serves to reveal possible contamination with ESBL-, AmpC-, or CP-producing *E. coli* in the different batches of meat/caeca and to produce a rough estimation of the level of background bacteria and cannot capture the full spectrum of the microbiota present in the matrix.

4.4 Performance in AST of the quality control (QC) strains

For quality control purposes, PT participants were asked to perform AST on the *E. coli* ATCC 25922 reference strain and the *A. baumannii* 2012-70-100-69 QC strain. Submitted AST results for the two QC strains were evaluated based on the published EUCAST QC range and a DTU-defined QC range, respectively (Appendix 5).

All participating laboratories performed MIC determination on the *E. coli* QC strain and reported results. In contrast, ten laboratories (29%) did not submit results on the *A. baumannii* QC strain. Of the submitted results, 96,4% were within the acceptable range (Appendix 5). For the *E. coli* reference strain, there were a total of ten deviations for seven antimicrobials across eight laboratories. No systematic errors were observed. For the *A. baumannii* QC strain, there were a total of 12 deviations for ten antimicrobials across five laboratories, including six deviations for laboratory #017 and three deviations for laboratory #016.

All laboratories with deviations in the AST of the QC strains, and particularly those with multiple deviations, should carefully evaluate these as part of their self-assessment of PT participation.

5. Conclusions

The 2025 Matrix PT demonstrated that participating laboratories have well-established methods for the isolation of ESBL-, AmpC- and carbapenemase-producing *E. coli* strains from meat or caecal samples. Laboratories may, however, face challenges in isolating strains with low-level carbapenem resistance. In this PT round, laboratories had difficulty isolating the carbapenemase-producing strain from sample M-11.8, which was likely due, in part, to the low viability of the spiked test strain in the caecal matrix. Similar challenges related to low viability of test strains in caecal matrices have been observed in previous Matrix PT rounds as well. In at least one case, laboratories appeared to have isolated more than one or an incorrect strain from the samples, leading to discrepancies in their submitted AST and ESBL/AmpC/CP phenotype classifications. This resulted in a relatively high number of deviations compared to previous Matrix PT rounds; however, performance was still high when excluding deviations associated with breakpoint issues and differential isolation of test strains.

In conclusion, the overall performance in this Matrix PT was high, demonstrating a strong capacity for the isolation and AST of *E. coli* strains from meat and caecal samples. While capacity for AST is more comprehensively assessed through the annual AST PTs, participation in Matrix PTs allows laboratories to additionally evaluate their isolation procedures under conditions that simulate real-life challenges associated with isolating ESBL-, AmpC- and carbapenemase-producing *E. coli* from complex matrices containing background microbiota. Therefore, in self-evaluations of performance in Matrix PTs, laboratories should include an assessment of their success in isolating test strains, particularly in the case of challenging strains, such as those with low-level carbapenemase production.

6. References

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 (relevant as of 01.01.2021).

EUCAST reading guide for broth microdilution, January 2024
https://www.eucast.org/fileadmin/eucast/pdf/MIC/Reading_guide_BMD_v_5.0_2024.pdf

7. Appendices

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Appendix 3. Protocol for Matrix PT 2025
Appendix 4. Examples of Test forms for Matrix PT 2025
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Appendices

for the report of

The 11th EURL-AMR Proficiency Test on selective isolation of *E. coli* with presumptive ESBL, AmpC or carbapenemase phenotypes from meat or caecal samples (2025)

EU Reference Laboratory for Antimicrobial Resistance

Authors: Dafni Paspaliari, Jette Kjeldgaard, Susanne Karlsmose Pedersen, Rene S. Hendriksen

PT Coordinator: Jette Kjeldgaard

Appendix 1: Pre-notification

EU Reference Laboratory for Antimicrobial Resistance (EURL-AMR) Proficiency Test (PT) for selective isolation of E. coli with presumptive ESBL, AmpC phenotypes or carbapenemases from meat or caecal samples

The EURL-AMR announces the launch of the 2025 PT on matrix samples, providing the opportunity for proficiency testing, which is considered an essential tool for the generation of reliable laboratory results of consistently good quality.

Content:
This PT consists of testing of eight matrix samples for selective isolation of ESBL, AmpC or carbapenemase-presumptive *E. coli*. These include:

- Four meat samples from cattle
- Four caecal samples from cattle

Additionally, quality control (QC) strains *E. coli* ATCC 25922 and *A. baumannii* 2012-70-100-69 will be included.

Participants:

This PT is targeted NRL's on antimicrobial resistance involved in the monitoring according to the EU Commission decision 2020/1729 and specifically processing meat and/or caecal samples in the specific monitoring for ESBL and carbapenemase producers. You may contact the PT-Coordinator if you wish to inform of changes in relation to your level of participation compared to previous years.

Non-EU-Member State NRLs in the EURL-AMR network are offered participation, however, a charge of 300 EUR is applied for these.

If your laboratory will not participate or will test only one of the matrix types, please inform the PT coordinator directly (see email address below).

TO AVOID DELAY IN SHIPPING THE ISOLATES TO YOUR LABORATORY
The content of the parcel is categorized as "UN3373, Biological Substance Category B". Eight samples which might contain ESBL, AmpC or carbapenemase-producing *E. coli* included in a matrix of beef meat (n=4) and/or cattle caecal content (n=4) will be shipped. Please provide the PT coordinator with documents or other information that can simplify customs procedures. We kindly ask you to send this information already at this stage.

TIMELINE FOR RESULTS TO BE RETURNED TO THE NATIONAL FOOD INSTITUTE
Shipment of isolates and protocol: The isolates are expected to be shipped the **first week of November 2025.** The protocol for this proficiency test will be available for download from the website (https://www.food.dtu.dk/english/topics/antimicrobial-resistance/eurl-ar/eqas).

Submission of results: Results must be submitted to the National Food Institute **no later than 16 December 2025 at 16:00** via the password-protected webtool. Upon reaching the deadline, and the PT coordinator has confirmed the opening of the results, each participating laboratory is kindly asked to enter the password-protected website once again to download an automatically generated evaluation report.

PT report: A report summarising and comparing results from all participants will be issued. In the report, laboratories will be presented coded, which ensures full anonymity. The EURL-AMR and the EU Commission, only, will have access to un-coded results. The report will be publicly available.

Please contact me if you have comments or questions regarding the PT.

Sincerely,

Jette Kjeldgaard, EURL-AMR PT-Coordinator
jetk@food.dtu.dk

Next PTs provided by the EURL-AMR:

The DTU Genomic PT 2025 is planned for mid-November 2025 and aims to facilitate harmonization and standardization in whole genome sequencing and data analysis of *Klebsiella pneumoniae*, *Campylobacter coli*, *C. jejuni*, and *Staphylococcus aureus* isolates. The goal is to produce comparable data for monitoring and research purposes.

Appendix 2: Test strains and reference values

Panel 1 = EUVSEC3

Strain	Genotype *bla*-	AMP	AZI	AMI	GEN	TGC	TAZ	FOT	COL	NAL	TET	TMP	SMX	CHL	MERO	CIP	ESBL Classificaition
EURL-M-11.1	NDM-5	>32	8	≤4	≤0.5	≤0.25	>8	>4	≤1	≤4	≤2	0.5	≤8	≤8	4	≤0.015	Carbapenemase
EURL-M-11.2	OXA-48	>32	4	≤4	≤0.5	≤0.25	≤0.25	1	≤1	16	>32	>16	>512	32	0.5	0.5	Carbapenemase
EURL-M-11.3																	Susc.
EURL-M-11.4	AmpC C-42T	>32	8	≤4	≤0.5	≤0.25	4	1	≤1	≤4	≤2	≤0.25	≤8	≤8	≤0.03	≤0.015	AmpC promoter
EURL-M-11.5	NDM-5, CTX-M-15	>32	16	≤4	≤0.5	≤0.25	>8	>4	≤1	>64	>32	>16	>512	≤8	8	>8	Carbapenemase
EURL-M-11.6	CTX-M-55	>32	32	≤4	>16	0.5	8	>4	≤1	16	>32	>16	>512	>64	≤0.03	1	ESBL
EURL-M-11.7																	
EURL-M-11.8	OXA-181	>32	8	≤4	>16	≤0.25	0.5	0.5	≤1	>64	>32	>16	>512	>64	1	>8	Carbapenemase

Strain	Genotype *bla*-	AMP	AZI	AMI	GEN	TGC	TAZ	FOT	COL	NAL	TET	TMP	SMX	CHL	MERO	CIP	ESBL Classificaition
EURL-M-11.1	NDM-5	R	S	S	S	S	R	R	S	S	S	S	S	S	R	S	Carbapenemase
EURL-M-11.2	OXA-48	R	S	S	S	S	S	R	S	R	R	R	R	R	R	R	Carbapenemase
EURL-M-11.3																	Susc.
EURL-M-11.4	AmpC C-42T	R	S	S	S	S	R	R	S	S	S	S	S	S	S	S	AmpC promoter
EURL-M-11.5	NDM-5, CTX-M-15	R	S	S	S	S	R	R	S	R	R	R	R	S	R	R	Carbapenemase
EURL-M-11.6	CTX-M-55	R	R	S	R	S	R	R	S	R	R	R	R	R	S	R	ESBL
EURL-M-11.7																	
EURL-M-11.8	OXA-181	R	S	S	R	R	S	R	S	R	R	R	R	R	R	R	Carbapenemase

Panel 2 = EUVSEC2

Strain	Genotype *bla*-	FOX	FOT	TRM	ETP	IMI	MERO	TAZ	FEP	F/C	T/C	ESBL Classificaition
EURL-M-11.1	NDM-5	>64	>64	32	>2	2	4	>128	16	>64/4	>128/4	Carbapenemase
EURL-M-11.2	OXA-48	4	1	>128	1	1	0.5	≤0.25	0.25	0.5/4	0.25/4	Carbapenemase
EURL-M-11.3												Susc.
EURL-M-11.4	AmpC C-42T	16	1	8	0,03	≤0.125	≤0.03	4	0.125	1/4	2/4	AmpC promoter
EURL-M-11.5	NDM-5, CTX-M-15	>64	>64	128	>2	4	8	>128	>32	>64/4	>128/4	Carbapenemase
EURL-M-11.6	CTX-M-55	8	>64	8	≤0.015	≤0.125	≤0.03	8	8	0.12/4	0.25/4	ESBL
EURL-M-11.7												
EURL-M-11.8	OXA-181	16	0.5	>128	2	0,5	0.5	≤0.25	0.25	0.5/4	0.25/4	Carbapenemase

Strain	Genotype *bla*-	FOX	FOT	TRM	ETP	IMI	MERO	TAZ	FEP	F/C	T/C	ESBL Classificaition
EURL-M-11.1	NDM-5	R	R	R	R	R	R	R	R	R	R	Carbapenemase
EURL-M-11.2	OXA-48	S	R	R	R	R	R	S	R	R	S	Carbapenemase
EURL-M-11.3												Susc.
EURL-M-11.4	AmpC C-42T	R	R	S	S	S	S	R	S	R	R	AmpC promoter
EURL-M-11.5	NDM-5, CTX-M-15	R	R	R	R	R	R	R	R	R	R	Carbapenemase
EURL-M-11.6	CTX-M-55	S	R	S	S	S	S	R	R	S	S	ESBL
EURL-M-11.7												
EURL-M-11.8	OXA-181	R	R	R	R	S	R	S	R	R	S	Carbapenemase

Appendix 3: Protocol for Matrix PT 2025

PROTOCOL

for selective isolation of presumptive ESBL-, AmpC- and carbapenemase-producing *Escherichia coli* from meat and caecal samples (Matrix PT)

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1 INTRODUCTION

The organisation and implementation of a Proficiency Testing for the selective isolation of presumptive extended spectrum beta-lactamase (ESBL)-, AmpC- or carbapenemase-producing *E. coli* is among the tasks of the EU Reference Laboratory for Antimicrobial Resistance (EURL-AMR). The PT assesses the selective isolation procedures and antimicrobial susceptibility testing (AST) of isolates obtained from eight samples of either meat or caecal content. In 2025, these eight samples will comprise four 25-g samples of beef meat and four 1-g samples of cattle caecal content, which may or may not contain *E. coli* producing either ESBL-, AmpC- or carbapenemase-enzymes.

Participating laboratories are expected to apply the same analytical procedures as for the EU monitoring activities, described in the regulation 2020/1729/EU, and to perform the selective isolation following the EU-recommended methods, published on the EURL-AMR website: https://www.food.dtu.dk/english/topics/antimicrobial-resistance/eurl-ar/protocols.

2 OBJECTIVES

This PT aims to assess and, if necessary, improve the quality of results obtained from the selective isolation of presumptive ESBL-, AmpC- or carbapenemase-producing *E. coli* from meat and caecal samples. Further objectives are to evaluate and improve the comparability of surveillance data on ESBL-, AmpC- or carbapenemase -producing *E. coli* reported to EFSA by different laboratories.

3 OUTLINE OF THE MATRIX PT 2025

3.1 Shipping, receipt and storage of samples

In November 2025, the National Reference Laboratories for Antimicrobial Resistance (NRL-AMR) will receive a parcel from the National Food Institute containing eight samples that may or may not be spiked with *E. coli* test and control strains. All strains used for spiking fall under UN3373, Biological substance, category B. Participants should expect that some of the strains will be producing ESBL, AmpC and/or carbapenemases.

The samples will be spiked matrices of either beef meat or cattle caecal content and will be distributed already weighed and ready to be tested, in tubes labelled from 11.1 to 11.8. Of those, 11.1 to 11.4 will be samples of meat (each 25 g) and 11.5 to 11.8 will be samples of caecal content (each 1 g).

It is expected that the matrix samples will be shipped on 03 November in frozen/chilled state in separate tubes contained in a cooling box together with a temperature logging device and freezing elements.

Upon arrival, it is very important to open the parcel as soon as possible and proceed with the analysis (following the normal procedures for sample testing in the monitoring).

It is required that participants:

- **When opening the parcel, note the date and exact time of opening**
- **Proceed with sample analysis immediately after opening the parcel**
- **Register the start date of analysis for each sample.**
- **Collect the temperature logging device from the parcel (small disc-shaped device located inside a bag inserted in a labelled tube);** open the tube and take out the bag containing the device. Place this bag with the device into the labelled bubble envelope provided and return it as normal letter to the EURL-AMR as soon as possible. Please note that you will have to arrange for stamps/postage (postal systems differ from country to country, so EURL-AMR cannot prepay or arrange shipping for this in advance).

3.2 QC reference strains

Include the *E. coli* ATCC 25922 and *Acinetobacter baumannii* 2012-70-100-69 reference strains in the MIC testing and report the results from these strains together with the results obtained from the PT isolates. Note that for the testing of the *E. coli* ATCC 25922 reference strain, the two compounds sulfamethoxazole and sulfisoxazole are regarded as comparable, i.e. the obtained MIC-value from the testing of sulfamethoxazole will be evaluated against the acceptance range listed in CLSI M100 for sulfisoxazole.

3.3 Selective isolation of ESBL-, AmpC- or carbapenemase (CP)-producing *E. coli* from the samples

The samples provided in each parcel are weighed beforehand and therefore no further weighing is required. Proceed immediately to the first enrichment step by adding the sample to the appropriate volume of media (225 ml of Buffered Peptone water for the meat samples and 9 ml for the caecal samples) as described in the EURL-AMR protocols. **Results should be generated according to the laboratory's routine procedures for antimicrobial susceptibility testing by MIC determination.** All subsequent procedures should be in accordance with the methods used for the monitoring for ESBL-, AmpC and CP-producing *E. coli* as outlined in the 2020/1729/EU Decision. If any modifications are made to the official protocols, these must be described in detail in the online database that can be found under the methods page of the webtool that will be used for result submission. The participants are responsible for ensuring the validity of the selective plates; therefore, the protocols entitled "Validation of selective MacConkey agar plates supplemented with 1 mg/L cefotaxime for monitoring of ESBL and AmpC-producing *E. coli* in meat and animals" and "Validation of selective and indicative agar plates for monitoring of carbapenemase-producing *E. coli*" should be run ahead of the analysis, as stated in the protocols found on the EURL-AMR webpage (see https://www.food.dtu.dk/english/topics/antimicrobial-resistance/eurl-ar/protocols).

The officially recommended protocols can be found on the EURL-AMR webpage (https://www.food.dtu.dk/english/topics/antimicrobial-resistance/eurl-ar/protocols):

- Follow the protocol for meat when testing samples 11.1 to 11.4.
- Follow the protocol for caecal content when testing samples 11.5 to 11.8.

As described in these protocols, any isolates obtained from the selective isolation procedure should be confirmed as being *E. coli* using the species identification methods routinely applied by your laboratory for the specific monitoring of ESBL-, AmpC-, and CP-producing *E. coli*.

Please store the isolates obtained during the isolation procedure and document the entire process, including all findings at each step.

As part of the online results submission, you will be requested to describe the enrichment and selective isolation processes you followed along with all findings, including the level of observed growth in the media, the isolation of suspected colonies, the results from the species identification and any findings of presumptive ESBL-, AmpC-, or CP-producing *E. coli* isolates (the latter will be evaluated as qualitative results by comparison with the expected results). These data can all be collected in the supporting document Test Forms.

3.4 Antimicrobial susceptibility testing (AST)

If the sample is deemed positive for ESBL-, AmpC- or CP -producing *E. coli*, one *E. coli* isolate per sample should be tested further for susceptibility to antimicrobials, as stated in the EU regulation (the targeted antimicrobials are listed in the Appendix 1 of this document). These results will be evaluated in the database against the expected results.

Reported AST results (from one isolate per sample) should be from:

- Any presumptive carbapenemase-positive *E. coli* isolates detected (isolated from carbapenemase or OXA-48 selective plates or found resistant to meropenem in the MIC test).
- Any presumptive ESBL- or AmpC-producing *E. coli* isolate detected, if no carbapenemase-positive isolate was found.

The AST should be performed exactly as performed by your laboratory as for the EFSA monitoring according to Decision 2020/1729/EU. Specifically, the two-step approach should be followed, i.e. including both testing panels, using the interpretative thresholds listed in Appendix 1.

Strains are categorised as “S” to a specific antimicrobial compound when the obtained MIC value for this compound is equal to, or less than, the respective ECOFF value, while strains are categorised as “R” when the obtained MIC value is greater than the ECOFF value.

Beta-lactam resistance

Confirmatory testing for ESBL and carbapenemase production is mandatory for all strains resistant to cefotaxime (FOT), ceftazidime (TAZ) and/or meropenem (MERO) and should be performed by AST on the second panel of antimicrobials (beta-lactams; EUVSEC2).

Confirmatory testing for ESBL production requires use of both cefotaxime (FOT) and ceftazidime (TAZ) alone as well as in combination with a β-lactamase inhibitor (clavulanic acid). Synergy is defined as a ≥ 3 two-fold-concentration decrease in the MIC for either antimicrobial agent (FOT or

TAZ) tested in combination with clavulanic acid vs. the MIC of the agent when tested alone (MIC FOT: FOT/CL or TAZ: TAZ/CL ratio ≥ 8). The presence of synergy indicates ESBL production.

Detection of AmpC-type beta-lactamases can be performed by testing bacterial susceptibility to cefoxitin (FOX). Resistance to FOX may indicate the presence of an AmpC-type beta-lactamase.

Confirmatory testing for carbapenemase production requires susceptibility testing to meropenem (MERO).

The classification of the phenotypic results should be based on the most recent EFSA recommendations (see Appendix 2).

Important note: For *E. coli*, there are two sets of relevant cut-off values for cefotaxime, ceftazidime and meropenem: 1) the EUCAST epidemiological cut-off values, which are used to define R/S phenotypes (see Appendix 1 and 2), and 2) the screening cut-off values (cefotaxime >1 and ceftazidime >1), which are used to categorise the resistance phenotypes, i.e. as ESBL, AmpC, carbapenemase, etc., based on the results from panel 2 (see Appendix 1 and 2).

4 REPORTING OF RESULTS AND EVALUATION

Test forms are available for recording your results before you enter them into the web tool.

4.1 General recommendations for data upload

We recommend reading carefully the description in paragraph 5 before entering your results in the web database. **Results must be submitted no later than 16 December 2025.** After the deadline, when all participants have uploaded results, you will be able to login to the database once again to view and print an automatically generated report evaluating your results. Results in agreement with the expected interpretation are categorised as 'correct', while results deviating from the expected interpretation are categorised as 'incorrect'.

If you experience difficulties in entering your results, please contact us directly.

All results will be summarized in a report which will be made publicly available. The data in the report will be presented under laboratory codes instead of laboratory names, to ensure anonymity. Each laboratory code will be known only to the respective laboratory, while the complete list of laboratories and their corresponding codes will remain confidential and known only to the EURL-AMR and the EU Commission. All conclusions will be public.

If you have any questions, please do not hesitate to contact the PT Coordinator:

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5 HOW TO ENTER RESULTS IN THE INTERACTIVE DATABASE

The 'guideline for submission of results via webtool' is available for download directly from the EURL-AMR website (https://www.food.dtu.dk/english/topics/antimicrobial-resistance/eurl-ar/protocols).

Access the webtool using this address: https://amr-eqas.dtu.dk. Please follow the guideline carefully and **remember to access the webtool via an 'incognito' website**.

When you submit your results, remember to have by your side the completed test forms.

Do not hesitate to contact us if you experience difficulties with the webtool.

Before finally submitting your input please ensure that you have filled in all the relevant fields, as **you can only 'finally submit' once!** 'Final submission' blocks further data entry.

⇨ About login to the webtool:

When you were first given access to login to the webtool, your **personal** loginID and password were sent to you by email on two email addresses (for primary and secondary contact) connected to each NRL-AMR.
Note that:

a) If the EURL-AMR has only one contact person for an NRL, this person is registered both as primary and secondary contact. Should you like to add another person as the secondary contact, please contact jetk@food.dtu.dk.
b) If your laboratory has two or more contact points on the EURL-AMR contact list, two of those have been defined as primary and secondary contact. Should you like to make changes to the primary and secondary contact or should you like to have more than two persons able to access the webtool, please contact jetk@food.dtu.dk.

All participants registered with an account in the submission webtool will receive a separate email with their personal username and password. The email will be sent after the webtool has gone through internal quality control and has been approved for user access. The EQAS Coordinator will let all participants know when to look out for it.

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APPENDIX 1 Criteria for interpretation of *Escherichia coli* MIC, panel 1 and 2 results

The following tables present the concentration range to be tested for each antimicrobial compound as well as the Epidemiological Cut-off values for the AMR phenotype categorisation as Resistant or Susceptible, as presented in Appendix B of the EFSA manual for reporting AMR data: EFSA (European Food Safety Authority), Amore G, Beloeil P-A, Garcia Fierro R, Rizzi V and Stoicescu A-V, 2025. Manual for reporting 2024 antimicrobial resistance data under Directive 2003/99/EC and Commission Implementing Decision (EU) 2020/1729. *EFSA supporting publication* 2025:EN-9238. 39 pp.. doi:10.2903/sp.efsa.2025.EN-9238

Criteria for interpretation of *E. coli* from *EFSA supporting publication* 2025:EN-9238. 39 pp.2024 Table B.1: Panel of antimicrobial substances to be included in AMR monitoring, interpretative thresholds for interpreting resistance and concentration ranges to be tested in *Salmonella* spp. and indicator commensal *E. coli.*

Antimicrobial	*Salmonella* EU surveillance 2024			*E. coli* EU surveillance 2024			Concentration range, mg/L (no of wells)
	ECOFF	EUCAST	EFSA	ECOFF	EUCAST	EFSA	
Amikacin[a]	4	x		8	x		4–128(6)
Ampicillin	8	x		8	x		1–32 (6)
Azithromycin	16	x		16		x	2–64 (6)
Cefepime[b]	0.125		x	0.125		x	0.064–32 (10)
Cefotaxime	0.5	x		0.25	x		0.25–4 (5)[c] 0.25–64 (9)[d]
Cefotaxime + clavulanic acid	0.5		x	0.25	x		0.064–64 (11)
Cefoxitin	8	x		8	x		0.5–64 (8)
Ceftazidime	2	x		0.5	x		0.25–8 (6)[c] 0.25–128 (10)[d]
Ceftazidime + clavulanic acid	2		x	0.5	x		0.125–128 (11)
Chloramphenicol	16	x		16	x		8–64 (4)
Ciprofloxacin	0.064	x		0.064	x		0.015–8 (10)
Colistin	2		x	2	x		1–16 (5)
Ertapenem[e]	0.064		x	0.064		x	0.015–2 (8)
Gentamicin	2	x		2	x		0.5–16 (6)
Imipenem	1	x		0.5	x		0.125–16 (8)
Meropenem	0.125		x	0.125	x		0.03–16 (10)
Nalidixic acid	8	x		8	x		4–64 (5)
Sulfamethoxazole	256		x	64		x	8–512 (7)
Temocillin	16		x	16	x		0.5–128 (9)
Tetracycline	8	x		8	x		2–32 (5)
Tigecycline	0.5		x	0.5	x		0.25–8 (6)
Trimethoprim	2	x		2	x		0.25–16 (7)

(a) : EUCAST epidemiological cut-off (ECOFF) value for *Salmonella* is tentative.

(b) : EUCAST epidemiological cut-off (ECOFF) value for *E. coli* is 0.25.

(c) : Range to be used when the substance is tested in panel 1.

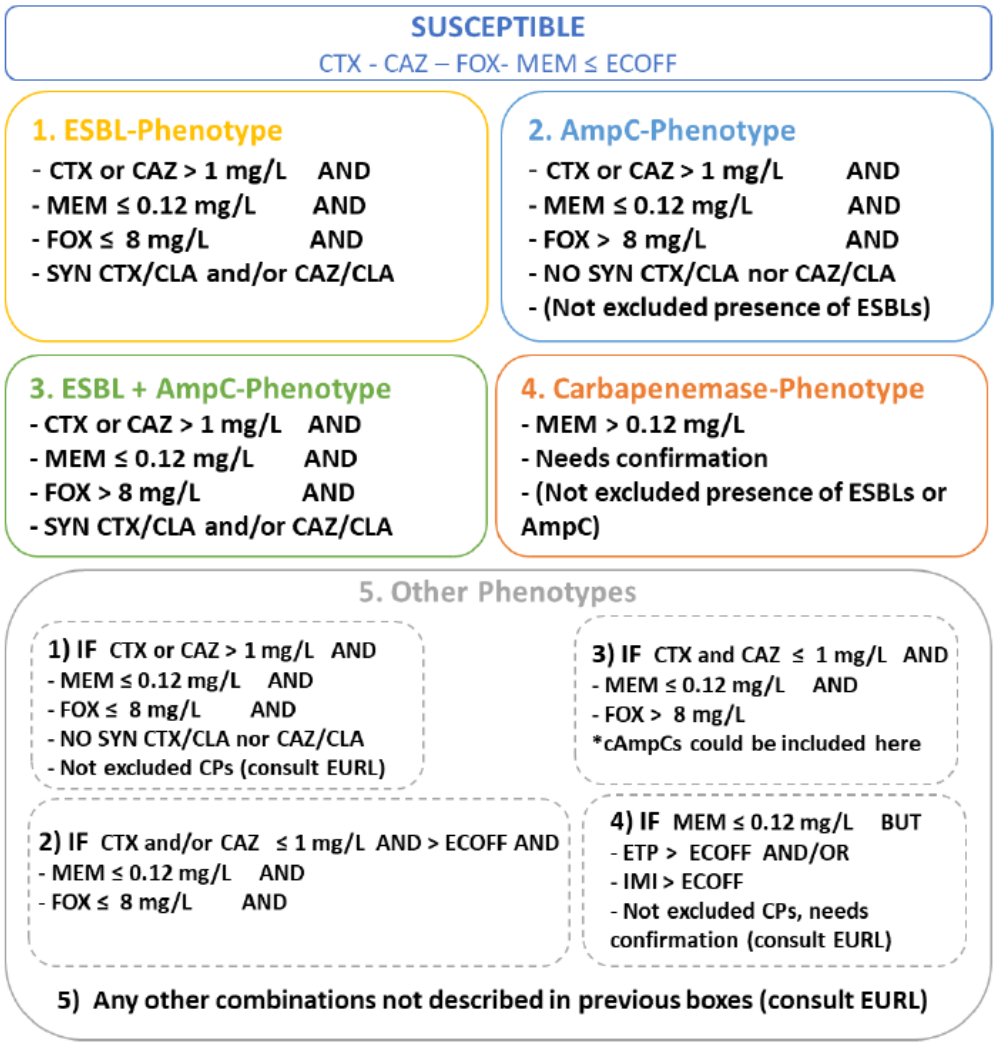
(d) : Range to be used when the substance is tested in panel 2.

(e) : EUCAST epidemiological cut-off (ECOFF) value for *E. coli* is tentative at 0.03.

APPENDIX 2 Criteria for categorisation of beta-lactam resistance phenotypes

Please use the scheme below to phenotypically identify presumptive ESBL-, AmpC-, and/or CP-producers. Five main categorizations of phenotypes are made: 1. Extended-Spectrum Beta-Lactamase-producing (ESBL phenotype), 2. AmpC Beta-Lactamase-producing (AmpC phenotype), 3. ESBL+AmpC phenotype, 4. Carbapenemase-producing (CP phenotype) and 5. Other.

The figure is from *EFSA and ECDC, 2025. The European Union Summary Report on Antimicrobial Resistance in zoonotic and indicator bacteria from humans, animals and food in 2022/2023. EFSA Journal. 2025;23:e9237.* https://doi.org/10.2903/j.efsa.2025.9237, Appendix A, Figure A.3.



Appendix 4: Examples of Test forms for Matrix PT 2025

Test forms,

Isolation of ESBL, AmpC and carbapenemase producers from matrices

Username:
Contact person:

Country:
Date for filling in test forms:

SAMPLES

Date and exact time the parcel with the proficiency testing samples was opened at the laboratory: (date and time is required)

Temperature of the contents of the parcel at arrival: °C

How many samples did your laboratory process in 2025 for the monitoring of ESBL/AmpC-producing *E. coli* in relation to 2020/1729/EU? (Choose only one option)

- ☐ none
- ☐ less than 100
- ☐ 101-200
- ☐ 201-300
- ☐ 301-400
- ☐ 401- 1000
- ☐ more than 1000

Which kind of samples did your laboratory process in 2025 for the monitoring of ESBL/AmpC-producing *E. coli* in relation to 2020/1729/EU? (You may choose more than one option)

- ☐ caecal, swine and cattle
- ☐ meat, pork and beef
- ☐ none
- ☐ other matrices, please specify:

How many samples did your laboratory process in 2025 for the monitoring of carbapenemase-producing *E. coli* in relation to 2020/1729/EU? (Choose only one option)

- ☐ none
- ☐ less than 100
- ☐ 101-200
- ☐ 201-300
- ☐ 301-400
- ☐ 401- 1000
- ☐ more than 1000

Which kind of samples did your laboratory process in 2025 for the monitoring of carbapenemase-producing *E. coli* in relation to 2020/1729/EU? (you may choose more than one option)

- ☐ caecal, swine and cattle
- ☐ meat, pork and beef
- ☐ none
- ☐ other matrices, please specify:

Any other comments:

METHODS

1- Method used for selective isolation of ESBL/AmpC-producing *E. coli* in this PT:

Regarding the methods used for the selective isolation of ESBL/AmpC-producing *E. coli* in this PT, please indicate if you made any modifications to the selective isolation procedure described in the EURL-recommended protocols referenced in EU decision 2020/1729/EU:

☐ The protocol was used without modifications (please jump to question 2)

☐ The protocol was used but the pre-enrichment was modified (please respond to question 1.1)

☐ The protocol was used but the selective isolation procedures were modified (please respond to question 1.2)

☐ The protocol was used but the incubation conditions for the selective plating were modified (please respond to question 1.3)

1.1- If you modified the pre-enrichment, please indicate the changes introduced:

Different sample amount (weight) used for the enrichment procedure:
g of meat samples
g of caecal samples

Different volume of enrichment in the isolation step:
ml for meat samples
ml for caecal samples

Different pre-enrichment medium:
Different incubation conditions during pre-enrichment °C/ h;
Please justify these changes:

1.2- Did you make changes in the selective isolation procedure:

Different concentration of cefotaxime**:** mg/L
Different antimicrobial
Different medium
Please justify these changes:

1.3- If you used different incubation conditions for selective plating, please indicate the conditions used: °C/ h;

Please justify these changes:

2- Method used for the selective isolation of carbapenemase producers in this PT:

Selective isolation procedure using the EURL-recommended protocols for isolation of carbapenemase producers:

☐ The protocol was used without modifications
☐ The protocol was modified

Plates used (brand/type)
Volume of sample plated
Please justify any changes:

Comments:

3- Method used for confirmation of *E. coli* species identification. Please indicate the primary *E. coli* identification method used (choose only one option; if you used more than one method, please explain in the comments field)

☐ PCR using published methods
☐ PCR using in-house method
☐ Biochemical tests
☐ MALDI-ToF
☐ DNA Sequencing
☐ Chromogenic media

Comments:

4- Method used for general antimicrobial susceptibility testing of the strains (choose only one option)

☐ Microbroth dilution test on EUVSEC3 panel
☐ Microbroth dilution test on another panel
☐ Agar dilution method
☐ E-test
☐ Disk diffusion test

5- Method used for phenotypic confirmatory testing of presumptive ESBL-/AmpC-/carbapenemase-producing strains (choose only one option)

☐ Microbroth dilution test on EUVSEC2 panel
☐ Microbroth dilution test on another panel
☐ Agar dilution method
☐ E-test
☐ Disk diffusion test

6- Additional comments. Please include here description and justification of your choice if you modified something from the method defined in the EU regulation 2020/1729/EU:

TEST FORM – SAMPLE 'EURL M-11.1'

Date the isolation procedure was started:

Please describe the results you observed regarding this sample:

Visible growth in pre-enrichment:
Yes ☐/ No☐

Growth on ESBL/AmpC-selective plates:
Yes ☐ / No ☐

Please describe the growth observed on ESBL/AmpC-selective plates. (choose only one option)
☐ Mixed culture containing typical *E. coli* colonies
☐ Mixed culture without typical *E. coli* colonies
☐ Pure culture of typical *E. coli* colonies
☐ Pure culture without typical *E. coli* colonies
☐ No growth

Results of species identification: (choose only one option)
☐ No isolates tested (sample negative)
☐ Presumptive ESBL/AmpC isolate identified as *E. coli* (sample considered positive)

Comments:

Growth on CARBA-selective plates:
Yes ☐ / No ☐

Growth on OXA-48 selective plates:
Yes ☐ / No ☐

Results of species identification (isolates from carbapenemase selective plating): (choose only one option)
☐ No isolates tested (sample negative)
☐ Presumptive carbapenemase isolate identified as *E. coli* (sample considered positive)
☐ Presumptive OXA-48 isolate identified as *E. coli* (sample considered positive)

Comments:

If you have found a presumptive carbapenemase-positive *E. coli* isolate, please insert the results of antimicrobial susceptibility testing for the isolate. If you do not have a carbapenemase-positive isolate and you have an ESBL presumptive isolate, please insert the results for this isolate (only one *E.coli* isolate is expected to be tested and these results will be evaluated in our database against the expected results).

Please confirm where the isolate tested for antimicrobial susceptibility originated from:

☐ ESBL/AmpC selective isolation on MacConkey agar plate with cefotaxime
☐ CARBA plate
☐ OXA-48 plate

Based on the results from the first AST panel, was the isolate found to be resistant to cefotaxime, ceftazidime or meropenem, thereby requiring testing with the second panel?

Yes ☐ / No ☐

AST results

Strain	Antimicrobial	Results and interpretation		
		≤ >	MIC-value (mg/L)	S / R
E. coli EURL M-11.1	Amikacin AMI			
	Ampicillin, AMP			
	Azithromycin, AZI			
	Cefotaxime, FOT or CTX			
	Ceftazidime, TAZ or CAZ			
	Chloramphenicol, CHL			
	Ciprofloxacin CIP			
	Colistin, COL			
	Gentamicin, GEN			
	Meropenem, MERO or MEM			
	Nalidixic acid, NAL			
	Sulfamethoxazole, SMX			
	Tetracycline, TET			
	Tigecycline, TGC			
	Trimethoprim, TMP			

Second *E. coli* AST panel (confirmatory testing for ESBL/AmpC/carbapenemase production)

Strain	Antimicrobial	Results and interpretation		
		≤ >	MIC-value (mg/L)	S / R
E. coli EURL M-11.1	Cefepime, FEP			
	Cefotaxime + clavulanic acid F/C or CTX/CLA			
	Cefotaxime, FOT or CTX			
	Cefoxitin, FOX			
	Ceftazidime, TAZ or CAZ			
	Ceftazidime+ clavulanic acid T/C or CAZ/CLA			
	Ertapenem, ETP			
	Imipenem, IMI			
	Meropenem, MERO or MEM			
	Temocillin, TRM			

Conclusions of confirmatory phenotypic testing: (choose only one option and please note that the final result will be evaluated by the database)

Interpretation of PANEL 2 results:

☐ Presumptive ESBL	☐ Presumptive AmpC	☐ Other phenotype
☐ Presumptive ESBL+ AmpC	☐ Presumptive carbapenemase	☐ Susceptible

Comments (include optional genotype or other results):

Appendix 5: *E. coli* ATCC25922 and *A. baumannii* 2012-70-100-69 QC ranges

Table 1. Quality control (QC) intervals for the reference strain *Escherichia coli* ATCC25922, based on CLSI M100, 35th ed.

Antimicrobial	**Accepted MIC range (mg/L)**
Amikacin	0.5-4
Ampicillin	2-8
Azithromyciin	-
Cefepime	0.016-0.12
Cefotaxime	0.03-0.12
Cefotaxime+Clavulanic acid	-
Cefoxitin	2-8
Ceftazidime	0.06-0.5
Ceftazidime+Clavulanic acid	-
Chloramphenicol	2-8
Ciprofloxacin	0.004-0.016
Colistin	-
Ertapenem	0.004-0.016
Gentamicin	0.25-1
Imipenem	0.06-0.5
Meropenem	0.008-0.06
Nalidixic acid	1-4
Sulfamethoxazole(1)	8-32
Temocillin	-
Tetracycline	0.5-2
Tigecycline	0.03-0.25
Trimethoprim	0.5-2

(1)*Sulfamethoxazole and sulfisoxazole are regarded as comparable, i.e., the obtained MIC value from the testing of sulfamethoxazole will be evaluated against the acceptance range listed in CLSI M100 for sulfisoxazole (Table 5A-1, CLSI M100, 35th ed. [3]).*

Table 2. Quality control (QC) intervals for the QC strain *Acinetobacter baumannii* 2012-70-100-69 QC strain, based on EURL-AMR reference values.

	Accepted MIC range (mg/L)	
Antimicrobial	**Lowest MIC**	**Highest MIC**
Amikacin	≤4	8
Ampicillin	8	32
Azithromyciin	≤2	4
Cefepime	1	4
Cefotaxime	4	16
Cefotaxime+Clavulanic acid	4	16
Cefoxitin	32	>64
Ceftazidime	2	8
Ceftazidime+Clavulanic acid	2	8
Chloramphenicol	32	>64
Ciprofloxacin	0.12	0.5
Colistin	≤1	4
Ertapenem	1	>2
Gentamicin	≤0.5	2
Imipenem	≤0.12	1
Meropenem	0.12	0.5
Nalidixic acid	≤4	8
Sulfamethoxazole[1]	≤8	16
Temocillin	128	>128
Tetracycline	8	>32
Tigecycline	≤0.25	0.5
Trimethoprim	8	>16

[1]*Sulfamethoxazole and sulfisoxazole are regarded as comparable, i.e., the obtained MIC value from the testing of sulfamethoxazole will be evaluated against the acceptance range listed in CLSI M100 for sulfisoxazole (Table 5A-1, CLSI M100, 35th ed. [3]).*

Appendix 6: List of deviations

Matrix test samples with no isolate recovered

Lab number	Samples with no isolate recovered
NRL-AR-016	EURL M-11.5

Deviations, AST results - full list

Lab number	Strain	Panel	Antimicrobial	Obtained operator	Expected operator	Obtained MIC value	Expected MIC value	Obtained interpretation	Expected interpretation	Score of interpretation
NRL-AR-004	EURL M-11.1	Panel2	Temocillin	=	=	16	32	S	R	0
NRL-AR-009	EURL M-11.1	Panel2	Temocillin	=	=	16	32	S	R	0
NRL-AR-016	EURL M-11.1	Panel2	Temocillin	=	=	16	32	S	R	0
NRL-AR-020	EURL M-11.1	Panel2	Temocillin	=	=	16	32	S	R	0
NRL-AR-023	EURL M-11.1	Panel1	Sulfamethoxazole	>	<=	512	8	R	S	0
NRL-AR-029	EURL M-11.1	Panel2	Temocillin	=	=	16	32	S	R	0
NRL-AR-038	EURL M-11.1	Panel1	Sulfamethoxazole	=	<=	128	8	R	S	0
NRL-AR-040	EURL M-11.1	Panel1	Sulfamethoxazole	>	<=	512	8	R	S	0
NRL-AR-045	EURL M-11.1	Panel2	Temocillin	=	=	16	32	S	R	0
NRL-AR-059	EURL M-11.1	Panel2	Temocillin	=	=	16	32	S	R	0
NRL-AR-019	EURL M-11.2	Panel1	Chloramphenicol	<=	=	16	32	S	R	0
NRL-AR-019	EURL M-11.2	Panel2	Cefepime	<=	=	0,12	0,25	S	R	0
NRL-AR-019	EURL M-11.2	Panel2	Cefotaxime-Clavulanic acid	<=	=	0,25	0,5	S	R	0
NRL-AR-019	EURL M-11.2	Panel2	Imipenem	<=	=	0,5	1	S	R	0
NRL-AR-020	EURL M-11.2	Panel2	Imipenem	=	=	0,5	1	S	R	0
NRL-AR-021	EURL M-11.2	Panel2	Cefotaxime-Clavulanic acid	=	=	0,5	0,5	S	R	0
NRL-AR-021	EURL M-11.2	Panel2	Cefoxitin	=	=	16	4	R	S	0
NRL-AR-026	EURL M-11.2	Panel1	Ceftazidime	>	<=	8	0,25	R	S	0
NRL-AR-026	EURL M-11.2	Panel1	Chloramphenicol	<=	=	8	32	S	R	0
NRL-AR-026	EURL M-11.2	Panel1	Ciprofloxacin	<=	=	0,015	0,5	S	R	0
NRL-AR-026	EURL M-11.2	Panel1	Nalidixic acid	<=	=	4	16	S	R	0
NRL-AR-026	EURL M-11.2	Panel1	Sulfamethoxazole	<=	>	8	512	S	R	0
NRL-AR-026	EURL M-11.2	Panel1	Tetracycline	<=	>	2	32	S	R	0
NRL-AR-026	EURL M-11.2	Panel1	Trimethoprim	<=	>	0,25	16	S	R	0
NRL-AR-026	EURL M-11.2	Panel2	Cefoxitin	>	=	64	4	R	S	0
NRL-AR-026	EURL M-11.2	Panel2	Ceftazidime	>	<=	128	0,25	R	S	0

NRL-AR-026	EURL M-11.2	Panel2	Ceftazidime-Clavulanic acid	>	<=	128	0,25	R	S	0
NRL-AR-040	EURL M-11.2	Panel1	Chloramphenicol	=	=	16	32	S	R	0
NRL-AR-040	EURL M-11.2	Panel1	Meropenem	=	=	0,12	0,5	S	R	0
NRL-AR-040	EURL M-11.2	Panel2	Imipenem	=	=	0,5	1	S	R	0
NRL-AR-040	EURL M-11.2	Panel2	Meropenem	=	=	0,12	0,5	S	R	0
NRL-AR-059	EURL M-11.2	Panel2	Imipenem	=	=	0,5	1	S	R	0
NRL-AR-062	EURL M-11.2	Panel1	Cefotaxime	<=	=	0,25	1	S	R	0
NRL-AR-062	EURL M-11.2	Panel1	Chloramphenicol	<=	=	8	32	S	R	0
NRL-AR-062	EURL M-11.2	Panel2	Cefepime	=	=	0,25	0,25	S	R	0
NRL-AR-062	EURL M-11.2	Panel2	Imipenem	=	=	0,5	1	S	R	0
NRL-AR-006	EURL M-11.4	Panel1	Meropenem	>	<=	16	0,03	R	S	0
NRL-AR-006	EURL M-11.4	Panel2	Ertapenem	>	=	2	0,03	R	S	0
NRL-AR-006	EURL M-11.4	Panel2	Imipenem	=	<=	16	0,125	R	S	0
NRL-AR-006	EURL M-11.4	Panel2	Meropenem	>	<=	16	0,03	R	S	0
NRL-AR-006	EURL M-11.4	Panel2	Temocillin	=	=	32	8	R	S	0
NRL-AR-012	EURL M-11.4	Panel2	Ertapenem	=	=	0,12	0,03	R	S	0
NRL-AR-017	EURL M-11.4	Panel2	Ertapenem	=	=	0,12	0,03	R	S	0
NRL-AR-021	EURL M-11.4	Panel2	Ceftazidime-Clavulanic acid	=	=	1	2	S	R	0
NRL-AR-023	EURL M-11.4	Panel2	Ertapenem	=	=	0,12	0,03	R	S	0
NRL-AR-025	EURL M-11.4	Panel2	Ertapenem	=	=	0,12	0,03	R	S	0
NRL-AR-034	EURL M-11.4	Panel2	Ertapenem	=	=	0,12	0,03	R	S	0
NRL-AR-037	EURL M-11.4	Panel2	Ceftazidime-Clavulanic acid	=	=	2	2	S	R	0
NRL-AR-040	EURL M-11.4	Panel1	Sulfamethoxazole	=	<=	256	8	R	S	0
NRL-AR-041	EURL M-11.4	Panel2	Ertapenem	=	=	0,125	0,03	R	S	0
NRL-AR-056	EURL M-11.4	Panel2	Imipenem	<=	<=	0,12	0,125	R	S	0
NRL-AR-040	EURL M-11.5	Panel2	Imipenem	=	=	0,5	4	S	R	0
NRL-AR-012	EURL M-11.6	Panel1	Tigecycline	=	=	1	0,5	R	S	0
NRL-AR-012	EURL M-11.6	Panel2	Temocillin	=	=	16	8	R	S	0
NRL-AR-016	EURL M-11.6	Panel1	Azithromycin	=	=	8	32	S	R	0

NRL-AR-016	EURL M-11.6	Panel1	Chloramphenicol	<=	>	8	64	S	R	0
NRL-AR-016	EURL M-11.6	Panel1	Ciprofloxacin	<=	=	0,015	1	S	R	0
NRL-AR-016	EURL M-11.6	Panel1	Gentamicin	=	>	1	16	S	R	0
NRL-AR-016	EURL M-11.6	Panel1	Meropenem	=	<=	8	0,03	R	S	0
NRL-AR-016	EURL M-11.6	Panel1	Nalidixic acid	<=	=	4	16	S	R	0
NRL-AR-016	EURL M-11.6	Panel1	Sulfamethoxazole	=	>	16	512	S	R	0
NRL-AR-016	EURL M-11.6	Panel1	Tetracycline	<=	>	2	32	S	R	0
NRL-AR-016	EURL M-11.6	Panel1	Trimethoprim	=	>	0,5	16	S	R	0
NRL-AR-016	EURL M-11.6	Panel2	Cefotaxime-Clavulanic acid	>	=	64	0,12	R	S	0
NRL-AR-016	EURL M-11.6	Panel2	Ceftazidime-Clavulanic acid	>	=	128	0,25	R	S	0
NRL-AR-016	EURL M-11.6	Panel2	Ertapenem	>	<=	2	0,015	R	S	0
NRL-AR-016	EURL M-11.6	Panel2	Imipenem	=	<=	4	0,125	R	S	0
NRL-AR-016	EURL M-11.6	Panel2	Meropenem	=	<=	8	0,03	R	S	0
NRL-AR-019	EURL M-11.6	Panel1	Ciprofloxacin	<=	=	1	1	S	R	0
NRL-AR-023	EURL M-11.6	Panel1	Nalidixic acid	<=	=	4	16	S	R	0
NRL-AR-040	EURL M-11.6	Panel2	Cefotaxime	=	>	0,12	64	S	R	0
NRL-AR-040	EURL M-11.6	Panel2	Cefotaxime-Clavulanic acid	=	=	64	0,12	R	S	0
NRL-AR-056	EURL M-11.6	Panel1	Azithromycin	=	=	16	32	S	R	0
NRL-AR-060	EURL M-11.6	Panel1	Tigecycline	=	=	1	0,5	R	S	0
NRL-AR-061	EURL M-11.6	Panel1	Azithromycin	=	=	64	32	S	R	0

*Grey shading indicates a 2-fold dilution deviation from the expected MIC value

Deviations, ESBL categorisation - full list

Lab number	Strain	Obtained interpretation	Expected interpretation	Score of interpretation
NRL-AR-006	EURL M-11.4	Carbapenemase-phenotype	AmpC-phenotype	0
NRL-AR-016	EURL M-11.6	Carbapenemase-phenotype	ESBL-phenotype¤ESBL+AmpC-phenotype	0
NRL-AR-017	EURL M-11.4	Other phenotype	AmpC-phenotype	0
NRL-AR-026	EURL M-11.3	Carbapenemase-phenotype	Susceptible	0
NRL-AR-040	EURL M-11.2	Other phenotype	Carbapenemase-phenotype	0
NRL-AR-056	EURL M-11.3	ESBL+AmpC-phenotype	Susceptible	0

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