EURL-PH-AMR

EU Reference Laboratory for public health in the field of AMR

101194806

Deliverable number: D7.4

Deliverable name: Plan for the phenotypic external quality assessment and genomic proficiency test for laboratories participating in EURGen-Net (2025)

Funded by the European Union

Document overview

Deliverable number	7.4
Deliverable name	Plan for the phenotypic external quality assessment and genomic proficiency test for laboratories participating in EURGen-Net (2025)
Work package number / name	7 / External quality assessments (EQAs)
Task number / name	Task 7.2 – Provision of phenotypic external quality assessment (EQA) and genomic proficiency testing (PT) to the national reference laboratories (EURGen-Net)
Due date	M7
Reviewed and agreed by ECDC	16.07.2025 Anke Kohlenberg, Marius Linkevicius and Pete Kinross
Revision (requested by the Commission)	
Dissemination level	Public
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Lead Beneficiary	SSI
Project website	EURL-PH-AMR website

Introduction

The European Antimicrobial Resistance Genes Surveillance Network (EURGen-Net) is a network for genomic-based surveillance of multidrug-resistant bacteria of public health importance, coordinated by the European Centre for Disease Prevention and Control (ECDC) (https://www.ecdc.europa.eu/en/about-us/who-we-work/disease-and-laboratory-networks/EURGen-net). Currently, National reference laboratories (NRLs) or equivalent laboratories of 37 European countries participate in EURGen-Net.

The targeted bacteria are healthcare-associated carbapenem- and/or colistin-resistant Enterobacterales (CCRE), *Pseudomonas aeruginos*a (CRPa), and *Acinetobacter baumannii* (CRAb). These are classified as 'bacterial priority pathogens' by the World Health Organization (WHO) (WHO, 2024) and are prioritised for surveillance by the ECDC (ECDC, 2024; ECDC, 2025b).

The objectives of EURGen-Net are to:

- determine the geographic distribution and population dynamics of multidrug-resistant clones and transmissible resistance elements;
- to inform risk assessment, prevention and control policies;
- to support countries in developing technical capability and proficiency for genomic-based surveillance of multidrug-resistant bacteria with epidemic potential.

To strengthen and improve the capacity for detection, identification and characterisation of CRE, CRAb and CRPa in the national reference laboratories participating in EURGen-Net, the EURL-PH-AMR consortium in coordination with the ECDC will conduct a phenotypic external quality assessment (EQA) and genomic proficiency testing (PT) yearly in the period 2025-2031, under grant agreement 101194806.

In this document, we outline the plan for the EURGen-Net phenotypic EQA and genomic PT 2025, in accordance with the Guide for EU-level EQAs for public health microbiology laboratories issued by ECDC in 2025.

The EURGen-Net phenotypic EQA and genomic PT will be conducted in compliance with recommendations by internationally recognised guidelines and standards if possible. At Statens Serum Institut (SSI) and Technical University of Denmark, National Food Institute (DTU Food), several microbiological analyses are accredited according to ISO 17025:2017 (equivalent to ISO 15189:2022) and antimicrobial susceptibility testing (AST) by broth microdilution is accredited according to ISO 20776-1:2020 by DANAK (SSI, accreditation no. 397; DTU, accreditation no. 350). Furthermore, DTU Food holds accreditation for provision of PT for the identification, serotyping and AST of zoonotic pathogens and indicator organisms according to ISO 17043:2023 (DANAK, accreditation no. 516), with concrete plans to have the EURGen-Net phenotypic EQA covered by this accreditation.

Objectives

The overall objective of the EURGen-Net phenotypic EQA and genomic PT is to assess the accuracy and reliability of results generated by the participating laboratories in the following areas:

- phenotypic characterisation of CRE, CRAb and CRPa including species identification and interpretation of AST results for a panel of antimicrobials specified further in this document;
- genomic characterisation of CRE, CRAb and/or CRPa, including whole-genome sequencing (WGS) and bioinformatics analyses of WGS data to determine specific genomic traits as explained further in this document.

Further specific objectives are:

- to enable participating laboratories to identify strengths and weaknesses of their technical and analytical set-up and implement appropriate actions to improve their performance in the phenotypic and genomic characterisation of CRE, CRAb and CRPa;
- to identify training and capacity building needs for the purpose of improving the detection and characterisation of CRE, CRAb and CRPa by phenotypic and genomic methods;
- to strengthen and maintain the high quality and comparability of national reference laboratory data of CRE, CRAb and CRPa for surveillance at the European level.

Participants and preparation

All national reference laboratories that are part of EURGen-Net and are eligible for the grant agreement 101194806 (n = 31) are invited to participate.

SSI and DTU Food will draft an information letter and set-up a registration form in the EU Survey tool. After ECDC agreement, SSI will e-mail the information letter (Annex 1) to all invited participants.

SSI will compile the list of participants and share it with DTU Food and ECDC.

Participating laboratories will be assigned a unique code, which will be used when presenting results. Only SSI and DTU Food will have access to the full list of codes, and each participating laboratory will only know its own code.

Timeline: the information letter and link to the registration form will be sent by end of June 2025. Registration will be open for two weeks after the e-mail is sent. Due to the summer holiday season, it may be possible to extend the registration period on an *ad hoc*

basis, but no later than the end of August 2025.

Methodology

Among the EURL-PH-AMR consortium members, DTU Food is the main responsible for the phenotypic EQA and SSI is the main responsible for the genomic PT. All steps relating to the preparation and execution of the EQA/PT, as well as communication with the participants, are carried out in coordination and agreement between DTU Food, SSI and ECDC.

The preparation and execution of the phenotypic EQA and genomic PT 2025 can be organised in three main components, including:

1. Selection, analysis and preparation of test materials;
2. Development of supporting documents including all information to be shared with participants and reports;
3. Set-up and management of web-based tools for submission of results.

The activities and timeline associated with each component are described in the protocol provided in Annex 2.

Distribution

DTU Food will prepare live cultures of the selected bacterial strains, including implementing quality assurance procedures to guarantee the viability of the bacterial cells.

DTU Food will prepare the swabs and the packages for each laboratory that registered for the phenotypic EQA/genomic PT 2025. The packages will be sent to each of the participating laboratories **(Milestone 20)**. The cultures are categorized as UN3373, biological substance category B and are packed following IATA packing instruction 650.

Each package will include a cover letter with safety instructions on how to handle the strains.

SSI will prepare the files in FASTQ and/or FASTA formats for sharing with participants who indicated this preference during registration. The files will be shared via SFTP.

Timeline: swabs will be prepared and shipped by the end of October 2025. The FASTQ and/or FASTA files will be shared when the strains are shipped.

Instructions for completion (minimum requirements)

The EQA and PT protocols, and the instructions and forms to report the results will be available on the EURL-PH-AMR website. Briefly, the participants will be asked to submit results generated with the methods in use in their laboratories and to report on the following:

- for the phenotypic EQA:
    - species identification;
    - AST (MIC values and/or inhibition zone diameters) for the antimicrobials listed in Annex 3;
    - interpretation of the AST results according to the most recent EUCAST clinical breakpoint tables (https://www.eucast.org/clinical_breakpoints);
    - information on the methods used for species identification and AST, including information about the manufacturers of instruments, disks, tablets, agars, broths, MIC panels, and gradient tests.

  The deadline for result submission will be 8 November 2025. The participants will receive an email informing that the individual evaluation reports and the certificate of participation can be downloaded via the secure webtool provided by DTU Food by the end of January 2026. The minimum requirement for obtaining a certificate of participation is submission of interpretation of AST results for all four strains.

- for the genomic PT:
    - multi-locus sequence typing (MLST);
    - core genome MLST (cgMLST);
    - genes and chromosomal mutations mediating resistance towards: i) aminoglycosides, carbapenems, third-generation cephalosporins, colistin and fluoroquinolones for all species; ii) trimethoprim-sulfamethoxazole for Enterobacterales and *A. baumannii*; and iii) fosfomycin for *E. coli*. For the purpose of the genomic PT, resistance is intended as a non-wild-type phenotype (i.e. above the epidemiological cutoff, ECOFF) and not necessarily as resistance according to clinical breakpoints. For more information about ECOFFs and clinical breakpoints, please see Kahlmeter and Turnidge, 2022 and the EUCAST website;
    - plasmid replicon types (limited to Enterobacterales);
    - information on the methods used for WGS and bioinformatics analyses of WGS data. This includes specifying, when relevant, the sequencing instrument used, the protocols and/or kits used for DNA extraction and library preparation, the processes for quality control of raw reads and assemblies, and the name and version number of software and databases used;
    - the FASTQ files produced during WGS for the purpose of evaluation of the sequence quality.

  The deadline for result submission will be 29 November 2025, and the individual

evaluation reports and certificate of participation will be e-mailed to the participants by the end of January 2026. The minimum requirement for obtaining a certificate of participation is submission of results for MLST, genes and chromosomal mutations mediating resistance towards the clinically important antimicrobials specified above and, limited to Enterobacterales, plasmid replicon types. The certificate will indicate the bacterial species for which the laboratory has submitted results since it is not mandatory to analyse all four strains to participate in the genomic PT. The certificate of participation will be issued in January 2026.

Of note, each participant will be allowed to submit one set of phenotypic results and one set of genomic results per test strain, irrespective of the methods used.

Data analysis

The data obtained through the phenotypic EQA and the genomic PT include information on the number of participants, the methods used by the participating laboratories, and the typing results for the test strains.

A descriptive analysis will be used to summarise and visualise all data obtained, which will be presented in anonymised form.

For the phenotypic EQA, a scoring system developed for the EARS-Net EQA that accounts for the "level of difficulty" and "severity of error" for each organism-antimicrobial combination will be used when evaluating the interpretation of AST results (ECDC, 2024), if the species of the isolate is identified correctly. Conversely, if the species is not identified correctly, the AST results for that isolate will not be evaluated further.

For the genomic PT, performance will be evaluated as concordance/discordance between expected and submitted results. There will be no scoring system as there are no internationally agreed performance standards for WGS and bioinformatics analyses of WGS data applicable to this context. However, following the results of the first genomic PT conducted by the EURL-PH-AMR, an attempt will be made to devise a scoring system in consultation with EURGen-Net members and ECDC for future genomic PT cycles.

The EQA/PT results will be discussed in dedicated sections of the reports shared with ECDC and the participants (described below in this document). The discussion will highlight the typing results for which concordance between expected and submitted results was highest and lowest, and the latter will be used to identify training and capacity building needs.

Reporting of results

The results of the EURGen-Net phenotypic EQA and genomic PT will be used to produce:

i) an individual report for each participating laboratory; ii) a report on the phenotypic EQA with aggregated, anonymised data; iii) a report on the genomic PT with aggregated, anonymised data; and iv) a report comparing the aggregated, anonymised results of the phenotypic EQA and the genomic PT. Further information about these reports is provided below.

In addition, SSI and DTU Food will organise a joint webinar to present the aggregated, anonymised results of the EURGen-Net phenotypic EQA and genomic PT 2025 by 30 April 2026 (**Milestone 21**). All participating laboratories, the National Focal Points for AMR, the EURGen-Net Operational Contact Points for Microbiology, ECDC, HaDEA and the European Commission (DG SANTE) will be invited to this webinar.

Reports to participants

Each participant will receive individual evaluations of the results obtained in the phenotypic EQA and in the genomic PT. The participants will be informed via e-mail when their laboratory reports are available, no later than 31 January 2026. Specifically:

- for the phenotypic EQA, the participants will be able to download the individual reports via the secure webtool provided by DTU Food. These reports will include, for each strain-antimicrobial combination, the expected and submitted AST results and respective interpretations, and the evaluation score;

- for the genomic PT, the participants will receive the individual reports as e-mail attachments in PDF format. These reports will include, for each strain, the expected and submitted results for MLST, cgMLST, genes and chromosomal mutations mediating resistance to the clinically important antimicrobials specified above and, limited to Enterobacterales, the plasmid replicon types.

Reports to ECDC

Reports containing aggregated, anonymised data will be produced for the phenotypic EQA and genomic PT. These reports will provide a description of the EQA/PT methodology, a summary of all results, and short conclusions on the capacity of participating laboratories along with recommendations for improvement where necessary. The reports will undergo written consultation with ECDC and the participants. The final reports, agreed with ECDC, will be published on the EURL-PH-AMR website by 30 April 2026.

Additionally, a report comparing the anonymised results of the phenotypic EQA and the genomic PT will be produced (**Deliverable 7.5**). This report will include a comparison of laboratories' performance in the phenotypic and genomic characterisation of CRE, CRAb and CRPa and, if needed, recommendations for improvement such as training and capacity building needs. The report will undergo written consultation with ECDC and the participants. The final report, agreed with ECDC, will be published on the EURL-PH-AMR website by 30 April 2026.

Participant survey

Participants will be invited to complete two short, anonymous surveys: one regarding the phenotypic EQA and one regarding the genomic PT. The surveys will aim at gathering feedback and suggestions for improving the phenotypic EQA and the genomic PT, and will be launched within two to three weeks after the release of the individual evaluation reports.

Key topics covered in the surveys will include:

- Corrective actions taken and/or planned if submitted results were not in agreement with expected results;
- Use of the results as documentation for accreditation or similar purposes;
- Satisfaction with the report of results specific to the participant's laboratory;
- Suggestions for improving the usefulness of the EURGen-Net phenotypic EQA and genomic PT.

The questions will be drafted by DTU Food and SSI, and agreed with ECDC.

The participants will be emailed the link to the survey hosted on a web platform (e.g. EU Survey tool) and will be given two weeks to reply.

The replies will be extracted, analysed, and presented in the final reports that will be published on the EURL-PH-AMR website.

Data management, ownership and sharing

Data processing and data sharing are done in compliance with Article 15 and 16, respectively, of Grant Agreement Project 101194806 for the EU Reference Laboratory for Public Health on Antimicrobial Resistance (EURL-PH-AMR).

Annex 1: Information letter

EURL-PH-AMR

EU Reference Laboratory for Public Health on Antimicrobial Resistance

101194806

European Antimicrobial Resistance Genes Surveillance Network (EURGen-Net) phenotypic external quality assessment (EQA) and genomic proficiency test (PT) 2025

Information letter

June 2025

STATENS SERUM INSTITUT

DTU

CLINICAL MICROBIOLOGY
KRONOBERG AND BLEKINGE
SWEDISH NRL FOR PHENOTYPIC AST
EUCAST DEVELOPMENT LABORATORY

Funded by the European Union

Background

The European Antimicrobial Resistance Genes Surveillance Network (EURGen-Net) phenotypic external quality assessment (EQA) and genomic proficiency test (PT) are conducted under the Grant Agreement Project 101194806 for the EU Reference Laboratory for Public Health on Antimicrobial Resistance (EURL-PH-AMR) awarded in response to a proposal to 'Direct grants to nominated EU reference laboratories (EU4H-2023-DGA-MS4-IBA; CP-g-23-05-01; 27 March 2024)'.

The Grant Agreement Project 101194806 is carried out jointly by the consortium led by Statens Serum Institut (SSI, Denmark) and comprising the National Food Institute at the Technical University of Denmark (DTU Food, Denmark) and the EUCAST Development Laboratory (EDL, Sweden).

The EURGen-Net phenotypic EQA and genomic PT 2025 are planned, coordinated and implemented in agreement with the 'Guide for EU-level external quality assessments (EQAs) for public health microbiology laboratories' published by the European Centre for Disease Prevention and Control (ECDC) in March 2025 (ECDC, 2025a).

The EURGen-Net phenotypic EQA and genomic PT 2025

Aims

The EURGen-Net phenotypic EQA and genomic PT 2025 focus on assessment of laboratory proficiency in the detection, identification and characterisation of carbapenem-resistant Enterobacterales (CRE), *Acinetobacter baumannii* (CRAb) and *Pseudomonas aeruginosa* (CRPa), that are classified among the 'bacterial priority pathogens' by the World Health Organization (WHO) (WHO, 2024) and are prioritised for surveillance by the European Centre for Disease Prevention and Control (ECDC) (ECDC, 2024; ECDC, 2025b)

The EURGen-Net phenotypic EQA and genomic PT 2025 aim to:

- enable participating laboratories to identify strengths and weaknesses of their technical and analytical set-up and implement appropriate actions to improve their performance in the phenotypic and genomic characterisation of CRE, CRAb and CRPa;
- identify training and capacity and capability building needs for the purpose of improving the detection and characterisation of CRE, CRAb and CRPa;
- strengthen and maintain the high quality and comparability of public health laboratory data of CRE, CRAb and CRPa at the European level.

Outline

The test materials are four live bacterial cultures. Exceptionally, for the genomic PT, the organisers can provide the sequence data (FASTQ or FASTA files, either from short-read or long-read sequencing) if laboratories cannot carry out whole-genome sequencing (WGS) in their settings. The participants must make this request via the registration form (see below).

The participants will be asked to submit the following results generated with the methods in use in the participating laboratories:

- for the phenotypic EQA: species identification, AST results (MIC values and/or inhibition zone diameters), and interpretation of the AST results according to the most recent EUCAST clinical breakpoint tables (https://www.eucast.org/clinical_breakpoints).
  In addition, the participants will be asked about detailed information on the methods used for species identification and AST. This includes specifying, when relevant, the instruments used, the manufacturers of disks, tablets, agars, broth, MIC panels, gradient tests.

- for the genomic PT: multi-locus sequence type (MLST), core genome MLST (cgMLST), genes and chromosomal mutations mediating resistance towards clinically important antimicrobials (that will be specified in the protocol) and, limited to Enterobacterales, plasmid replicon types.
  Additionally, the participants will be asked to report detailed information on the methods used for WGS and bioinformatics analyses, and will be invited to submit the FASTQ files produced during WGS for the purpose of evaluation of the sequence quality.

Results should be uploaded separately for the phenotypic EQA, that is provided by DTU Food, and the genomic PT, that is provided by SSI.

The protocols with detailed instructions and other supporting materials will be available to download on the EURL-PH-AMR website before dispatching and shipping the test materials.

After submitting the results, each participating laboratory will receive:

i. individual evaluations of the results obtained in the phenotypic EQA and/or the genomic PT;
ii. technical follow-up and support to identify corrective measures by the EURL-PH-

AMR, upon request;

iii. a short survey to provide feedback on the EURGen-Net phenotypic EQA and the genomic PT 2025, and support improvement of future phenotypic EQA and genomic PT iterations; and

iv. a certificate of participation. Minimum requirements for receiving a certificate of participation are:

- for the phenotypic EQA: submission of interpretation of AST results for all four strains;
- for the genomic PT: submission of results for MLST, genes and chromosomal mutations mediating resistance towards clinically important antimicrobials (that will be specified in the protocol) and, limited to Enterobacterales, plasmid replicon types. The certificate will indicate the bacterial species for which the laboratory has submitted results. It is not mandatory to analyse all four strains to participate in the genomic PT.

The reports summarising the aggregated results in an anonymised form for the phenotypic EQA and the genomic PT will be published on the EURL-PH-AMR website after written consultation with the participants.

Timeline of the EURGen-Net phenotypic EQA and genomic PT 2025

Item	Timeline
Registration	25 June – 10 July 2025
Protocols made available on the EURL-PH-AMR website	September 2025
Test material shipped	Early October 2025
Deadline for result submission for phenotypic EQA	8 November 2025
Individual evaluation reports for phenotypic EQA available to the participants	January 2026
Certificate of participation in phenotypic EQA	January 2026
Survey to gather participants' feedback on phenotypic EQA	Two weeks after release of the individual evaluation reports
Deadline for result submission for genomic PT	29 November 2025
Individual evaluation reports for genomic PT available to the participants	January 2026
Certificate of participation in genomic PT	January 2026
Survey to gather participants' feedback on genomic PT	Two weeks after release of the individual evaluation reports
Final reports with aggregated data made available for consultation by the participants	April 2026

Item	Timeline
Final reports with aggregated data published on the EURL-PH-AMR website	Q3 2026

Invited participants and registration

All laboratories that are part of EURGen-Net and eligible for the grant agreement 101194806 are invited to participate.

We kindly ask all invited laboratories to complete the registration form and indicate their plans for participation in the EURGen-Net phenotypic EQA and/or genomic PT 2025. Please complete the registration form, even if you do not intend to participate, as there is an option to indicate this.

Link to the registration form:
https://ec.europa.eu/eusurvey/runner/EURGen-Net_EQA-PT_2025.

Costs for participation

There is no participation fee. However, the participating laboratories are expected to cover the costs of handling and analysing the test material associated to participation in the phenotypic EQA and genomic PT.

Data protection

Data processing is done in compliance with Article 15 of Grant Agreement Project 101194806 for the EU Reference Laboratory for Public Health on Antimicrobial Resistance (EURL-PH-AMR).

Contact

For any questions, please write to EURL-PH-AMR@ssi.dk specifying in the subject line if your request is about EURGen-Net phenotypic EQA, genomic PT or both.

Annex 2 – Protocol for the organisation and execution of the EURGen-Net phenotypic EQA and genomic PT 2025

Among the EURL-PH-AMR consortium members, DTU Food is the main responsible for the phenotypic EQA and SSI is the main responsible for the genomic PT. All steps relating to the preparation and execution of the EQA/PT, as well as communication with the participants, are carried out in coordination and agreement between DTU Food, SSI and ECDC.

1. Selection, analysis and preparation of test materials

Steps in delivery

Item	Timeline
Select candidate strains	At the latest, six months before planned shipment of strains
Test stability of phenotype and genotype	-
Select test strains	At the latest, five months before planned shipment of strains
Share test strains with reference laboratories for generating additional set of results	At the latest, five months before planned shipment of strains
Establish the expected results	At the latest, one months before planned shipment of strains
Prepare list of participants and assign codes for anonymisation of results	At the latest, three months before planned shipment of strains
Preparation and shipment of test materials	October 2025

Description

The test materials for the phenotypic external quality assessment (EQA) and genomic proficiency testing (PT) 2025 are four live bacterial cultures of Enterobacterales, *Acinetobacter baumannii* and/or *Pseudomonas aeruginosa*. Exceptionally, for the genomic PT, the organisers can provide the sequence data (in FASTQ or FASTA format, either from short-read or long-read sequencing) if laboratories cannot carry out whole genome sequencing (WGS) in their settings. The participants have the opportunity to make this request via the registration form.

No later than six months before the planned launch of the phenotypic EQA and genomic PT, the candidate strains are selected from the Statens Serum Institut (SSI), Technical University of Denmark, National Food Institute (DTU Food), and EUCAST Development Laboratory (EDL) biobanks to encompass phenotypes and genotypes of public health relevance based on contemporary epidemiological information. Selected candidate strains must be available as live cultures and accompanied by WGS data produced using Illumina and Nanopore technologies. There must be no issues regarding the Material Transfer Agreement for sharing with other laboratories, nor for uploading the WGS data on the European Nucleotide Archive (ENA). The number of candidate strains is usually double that of test strains to have a backup in case of issues with the repeatability and reproducibility of results.

SSI tests for stability of the phenotype and genotype by performing antimicrobial susceptibility testing (AST, by broth microdilution and disk diffusion) and WGS (by Illumina) on cultures at Day 0 and Day 5, whereby the Day 0 culture is obtained after thawing from cryopreservation and the Day 5 culture is obtained after daily subcultures. Based on these results, the test strains are chosen. The test strains are shared with additional laboratories: SSI and DTU Food serve as reference laboratories for the WGS, and DTU Food and EDL serve as reference laboratories for the AST. Results from the reference laboratories are used to define the EQA/PT expected results.

Results generated include:

- AST by broth microdilution and disk diffusion according to EUCAST guidance, and interpretation of minimum inhibitory concentration and inhibition zone diameter results according to the most recent EUCAST clinical breakpoint tables;
- species identification and typing information (specified in the section ‘Instructions for completion’ of the main document) conducted on Illumina- and Nanopore-generated WGS data using the methods routinely applied in the two laboratories. The methods to obtain the expected results will be described in detail in the final reports (i.e. reports with aggregated, anonymised data described in the section ‘Reporting of results’ of the main document).

For preparation and shipment of test materials, details are described in the section ‘Distribution’ of the main document.

2. Development of supporting documents including all information to be shared with participants and reports

Steps in delivery

Item	Timeline
Prepare and send information letter and registration form, along with deadline for registration	At the latest, three months before planned shipment of strains. Registration is open for two weeks.
Prepare and upload the EQA/PT protocols and manuals for submission of results to the EURL-PH-AMR website.	At the latest, one month before planned shipment of strains
Check submissions of results a few days before the deadline and send reminders if needed	Deadlines: - for phenotypic EQA: 8 November 2025; - for genomic PT: 29 November 2025
Prepare and send individual evaluation reports. Inform participants that technical follow-up and support to identify corrective measures is available from the EURL-PH-AMR upon request	At the latest, three months after submission deadline
Prepare and send certificate of participation	At the time of release of individual evaluation reports
Prepare and send surveys to gather participants' feedback	Within two to three weeks after release of the individual evaluation reports
Prepare and share reports with aggregated, anonymised data for consultation with the participants	Consultation period is two weeks. The consultation should be finalised within five months after the submission deadline.
Organise a webinar to present the aggregated, anonymised results of the EURGen-Net phenotypic EQA and genomic PT	At the latest, five months after the submission deadline
Publish final revised reports on the EURL-PH-AMR website and inform all stakeholders	End of April 2026

Description

Details on the steps above are described in the main document.

3. Set-up and management of web-based tools for submission of results

Steps in delivery

Item	Timeline
Set-up and test of the web-based tools for submission of results	Work starts at the latest three months before planned shipment of strains
Launch of the web-based tools for submission of results	At the latest, on the day of shipment of strains
Manage the web-based tool	Ongoing during the full EQA/PT 2025 cycle

Description

The participants will be asked to upload information on used methods and obtained results to web-based tools, including a system developed and hosted at DTU Food for the phenotypic EQA and a submission page implemented using the EU Survey tool or similar software for the genomic PT. Access to the web-based tools is password-protected, and each participant will receive their own login details.

The web-based tools will allow each participant to submit one set of phenotypic results and one set of genomic results per test strain, irrespective of the methods used.

The web-based tools will be thoroughly tested prior to launch and will be regularly monitored and managed as needed during the full EQA/PT 2025 cycle.

Annex 3. List of antimicrobials for the EURGen-Net phenotypic EQA 2025

Escherichia coli

Amikacin	AMK
Aztreonam	ATM
Aztreonam-avibactam (fixed 4)	AZA
Cefiderocol	FDC
Cefotaxime	CTX
Ceftazidime	CAZ
Ceftazidime-avibactam (fixed 4)	CZA
Ceftolozane-tazobactam (fixed 4)	CZT
Ciprofloxacin	CIP
Colistin	COL
Ertapenem	ETP
Gentamicin	GEN
Imipenem	IPM
Imipenem-relebactam (fixed 4)	IMR
Levofloxacin	LVX
Meropenem	MEM
Meropenem-vaborbactam (fixed 8)	MEV
Piperacillin-tazobactam (fixed 4)	TZP
Tigecycline	TGC
Tobramycin	TOB
Trimethoprim-sulfamethoxazole (ratio 1:19)	SXT
Fosfomycin	FOS

Klebsiella pneumoniae

Amikacin	AMK
Aztreonam	ATM
Aztreonam-avibactam (fixed 4)	AZA
Cefiderocol	FDC
Cefotaxime	CTX
Ceftazidime	CAZ
Ceftazidime-avibactam (fixed 4)	CZA
Ceftolozane-tazobactam (fixed 4)	CZT
Ciprofloxacin	CIP
Colistin	COL
Ertapenem	ETP
Gentamicin	GEN
Imipenem	IPM
Imipenem-relebactam (fixed 4)	IMR
Levofloxacin	LVX
Meropenem	MEM
Meropenem-vaborbactam (fixed 8)	MEV
Piperacillin-tazobactam (fixed 4)	TZP
Tobramycin	TOB
Trimethoprim-sulfamethoxazole (ratio 1:19)	SXT

Acinetobacter baumannii

Amikacin	AMK
Cefiderocol	FDC
Ciprofloxacin	CIP
Colistin	COL
Gentamicin	GEN
Imipenem	IPM
Levofloxacin	LVX
Meropenem	MEM
Tobramycin	TOB
Trimethoprim-sulfamethoxazole (ratio 1:19)	SXT

Pseudomonas aeruginosa

Amikacin	AMK
Aztreonam	ATM
Cefiderocol	FDC
Ceftazidime	CAZ
Ceftazidime-avibactam (fixed 4)	CZA
Ceftolozane-tazobactam (fixed 4)	CZT
Ciprofloxacin	CIP
Colistin	COL
Imipenem	IPM
Imipenem-relebactam (fixed 4)	IMR
Levofloxacin	LVX
Meropenem	MEM
Meropenem-vaborbactam (fixed 8)	MEV
Piperacillin-tazobactam (fixed 4)	TZP
Tobramycin	TOB