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External quality assessment for identification, antimicrobial susceptibility testing and molecular typing of *Neisseria meningitidis*, 2026

ECDC MONITORING

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On behalf of the IBDLabNet surveillance network

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Abbreviations

AST	antimicrobial susceptibility testing
BIGSdb	Bacterial Isolate Genome Sequence Database
CSF	cerebrospinal fluid
Ct	cycle threshold
DNA	deoxyribonucleic acid
ECDC	European Centre for Disease Prevention and Control
EMGM	European Meningococcal and Haemophilus Disease Society
EQA	external quality assessment
EUCAST	European Committee on Antimicrobial Susceptibility Testing
EU/EEA	European Union/European Economic Area
IBDLabNet	Invasive Bacterial Diseases Laboratory Network
IMD	invasive meningococcal disease
MALDI-TOF	matrix-assisted laser desorption ionisation time-of-flight
MIC	minimum inhibitory concentration
N. meningitidis	*Neisseria meningitidis*
PCR	polymerase chain reaction
REDCap	Research Electronic Data Capture
WGS	whole-genome sequencing

Executive summary

Invasive meningococcal disease remains a major public health concern because of its rapid progression, severity, outbreak potential and relevance for vaccine-preventable disease surveillance. High-quality laboratory capacity is essential to ensure timely detection, reliable serogroup determination, antimicrobial susceptibility testing and genomic characterisation of *Neisseria meningitidis*, including for culture-negative cases.

This external quality assessment was organised within the IBDLabNet framework to assess current European Union/European Economic Area (EU/EEA) laboratory capacity for the diagnosis and characterisation of *N. meningitidis* in both non-culture and culture-based settings, and to identify areas requiring further harmonisation or technical support. The exercise included a shared non-culture panel and an optional meningococcal culture panel. Samples were shipped in December 2025, the online response form was made available in January 2026, and the submission deadline was 15 April 2026.

A total of 34 EU/EEA laboratories from 24 countries were included in the EU/EEA analysis. All 34 EU/EEA laboratories received the non-culture panel, and 32/34 submitted at least one non-culture sample result in REDCap. The meningococcal culture panel was requested by 26 laboratories overall, with 25 EU/EEA laboratories providing analysable isolate-level results.

Overall, the exercise showed strong performance for culture-based meningococcal identification and serogroup determination. All laboratories with analysable results correctly identified both cultured isolates as *N. meningitidis*, and serogroup assignment was highly concordant. AST uptake was high among laboratories providing culture-panel results. Comparative MIC analysis showed higher agreement for cefotaxime and ciprofloxacin, while greater dispersion was observed for penicillin G, amoxicillin, rifampicin and ceftriaxone where reported. Complementary European Committee on Antimicrobial Susceptibility Testing (EUCAST)-based analysis showed that ciprofloxacin resistance in N1 sample was recognised by 19/21 laboratories reporting a numeric ciprofloxacin MIC, while cefinase/beta-lactamase positivity in N2 sample was reported by 10/25 isolate responders and by 10/12 laboratories providing an interpretable Yes/No result.

Whole-genome sequencing (WGS) was reported by approximately two-thirds of laboratories with analysable meningococcal culture-panel results. Among WGS-positive submissions, reporting completeness was high for core surveillance outputs such as sequence type, clonal complex and major antigenic markers. More specialised outputs, including some resistance-associated loci and extended nomenclature fields, were less consistently reported.

By contrast, performance on non-culture meningococcal samples was more heterogeneous. Correct pathogen detection was lower than for cultured isolates, and the main error pattern was false-negative reporting rather than misidentification as another pathogen. Among laboratories that reported a serogroup result, the serogroup was usually assigned correctly (approximately 72–74% of typed submissions). However overall sample-level success remained lower because many laboratories did not report a serogroup, in addition to those that failed to detect the pathogen. These findings indicate that non-culture molecular workflows remain the main area of variability across the participating network.

The EQA confirms that EU/EEA laboratories participating in IBDLabNet have strong capacity for isolate-based meningococcal confirmation and characterisation, high AST uptake and substantial WGS-supported surveillance capacity. Priority areas for improvement include strengthening non-culture molecular detection, improving completeness of serogroup assignment from clinical material, maintaining standardised MIC reporting, improving recognition and reporting of resistance-relevant phenotypes, and further harmonising WGS-derived outputs.

The design of the exercise was appropriate to document current practice and identify surveillance-relevant gaps across the network. Interpretation should take into account the limited number of meningococcal samples, the absence of a negative non-culture sample, optional participation in the culture component, the use of participant modal MICs for comparative AST analysis, and the descriptive nature of the WGS assessment.

Recommended next steps include continued regular EQA rounds, targeted feedback to participating laboratories, improved collection of methodological information for non-culture workflows, focused training on molecular detection and serogrouping from non-culture material, continued support for standardised AST reporting, and progressive harmonisation of WGS-based reporting. These actions would further strengthen the quality and comparability of IMD surveillance data across the EU/EEA.

1 Introduction

Invasive meningococcal disease, caused by *N. meningitidis*, remains an important cause of severe bacterial infection in Europe despite its relatively low incidence compared with other invasive bacterial diseases [1]. In 2023, 1 895 confirmed IMD cases were reported in 30 EU/EEA countries, with the highest notification rates observed in infants under one year of age, followed by children aged 1–4 years and adolescents and young adults aged 15–24 years [1]. Beyond the classical presentations of meningitis and septicaemia, IMD is now recognised as having a broader clinical spectrum that includes extra-meningeal manifestations, which may complicate diagnosis and delay appropriate management [2,3].

Laboratory confirmation and characterisation are central to IMD surveillance because they support case confirmation, serogroup monitoring, outbreak detection, antimicrobial susceptibility surveillance and public health decision-making, including vaccination strategies [1-4]. Across the EU/EEA, surveillance of invasive bacterial diseases relies on coordinated contributions from clinical microbiology laboratories, national reference laboratories and ECDC disease networks [4]. Within this framework, harmonised laboratory practices are essential to ensure comparability of data between countries and over time.

The present EQA was organised within IBDLabNet on behalf of ECDC as part of the first-year implementation of the EU invasive bacterial diseases laboratory network activities [4,5]. The exercise was designed to assess the capacity of participating laboratories to detect and characterise *N. meningitidis* from both non-culture and culture-based materials, including species identification, serogroup determination, AST, and, where available, WGS-derived characterisation. In addition, the exercise aimed to describe the routine methods currently used by participating laboratories and to identify areas where further harmonisation, targeted support or training may be beneficial [5].

This EQA addressed a surveillance-oriented need that is not fully covered by routine national practice or by narrower method-specific proficiency schemes, namely the integrated assessment of laboratory performance across the main microbiological dimensions relevant for meningococcal surveillance in the EU/EEA context: molecular detection from non-culture material, culture-based identification and serogrouping, AST, and optional WGS-based characterisation [1,4,5]. The specific objectives of this EQA were therefore to: (i) assess laboratory performance for the detection and identification of *N. meningitidis* in shared non-culture and culture-based samples; (ii) assess the concordance of meningococcal serogroup determination; (iii) describe AST practices, compare reported MICs across laboratories, and provide complementary EUCAST-based phenotypic readings for predefined informative resistance-associated combinations; and (iv) describe the uptake and outputs of WGS among laboratories performing sequencing.

2 Study design and methods

Organisation of the scheme

The EQA was organised by the IBDLabNet coordination team at Institut Pasteur Paris, on behalf of ECDC, in accordance with the first-year workplan and EQA implementation plan of the network. ECDC provided oversight and approval of the invitation documents, protocols, safety instructions and shipment documentation, while the organising team was responsible for panel design, preparation, quality control, shipment, data capture, analysis and reporting. The overall structure of the scheme followed ECDC principles for EU-level EQAs for public health microbiology laboratories [6].

Participants and recruitment

Invitation letters and pre-registration forms were disseminated through the ECDC disease network to national focal points and operational contact points, who could participate directly or relay the invitation to relevant national laboratories. A total of 34 laboratories from 24 countries registered for the exercise. All registered laboratories completed the registration process; response completeness varied by module, sample and variable.

Panel design

The EQA combined one shared non-culture panel and optional culture panels. The non-culture panel consisted of six lyophilised samples distributed to all participating laboratories. All six non-culture samples were positive samples; no negative sample was included in this edition of the scheme. The culture component consisted of up to six isolates in total, corresponding to two isolates each for *N. meningitidis*, *Haemophilus influenzae* and *Streptococcus pneumoniae*, according to the panels requested by participants at pre-registration. All 34 laboratories received the non-culture panel, 26 received the meningococcal culture panel, 23 the *H. influenzae* culture panel, and 24 the pneumococcal culture panel. In the EU/EEA aggregate analysis, 25 laboratories provided responses for the meningococcal culture isolates.

This pathogen-specific report presents the meningococcal components of the shared EQA scheme, namely the *N. meningitidis* non-culture targets and the two meningococcal culture isolates included in the exercise.

Distribution, testing window and instructions

Shipments started on 3 December 2025 and continued until 17 December 2025. The online response form was made available on 12 January 2026 and the submission deadline was 15 April 2026. Participating laboratories were instructed to apply only the methods routinely available in their laboratories. Non-culture samples were to be reconstituted according to the instructions provided in the shipment documents, whereas cultured isolates were shipped in Amies charcoal transport swabs and had to be re-isolated on appropriate media upon receipt. Panels were shipped and handled according to the operational protocol approved for the EQA [5].

Laboratory procedures assessed

For non-culture samples, laboratories were asked to perform routine pathogen-specific molecular detection and, when positive and feasible locally, molecular group determination and additional typing. Ct values for species detection and, where applicable, for group determination were recorded. For cultured isolates, laboratories were asked to perform routine identification, serogrouping, AST and molecular typing. Acceptable approaches included routine phenotypic methods, MALDI-TOF, validated molecular methods, and WGS where available. For AST, laboratories were asked to report the method used, the standard used for interpretation, and raw MIC values when determined. Most participants reported the use of EUCAST breakpoints [9].

Whole-genome sequencing

WGS was optional. Laboratories performing WGS were asked to report the sequencing technology used, whether assembly had been performed, and the genomic typing outputs routinely available in their practice. Because no full internal truth table had been established for all genomic fields across all samples, WGS analyses were primarily descriptive. A minimal WGS analysis was conducted for uptake, technology and assembly practices, and an extended descriptive analysis was performed for variables actually reported by participants, with denominators stated for each variable.

Data capture and confidentiality

Study data were collected and managed using REDCap hosted at Institut Pasteur, Paris [7,8]. Separate modules captured laboratory information, non-culture results and culture-set results. Laboratories were pseudonymised using laboratory identifiers. Aggregated outputs in the report are presented in pseudonymised form. Full laboratory identification remained available only to the organising centre and ECDC.

Expected results and performance assessment

Expected species identification and serogroup results were predefined by the organising centre on the basis of the panel composition. For the meningococcal culture panel, the expected serogroups were W and Y, and the isolates were selected to include relevant resistance-associated phenotypes. No predefined target MIC values were assigned for the exercise. Accordingly, identification and serogroup determination were assessed against the expected results defined for each sample, whereas AST results were analysed comparatively across participants using modal MICs, with complementary phenotype recognition summaries for predefined informative resistance-associated combinations.

In line with the exercise protocol, agreement for MIC results was assessed against the modal participant result, and results within one doubling dilution of the modal MIC were considered concordant for comparative analyses. For predefined informative resistance-associated combinations, a complementary descriptive EUCAST v16.0 reading was added where relevant; this was not applied as a formal scoring framework for all antibiotic-isolate combinations.

Ct values were analysed descriptively because no predefined target Ct values had been assigned to the panel. Results are presented as counts and percentages using the available denominator for each sample and variable. Because not all laboratories requested all culture panels and not all participants performed all methods, denominators vary across analyses and are stated explicitly.

3 Results

3.1 Participation and laboratory methods

A total of 34 EU/EEA laboratories from 24 countries were included in the EU/EEA analysis. All 34 EU/EEA laboratories received the non-culture panel by design. Of these, 32/34 submitted at least one non-culture sample result in REDCap. Performance analyses for individual non-culture samples used the number of laboratories with an interpretable response for that sample as the denominator.
Overall, 26 laboratories requested and received the meningococcal culture panel; 25 EU/EEA laboratories provided responses for N1 and N2 and were included in the aggregate analysis.

Reported routine methods showed substantial heterogeneity across laboratories. For meningococcal detection in non-culture material, 16/34 laboratories (47.1%) reported using *ctrA*, 12/34 (35.3%) reported *sodC*, and 8/34 (23.5%) reported other molecular targets; *porA* was not reported as a routine non-culture detection target. Multiple targets could be reported by the same laboratory.

For culture-based meningococcal identification, molecular methods were reported by 15/25 laboratories (60.0%), MALDI-TOF by 11/25 (44.0%) and other phenotypic methods by 10/25 (40.0%). For serogroup determination on cultured isolates, phenotypic methods were reported by 17/25 laboratories (68.0%), molecular methods by 16/25 (64.0%) and other methods by 2/25 (8.0%).

AST methods also varied, although gradient-based MIC testing was predominant. E-test was reported by 20/25 laboratories (80.0%), broth microdilution by 2/25 (8.0%), antimicrobial gradient methods by 2/25 (8.0%) and agar dilution by 1/25 (4.0%). EUCAST was the main interpretive standard, reported by 22/25 laboratories (88.0%).

Among laboratories reporting WGS for meningococcal isolates, Illumina was the most frequently used platform, reported by 14/16 laboratories (87.5%). Assembly was reported as performed by 13/16 WGS-positive laboratories (81.2%). These results describe the range of methods reported across molecular detection, serogrouping, AST and WGS workflows.

Table 1. Overview of aggregated EU/EEA results for the meningococcal component of the EQA

EQA component	Sample/isolate	Expected result	Denominator	Correct result, n/N (%)
Non-culture pathogen identification	NC1	*N. meningitidis*	32	22/32 (68.8%)
Non-culture serogroup assignment among all responders	NC1	Serogroup B	32	13/32 (40.6%)
Non-culture serogroup assignment among typed submissions	NC1	Serogroup B	18	13/18 (72.2%)
Non-culture pathogen identification	NC4	*N. meningitidis*	32	26/32 (81.2%)
Non-culture serogroup assignment among all responders	NC4	Serogroup W	32	14/32 (43.8%)
Non-culture serogroup assignment among typed submissions	NC4	Serogroup W	19	14/19 (73.7%)
Culture-based species identification	N1	*N. meningitidis*	25	25/25 (100%)
Culture-based serogroup assignment	N1	Serogroup W	25	23/25 (92.0%)
Culture-based species identification	N2	*N. meningitidis*	25	25/25 (100%)
Culture-based serogroup assignment	N2	Serogroup Y	25	22/25 (88.0%)
AST uptake	N1	MIC reported	25	23/25 (92.0%)
AST uptake	N2	MIC reported	25	23/25 (92.0%)
WGS uptake	N1	WGS performed	25	16/25 (64.0%)
WGS uptake	N2	WGS performed	25	16/25 (64.0%)

Denominators vary according to the number of laboratories providing an interpretable result for the relevant sample or isolate, and according to whether group assignment was reported.

3.2 Performance on non-culture samples

The meningococcal non-culture component comprised two positive samples: NC1, expected to contain *N. meningitidis* serogroup B, and NC4, expected to contain *N. meningitidis* serogroup W. Performance was analysed using the available denominator for each sample and variable.

NC1

For NC1, 32 laboratories provided an interpretable pathogen response. Of these, 22/32 (68.8%) correctly identified *N. meningitidis*, while 10/32 (31.3%) reported a negative result. No laboratory reported another pathogen or a non-conclusive result for this sample.

Serogroup information was available from 18 laboratories. Thirteen of 18 laboratories (72.2%) correctly reported serogroup B among typed submissions, corresponding to 13/32 (40.6%) of all laboratories with an interpretable pathogen response. The remaining type calls consisted of serogroup X in 2/18 laboratories (11.1%) and "None of the above" in 3/18 laboratories (16.7%).

Ct values for species detection were available from 19 laboratories and showed a median of 34.0 (IQR: 33.1–34.9). Ct values for serogroup determination were available from 14 laboratories and showed a median of 35.7 (IQR: 35.0–36.0).

NC4

For NC4, 32 laboratories provided an interpretable pathogen response. Of these, 26/32 (81.2%) correctly identified *N. meningitidis*, while 6/32 (18.8%) reported a negative result.

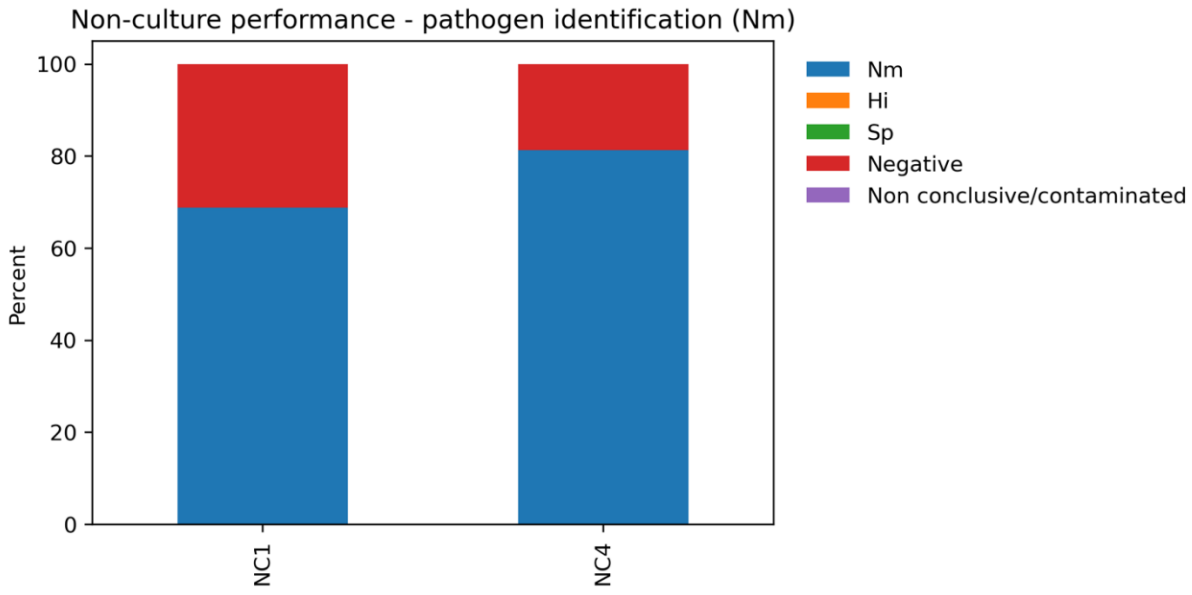
Meningococcal serogroup information was reported by 19 laboratories for NC4. Fourteen of 19 laboratories (73.7%) correctly identified serogroup W among typed submissions, corresponding to 14/32 (43.8%) of all responders. The remaining type calls were serogroup X in 2/19 laboratories (10.5%), serogroup B in 1/19 (5.3%), serogroup C in 1/19 (5.3%) and "None of the above" in 1/19 (5.3%).

Ct values for species detection were available from 20 laboratories and showed a median of 32.7 (IQR: 30.9–34.3). Ct values for group determination were available from 15 laboratories and showed a median of 34.0 (IQR: 30.4–35.7).

Overall non-culture performance

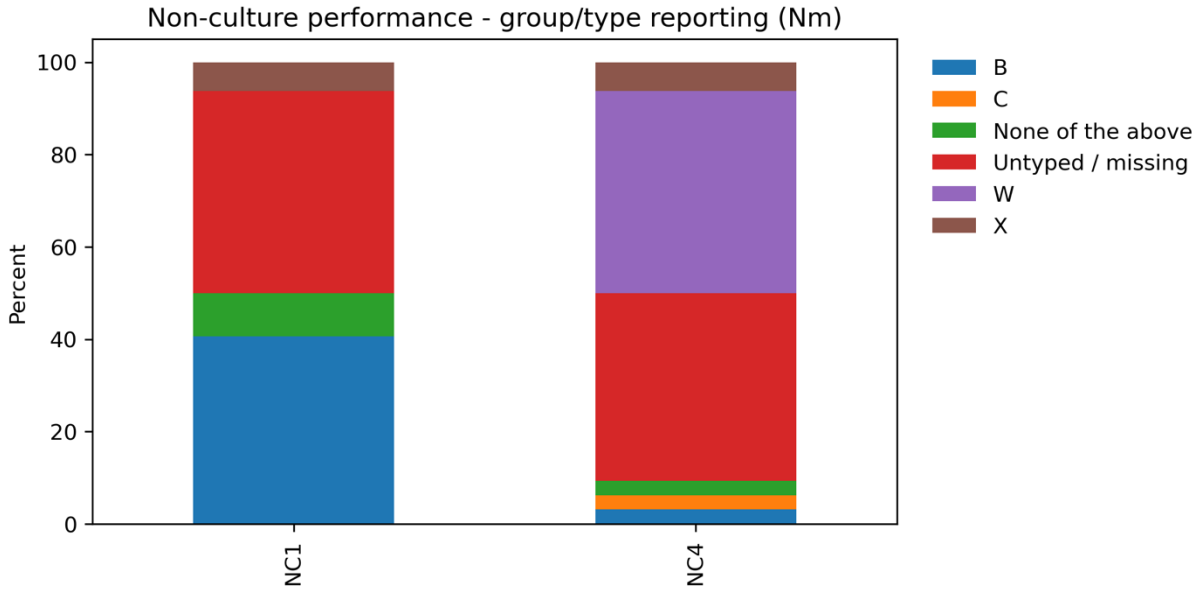
Across the two meningococcal non-culture samples, the proportion of correct pathogen identification was 68.8% for NC1 and 81.2% for NC4. Among laboratories reporting a serogroup result, the proportion of correct serogroup assignment was 72.2% for NC1 and 73.7% for NC4. When expressed against all laboratories with an interpretable pathogen response, the proportion of correct serogroup assignment was 40.6% for NC1 and 43.8% for NC4.

Figure 1. Performance on meningococcal non-culture samples: pathogen identification for NC1 and NC4 (*N. meningitidis* expected in both samples)



Percentages are based on laboratories providing an interpretable pathogen response (NC1: n=32; NC4: n=32).

Figure 2. Performance on meningococcal non-culture samples: serogroup reporting for NC1 and NC4 (expected: serogroup B for NC1 and serogroup W for NC4)



Percentages are based on all laboratories providing an interpretable pathogen response (NC1: n=32; NC4: n=32); untyped or missing serogroup results are shown as a separate category.

3.3 Performance on cultured isolates

The meningococcal culture panel included two isolates: N1 (expected serogroup W) and N2 (expected serogroup Y).

N1

A total of 25 EU/EEA laboratories reported a response for N1. All 25/25 laboratories (100%) correctly identified the isolate as *N. meningitidis*. Serogroup information was reported by all 25 laboratories, and 23/25 (92.0%) correctly assigned serogroup W. The two discordant results consisted of one report of serogroup C and one report of "None of the above".

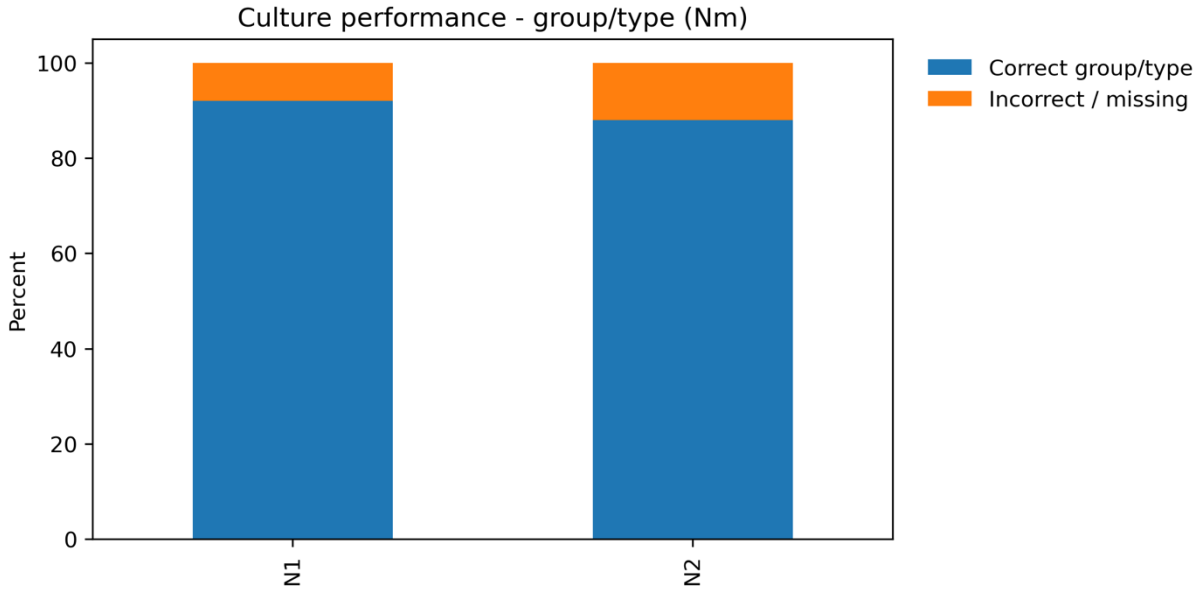
N2

A total of 25 EU/EEA laboratories reported a response for N2. All 25/25 laboratories (100%) correctly identified the isolate as *N. meningitidis*. Serogroup information was reported by 23 laboratories, and 22/23 (95.7%) correctly assigned serogroup Y, corresponding to 22/25 (88.0%) when expressed against all responding laboratories. The only discordant grouped result was "None of the above".

Overall culture-based performance

Across the two cultured meningococcal isolates, correct species identification was reported by 25/25 laboratories for both N1 and N2. Correct serogroup assignment among all responding laboratories was 23/25 (92.0%) for N1 and 22/25 (88.0%) for N2.

Figure 3. Culture-based serogroup performance for meningococcal isolates N1 and N2 (expected: serogroup W for N1 and serogroup Y for N2)



Percentages are based on all laboratories reporting a result for the isolate (N1: n=25; N2: n=25).

3.4 Antimicrobial susceptibility testing

AST uptake was high for both meningococcal isolates. MIC testing was reported for 23/25 laboratories (92.0%) for N1 and 23/25 (92.0%) for N2 in the final analysed EU/EEA dataset. As predefined target MIC values were not assigned for this exercise, MIC reproducibility was assessed comparatively against the participant modal MIC, with concordance defined as a result within one doubling dilution of the modal MIC. In addition, EUCAST v16.0 criteria were applied to predefined informative resistance-associated isolate-antibiotic combinations as a complementary descriptive reading of expected phenotype recognition.

N1

For N1, the participant modal MICs for the selected antibiotics were 1.0 for penicillin G, 1.0 for amoxicillin, 0.032 for cefotaxime, 0.004 for ceftriaxone, 0.064 for ciprofloxacin and 0.016 for rifampicin.

Concordance within one doubling dilution of the modal MIC was:

- 88.9% for penicillin G;
- 90.0% for amoxicillin;
- 90.0% for cefotaxime;
- 58.3% for ceftriaxone;
- 86.4% for ciprofloxacin; and
- 54.5% for rifampicin.

For the predefined informative phenotype, ciprofloxacin resistance was identified in 19/22 laboratories (86.4%) with an interpretable numeric ciprofloxacin MIC.

N2

For N2, the participant modal MICs were 8.0 for penicillin G, 4.0 for amoxicillin, 0.016 for cefotaxime, 0.002 for ceftriaxone, 0.004 for ciprofloxacin and 0.016 for rifampicin.

Concordance within one doubling dilution of the participant modal MIC was:

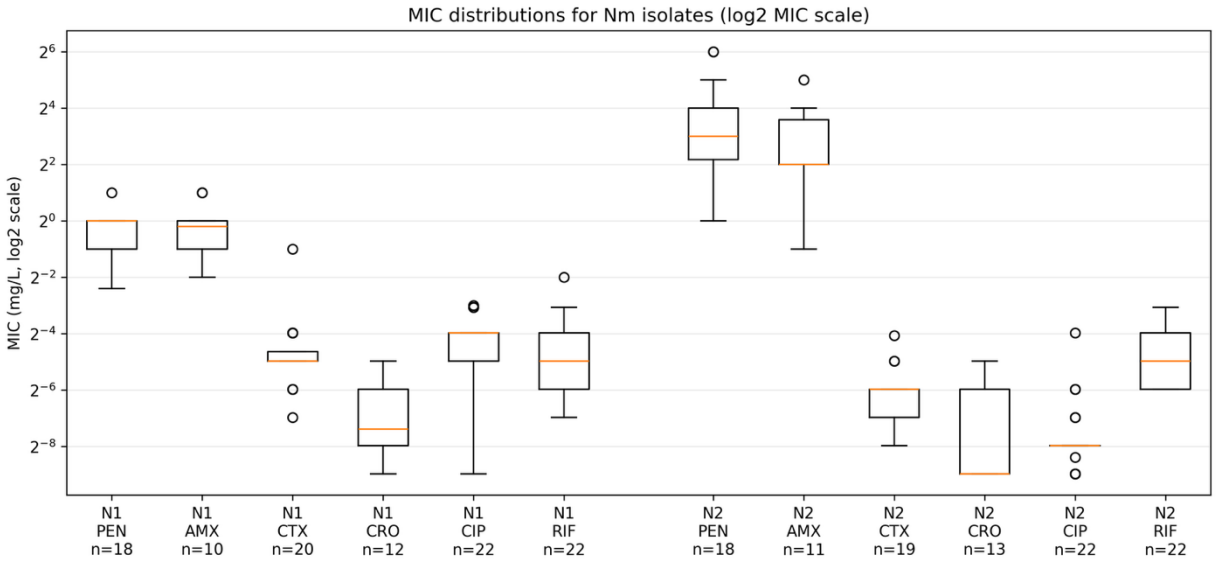
- 66.7% for penicillin G;
- 63.6% for amoxicillin;
- 84.2% for cefotaxime;
- 61.5% for ceftriaxone;
- 86.4% for ciprofloxacin; and
- 68.2% for rifampicin.

Cefinase/beta-lactamase positivity was reported by 10/25 laboratories (40.0%) when all isolate responders were used as the denominator, and by 10/12 laboratories (83.3%) among laboratories providing an interpretable Yes/No result.

Overall AST results

Overall, MIC agreement was higher for cefotaxime and ciprofloxacin than for penicillin G, amoxicillin and rifampicin. For N1 ciprofloxacin, 19/22 numeric MIC results were categorised as resistant. For N2 cefinase/beta-lactamase, 10/25 isolate responders reported positivity, corresponding to 10/12 among laboratories with a Yes/No result.

Figure 4. Distribution of reported MIC values for selected antibiotics for meningococcal isolates N1 and N2, displayed on a log2 MIC scale



Only isolate–antibiotic combinations with available numeric MIC values are shown. The number below each antibiotic label indicates the number of numeric MIC values included for that isolate–antibiotic combination.

3.5 Whole-genome sequencing uptake and reported outputs

WGS uptake was 16/25 laboratories (64.0%) for N1 and 16/25 (64.0%) for N2.

Among WGS-positive laboratories, reporting completeness was 32/32 (100%) for clonal complex, sequence type, VR1, VR2 and fetA at pooled pathogen level. LINcode was reported in 16/32 submissions (50.0%). Resistance-associated loci were reported in 28/32 submissions (87.5%) for penA, 28/32 (87.5%) for gyrA and 26/32 (81.3%) for rpoB.

The isolate-specific WGS completeness results for N1 and N2 were identical:

- 16/16 (100%) for clonal complex;
- 16/16 (100%) for sequence type;
- 16/16 (100%) for VR1;
- 16/16 (100%) for VR2;
- 16/16 (100%) for fetA;
- 8/16 (50.0%) for LINcode;
- 14/16 (87.5%) for penA;
- 13/16 (81.3%) for rpoB; and
- 14/16 (87.5%) for gyrA.

Figure 5. Uptake of whole-genome sequencing for meningococcal isolates N1 and N2 (N1: n=25; N2: n=25)

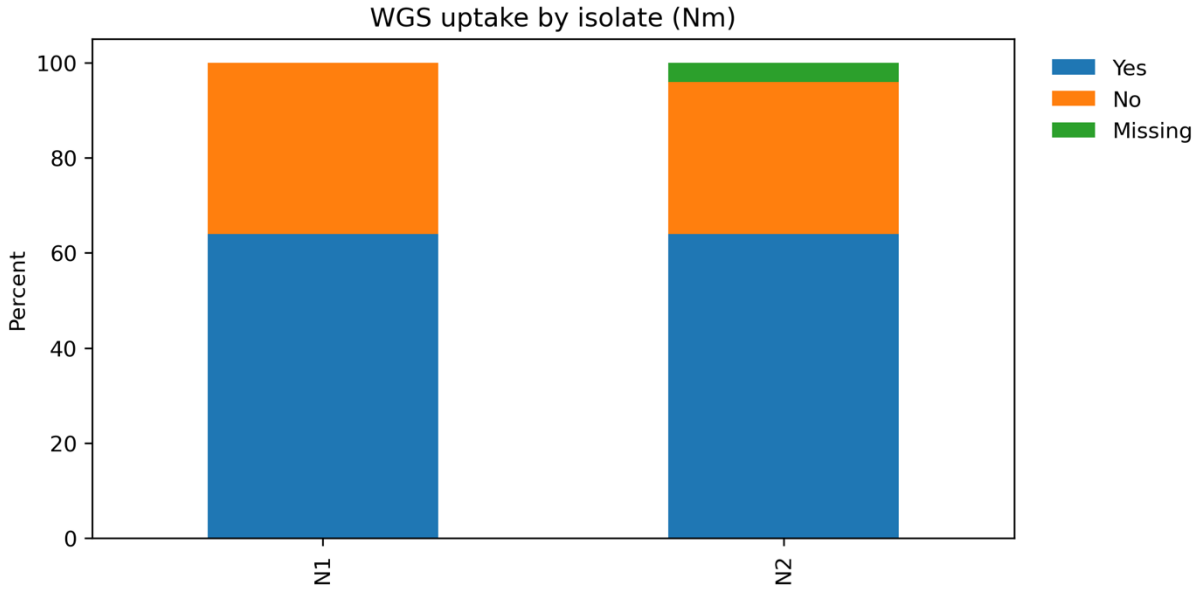
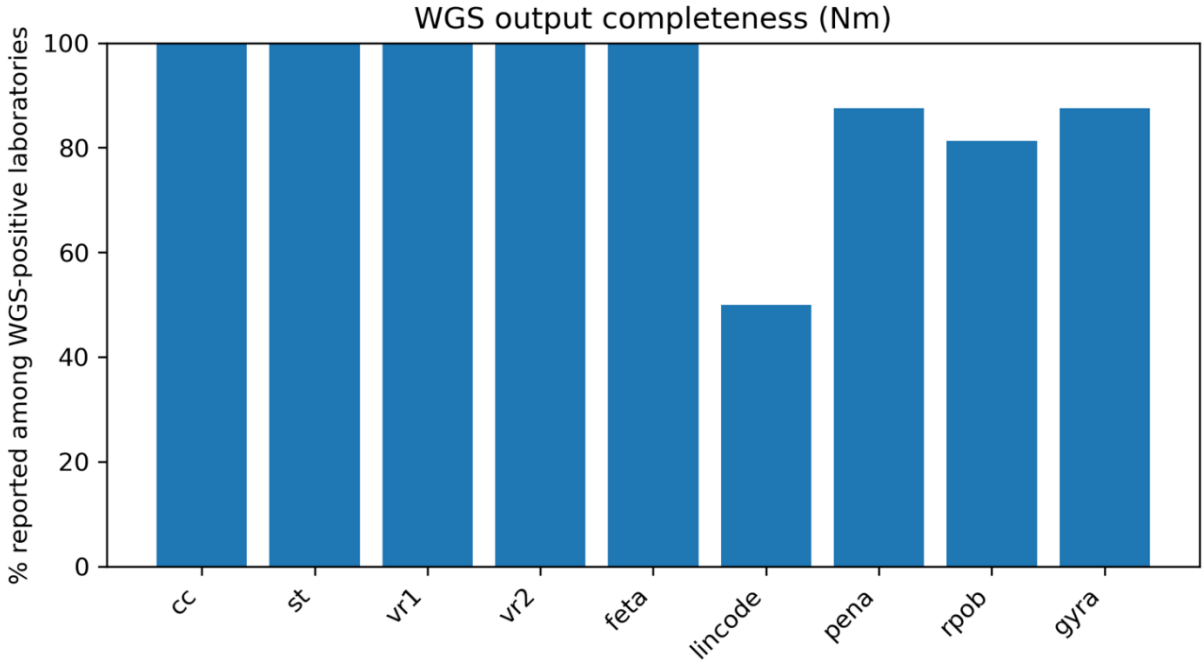


Figure 6. Completeness of reported WGS outputs among WGS-positive submissions for meningococcal isolates



Percentages are based on WGS-positive submissions only (pooled N1 and N2 submissions: n=32; per isolate: n=16).

4 Discussion

This EQA provides an overview of current EU/EEA laboratory capacity for the detection, identification, serogroup determination, AST and genomic characterisation of *N. meningitidis*. Overall, the results show strong and consistent performance for culture-based meningococcal identification, high uptake of AST among laboratories providing analysable culture-panel responses, and substantial implementation of WGS in routine or reference workflows. In contrast, performance on non-culture samples was more heterogeneous, particularly for pathogen detection and complete serogroup reporting. This general pattern is consistent with previous European meningococcal EQA exercises and with the broader role of EQA in documenting inter-laboratory variability and identifying areas requiring harmonisation or targeted support [5,6,10–14].

The 2026 meningococcal EQA should be interpreted in continuity with earlier exercises performed in European laboratory networks. Direct comparison must remain cautious because the 2009, 2011, 2012 and 2014 ECDC IBDLabNet schemes, the 2022 EMGM interlaboratory study and the present EQA differed in panel composition, participant networks, matrices, expected outputs and scoring approaches [10–14]. Nevertheless, several recurring observations emerge across exercises. Earlier ECDC-funded schemes showed that laboratories differed not only in analytical performance but also in the extent of meningococcal characterisation performed and reported, especially for molecular typing and non-culture testing [10–13]. The 2022 EMGM study similarly highlighted that performance was generally strong for typical cultured isolates, but more variable for atypical *Neisseria* and non-culture samples [14]. Taken together, these exercises support the continued value of repeated EQA rounds as tools for benchmarking, documenting progress and identifying persistent technical and reporting gaps relevant to surveillance.

Culture-based species identification represented the strongest component of the present exercise. All laboratories reporting analysable results for N1 and N2 samples correctly identified the isolates as *N. meningitidis*, and serogroup assignment was also highly concordant. These findings indicate robust routine capacity for core meningococcal identification once a viable isolate is available. This is particularly important because serogroup data remain central to IMD surveillance, outbreak investigation and vaccine-prevention policy [1,4]. The findings are also consistent with earlier European exercises. In the 2014 ECDC EQA, culture-based meningococcal characterisation was generally stronger than non-culture molecular characterisation [10]. In the 2022 EMGM interlaboratory study, MenY, MenW and MenC isolates were correctly identified by all 15 participating laboratories, whereas *Neisseria bergeri* was correctly identified by 60%, or by 93% when identification as non-*N. meningitidis* or *Neisseria* sp. was considered acceptable [14]. The present results therefore support sustained high proficiency for culture-based identification of typical *N. meningitidis* isolates, while also underlining the educational value of including atypical or closely related *Neisseria* species in future exercises.

Non-culture testing showed lower and more variable performance. For both meningococcal non-culture samples, the main error pattern was false-negative reporting rather than misidentification as another pathogen. Among laboratories that reported a serogroup result, typing accuracy was reasonably similar between NC1 and NC4 samples. However, when expressed against all laboratories with an interpretable pathogen response, correct serogroup assignment was lower because several laboratories did not report a serogroup result. This distinction is important for surveillance interpretation: once laboratories proceed to serogrouping, performance is generally acceptable, but overall sample-level completeness remains limited by the combined effect of false-negative pathogen detection and incomplete group determination. Similar observations were reported in earlier European EQAs, where non-culture meningococcal detection and genogrouping were more variable than culture-based characterisation [10–14].

The difference observed between NC1 and NC4 samples may partly reflect analytical sensitivity requirements. Species-level Ct values were higher for NC1 than for NC4, suggesting a lower detectable target concentration or a more challenging amplification profile for NC1. Serogroup Ct values were also high, particularly for NC1. These findings should not be interpreted as direct quantitative comparisons across laboratories, because Ct values are assay-dependent and influenced by extraction method, platform, reagents and positivity thresholds. In addition, variability related to reconstitution of lyophilised material and possible degradation during transport cannot be excluded as contributing factors. Comparison of Ct distributions across the full non-culture panel may help distinguish intrinsic sample characteristics from broader technical variability, although such comparisons remain descriptive because different pathogens and assays are involved. Nevertheless, the results suggest that NC1 appeared to test a relatively low-signal range of routine molecular workflows. This interpretation is consistent with previous exercises. In the 2014 ECDC EQA, 83% of laboratories detected *N. meningitidis* in non-culture samples, whereas genogroup confirmation was lower, at 63–73% depending on the sample [10]. In the 2022 EMGM non-culture panel, MenB and MenW samples were correctly identified by 88% of participants, while a non-groupable *N. meningitidis* sample was identified by only 56% [14]. Together, these findings indicate that non-culture meningococcal molecular detection and group determination remain key areas for harmonisation and training.

Variation in molecular targets may also have contributed to the observed differences. In the present exercise, laboratories reported the routine use of several meningococcal molecular targets, including *ctrA*, *sodC* and other locally used assays. Target choice can influence performance because capsule-associated targets may be affected by genetic variation, capsule-null loci or assay design, whereas alternative species targets may differ in sensitivity

and specificity [15–17]. The *sodC* target has been proposed as a sensitive and specific target for *N. meningitidis* detection, including in settings where capsule-associated targets may be problematic [15]. Conversely, false-negative real-time PCR results associated with polymorphisms in *ctrA* have been reported [17]. The present dataset was not designed to formally compare performance according to molecular target, extraction method or platform, and the number of samples was limited. Therefore, no causal attribution can be made at laboratory or assay level. However, the results support the value of collecting more structured methodological information in future EQA rounds, including extraction workflow, input volume, internal inhibition controls, PCR target combinations, Ct cut-off policy and whether serogroup PCR is performed only after species-level positivity or in parallel.

AST participation was high among laboratories with analysable isolate-level responses, with MIC testing reported for 23/25 laboratories for both meningococcal isolates. Because no predefined reference MIC values were assigned for this exercise, performance was assessed comparatively against participant modal MICs, with concordance defined as a result falling within one doubling dilution of the modal value. This approach is suitable for descriptive comparison but should not be interpreted as formal susceptibility scoring against an independent reference standard. In the present exercise, agreement was good for cefotaxime and ciprofloxacin, whereas broader dispersion was observed for penicillin G, amoxicillin and rifampicin. Ceftriaxone results, available from fewer laboratories, also showed greater dispersion than cefotaxime. Several factors may contribute to this variability, including differences in gradient diffusion systems, strip ranges, inoculum preparation, incubation conditions, endpoint reading and local reporting conventions. Previous EQA reports have similarly emphasised the need for standardised methodology and raw MIC reporting to enable valid inter-laboratory comparison [9,10,13]. The present results therefore support continued reporting of raw MICs, clear documentation of the method used and alignment with current EUCAST recommendations when interpretive categories are required [9].

The two meningococcal isolates also illustrated the usefulness of including resistance-relevant phenotypes in surveillance-oriented EQA panels. N1 was selected as a MenW isolate with a ciprofloxacin-resistant phenotype. Using the complementary EUCAST v16.0 interpretation of reported raw MICs, ciprofloxacin resistance was recognised in 19/22 laboratories with numeric ciprofloxacin MIC results. N2 was selected as a MenY cefinase-positive isolate. Cefinase/beta-lactamase positivity was reported by 10/25 laboratories among all isolate responders, but by 10/12 laboratories among those providing an interpretable Yes/No cefinase result. This distinction suggests that recognition of the expected phenotype was good among laboratories that performed and reported the test, whereas overall completeness was limited by non-testing or missing reporting. These findings show the added value of presenting both MIC concordance and clinically informative phenotype recognition. This is important because AST surveillance for *N. meningitidis* informs treatment recommendations, chemoprophylaxis policy and early detection of emerging resistance [1,4]. The available 2022 EMGM abstract did not provide detailed meningococcal MIC performance data, so comparison with that exercise is mainly informative for culture identification and non-culture molecular detection rather than for AST [14]. Even so, the present EQA reinforces the interest of combining phenotypic MIC data with genomic markers where these are available.

WGS was reported by 16/25 laboratories for both meningococcal isolates, indicating substantial integration of sequencing into current reference-laboratory practice. Among WGS-positive submissions, completeness was high for core surveillance outputs, including sequence type, clonal complex, PorA VR1, PorA VR2 and FetA. More specialised outputs, including LINcode and resistance-associated loci such as *penA*, *rpoB* and *gyrA*, were less consistently reported. This suggests that the main challenge has shifted from access to sequencing alone towards harmonisation of downstream bioinformatic analysis, nomenclature, quality thresholds and reporting formats. This is an important development compared with earlier IBDLabNet exercises, which focused mainly on classical sequence-based fine typing and already highlighted variation in the completeness of reported molecular outputs [10–13]. Standardised meningococcal molecular nomenclature has long relied on reporting of serogroup, PorA variable regions, FetA, sequence type and clonal complex [18]. The development of BIGSdb and gene-by-gene genomic approaches has since enabled scalable extraction, storage and comparison of these outputs from WGS data [19,20]. In this context, the present EQA reflects a transitional stage in which WGS is already widely implemented in a substantial proportion of laboratories, but reporting of extended genomic outputs remains heterogeneous.

The public health implications of these findings are substantial. IMD surveillance depends not only on confirmation of *N. meningitidis*, but also on timely and comparable serogroup, AST and lineage information. Incomplete non-culture detection or serogrouping may reduce the completeness of surveillance data, particularly for culture-negative cases, which are common after antibiotic administration or when only clinical material is available. Missing serogroup information can affect estimation of vaccine-preventable disease burden and reduce the precision of outbreak detection and response. Conversely, robust culture-based identification, high AST uptake and increasing WGS capacity strengthen the ability of the network to monitor circulating lineages, identify resistance signals and support cross-border public health action [1,4]. These priorities are especially relevant in a context of changing epidemiology and evolving clinical presentation of IMD [2,3].

Several limitations should be considered. Firstly, the meningococcal component included only two positive non-culture samples and two cultured isolates and therefore cannot capture the full diversity of meningococcal lineages, serogroups, resistance phenotypes or clinical matrices encountered in routine surveillance. Secondly, no negative non-culture sample was included in this edition, limiting assessment of specificity and false-positive reporting. Thirdly, culture participation was optional and denominators varied across analyses because not all

laboratories requested the culture panel and not all participating laboratories performed all tests. Fourthly, the non-culture samples were simulated and lyophilised and may not fully reproduce the composition, inhibitors, degradation patterns or bacterial load distribution of clinical CSF or blood samples. Fifthly, Ct values were collected descriptively and are not directly comparable across laboratories without harmonised assays or calibrated standards. Sixthly, AST analysis relied primarily on participant modal MICs rather than predefined reference MIC values; complementary EUCAST-based interpretation was therefore restricted to selected predefined informative phenotype–antibiotic combinations. Finally, WGS outputs were analysed descriptively. A fully predefined reference dataset was not available for all genomic fields included in the questionnaire, and WGS reporting was not required from all participants. This approach reflects the current heterogeneity in WGS implementation across EU/EEA laboratories, as also shown in previous EQA exercises [10–13], and the inclusion of optional WGS fields was intended primarily to document implementation and identify areas for harmonisation rather than to provide formal performance scoring against predefined reference values.

Despite these limitations, the EQA provides a useful benchmark for both individual laboratories and the wider European network. For participants, the results can support internal review of false-negative molecular results, serogrouping discrepancies, MIC outliers, incomplete cefinase or beta-lactamase reporting and incomplete WGS outputs and may contribute to quality-management and accreditation documentation. At network level, the findings identify clear priorities for capacity strengthening: improving non-culture molecular detection and group determination, encouraging structured reporting of molecular targets and controls, maintaining standardised raw MIC reporting, documenting recognition of resistance-relevant phenotypes, and harmonising WGS-derived nomenclature and resistance-marker outputs. These priorities are aligned with the objectives of ECDC EQA activities, which aim to support harmonisation, identify training needs and improve the comparability of surveillance data across the EU/EEA [5,6].

Overall, the 2026 meningococcal EQA shows that EU/EEA laboratories participating in IBDLabNet have strong proficiency for culture-based meningococcal identification and generally high capacity for AST and WGS-supported characterisation. The main residual gaps concern non-culture sensitivity, completeness of serogroup reporting, completeness of selected phenotype reporting, and harmonisation of specialised genomic outputs. Regular EQA rounds, targeted feedback, structured method questionnaires and focused training on non-culture molecular workflows, AST reporting and WGS output harmonisation would help address these gaps and further strengthen the quality and comparability of IMD surveillance data across the EU/EEA.

5 Conclusions

The 2026 IBDLabNet EQA for *N. meningitidis* showed overall strong performance among participating EU/EEA laboratories, particularly for culture-based species identification and serogroup determination. All laboratories with analysable isolate-level responses correctly identified both meningococcal isolates, and serogroup assignment was highly concordant. AST uptake was high among laboratories providing culture-panel results, and WGS was already implemented by a substantial proportion of participants, with good reporting completeness for core surveillance outputs such as sequence type, clonal complex and major antigenic markers.

In contrast, the non-culture component showed more heterogeneous performance. The main limitations were false-negative molecular detection and incomplete serogroup reporting rather than frequent misidentification as another pathogen. These findings indicate that, within the participating network, culture-based meningococcal characterisation is well established, whereas non-culture workflows remain more variable and represent the main area requiring further harmonisation.

The AST results provided useful complementary information. Comparative analysis of MICs showed higher agreement for cefotaxime and ciprofloxacin, with greater dispersion for penicillin G, amoxicillin, rifampicin and ceftriaxone where reported. The complementary EUCAST-based reading of selected informative phenotypes showed that ciprofloxacin resistance in N1 was recognised by most laboratories reporting a numeric ciprofloxacin MIC, whereas cefinase positivity in N2 was frequently recognised among laboratories providing an interpretable Yes/No result but less completely documented when all isolate responders were considered. These findings support the value of reporting both raw MIC concordance and recognition of predefined resistance-relevant phenotypes.

From a surveillance perspective, the EQA confirms that the network has strong capacity to support isolate-based confirmation and characterisation of IMD. However, improving the completeness and robustness of non-culture molecular detection and serogroup assignment remains important, particularly for culture-negative cases where clinical material may provide the only laboratory basis for public health interpretation. Further harmonisation of AST reporting and WGS-derived outputs would also strengthen the comparability of meningococcal surveillance data across the EU/EEA.

The design of this EQA was appropriate for documenting current practice across the network and identifying priority gaps relevant to surveillance, AST and genomic characterisation. At the same time, the limited number of samples, the absence of a negative non-culture sample, optional participation in some components, reliance on participant modal MICs for comparative AST analysis, and the descriptive nature of the WGS assessment should be taken into account when interpreting the results. Overall, this exercise provides a useful baseline for future EQA rounds and for monitoring progress in network harmonisation over time.

6 Recommendations

Based on the findings of this EQA, the following actions are recommended for future rounds and follow-up activities:

1. **Prioritise improvement of non-culture molecular workflows.**
   Future capacity-strengthening activities should focus on reducing false-negative detection and improving completeness of serogroup reporting from non-culture material. This could include targeted technical guidance or training on nucleic acid extraction, inhibition controls, molecular target selection, assay sensitivity, Ct interpretation and reporting algorithms.
2. **Collect more structured methodological information and use it to guide support.**
   Future questionnaires should capture more standardised information on molecular workflows, including extraction method, input volume, internal controls, PCR targets used, Ct cut-off policies, and whether serogroup PCR is performed only after species-level positivity or in parallel. These data should be used to interpret inter-laboratory differences and prioritise training or technical exchanges across non-culture detection, culture identification, serogrouping, AST and WGS workflows.
3. **Maintain and strengthen standardised AST reporting.**
   Laboratories should continue to report raw MIC values together with the method used and the interpretive standard applied. Future analyses should continue to present MIC distributions and concordance around the participant modal MIC, while also including predefined informative phenotype readings where relevant and applicable, using current EUCAST breakpoints. For meningococcal isolates, this includes resistance-relevant phenotypes such as ciprofloxacin resistance and cefinase/beta-lactamase detection.
4. **Improve reporting of cefinase/beta-lactamase results.**
   When cefinase or beta-lactamase testing is relevant to the expected phenotype of an isolate, future EQA forms should clearly distinguish between "tested negative", "tested positive", "not tested" and "missing". This would allow more accurate interpretation of whether an expected resistance mechanism was not detected, not assessed or not reported.
5. **Further harmonise WGS-derived reporting.**
   Future EQA exercises should continue to include WGS components, while progressively improving standardisation of reported outputs, particularly for resistance-associated loci and extended genomic nomenclature. Where feasible, predefined expected genomic outputs should be expanded for selected markers, so future WGS analyses can move from descriptive assessment towards more formal performance evaluation.
6. **Strengthen the educational value of future panels.**
   Future meningococcal EQAs could include a broader range of sample types and challenge materials, such as negative controls, lower-signal non-culture samples, atypical or closely related *Neisseria* species, and isolates with predefined resistance-relevant phenotypes. This would allow better assessment of specificity, sensitivity, discriminatory performance and resistance recognition.
7. **Maintain repeated EQA implementation and network-level feedback.**
   Regular EQA rounds should be maintained to monitor progress, document persistent gaps and evaluate the effect of follow-up actions at laboratory and network level. Outputs from this exercise should inform targeted feedback, technical exchanges, training modules and harmonisation work relevant to meningococcal surveillance in the EU/EEA, particularly for non-culture confirmation, serogroup assignment, AST reporting, resistance-marker reporting and WGS-derived characterisation.

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Annex 1. Participating laboratories and countries

Table 1A. EU/EEA participating laboratories

Country	Laboratory / institute	Non-culture panel	Meningococcal culture panel
Austria	National reference center for meningococci, pneumococci and *Haemophilus influenzae* / Austrian Agency for Health and Food Safety	Yes	Yes
Bulgaria	National Center of Infectious and Parasitic Diseases	Yes	Yes
Belgium	LHUB-ULB - CNR *Haemophilus influenzae*	Yes	No
Latvia	Riga East University Hospital, Laboratory service, National Microbiology Reference Laboratory	Yes	Yes
Portugal	Laboratório de Referência de Infeções Respiratórias – agentes bacterianos / Instituto Nacional de Saúde Doutor Ricardo Jorge	Yes	Yes
Slovakia	National Reference Center for Meningococci, Public Health Authority of Slovakia	Yes	Yes
Belgium	NRC Neisseria / Sciensano	Yes	Yes
Italy	Department of Infectious Diseases, Istituto Superiore di Sanità, Roma, Italy	Yes	Yes
Italy	Istituto Superiore di Sanità	Yes	No
Bulgaria	National Center of Infectious and Parasitic Diseases, Laboratory for Molecular Microbiology	Yes	Yes
Czechia	National Reference Laboratory for Streptococcal Infections, National Institute of Public Health	Yes	No
Sweden	Department of Laboratory Medicine, Clinical Microbiology, University Hospital Örebro	Yes	Yes
France	Centre National de Référence des Pneumocoques / Centre Hospitalier Intercommunal de Créteil	Yes	No
Norway	Norwegian Institute of Public Health	Yes	Yes
Germany	National reference center for meningococci and *Haemophilus influenzae*	Yes	Yes
Spain	Spanish Pneumococcal Reference Laboratory	Yes	No
Estonia	Republic of Estonia Health Board (communicable diseases laboratory)	Yes	Yes
Spain	Neisseria, Listeria and Bordetella Unit / Reference and Research Laboratory for Vaccine Preventable Bacterial Diseases / National Centre for Microbiology / Instituto de Salud Carlos III	Yes	Yes
Poland	National Reference Centre for Bacterial Meningitis, National Medicines Institute	Yes	Yes
Romania	Bacterial Respiratory Infections Laboratory / Cantacuzino National Military Medical Institute for Research and Development	Yes	No
Hungary	National Center for Public Health and Pharmacy	Yes	Yes
Italy	Istituto Superiore di Sanità	Yes	No
Romania	INCDMMCantacuzino	Yes	Yes
Finland	Finnish Institute for Health and Welfare (THL)	Yes	Yes
Denmark	Neisseria and Streptococci Reference Laboratory, Statens Serum Institut	Yes	Yes
Lithuania	National Public Health Surveillance Laboratory	Yes	Yes
Greece	Infectious Diseases and Chemotherapy Research Laboratory, First Department of Pediatrics, Medical School, National and Kapodistrian University of Athens, “Aghia Sophia” Children’s Hospital	Yes	No
Cyprus	Microbiology Department, Nicosia General Hospital	Yes	Yes
Greece	Hellenic National Meningitis Reference Laboratory	Yes	Yes
Czechia	National Reference Laboratory for *Haemophilus* Infections, National Institute of Public Health	Yes	No
Malta	Bacteriology Laboratory, Mater Dei Hospital	Yes	Yes
Czechia	National Reference Laboratory for Meningococcal Infections	Yes	Yes
The Netherlands	Netherlands Reference Laboratory for Bacterial Meningitis	Yes	Yes
France	Centre National de Référence des Méningocoques et *Haemophilus influenzae*	Yes	Yes

Annex 2. Meningococcal panel composition and expected results

Annex 2A. Non-culture samples

Sample code	Material type	Expected pathogen	Expected serogroup	Purpose in the EQA
NC1	Lyophilised non-culture sample	*Neisseria meningitidis*	B	Assessment of molecular detection and serogroup determination from non-culture material
NC4	Lyophilised non-culture sample	*Neisseria meningitidis*	W	Assessment of molecular detection and serogroup determination from non-culture material

Annex 2B. Cultured isolates

Isolate code	Material type	Expected pathogen	Expected serogroup	Additional note
N1	Cultured isolate	*Neisseria meningitidis*	W	menW ciprofloxacin-resistant isolate
N2	Cultured isolate	*Neisseria meningitidis*	Y	menY cefinase-positive isolate

Annex 2C. Performance variables assessed for the meningococcal component

EQA component	Variables assessed
Non-culture panel	Pathogen detection, serogroup determination, reported Ct values for species detection and serogroup determination
Culture panel	Species identification, serogroup determination, antimicrobial susceptibility testing, cefinase/beta-lactamase detection where relevant, and, where performed, WGS uptake and reported outputs

Annex 3. Supplementary detailed result tables

This annex provides supplementary aggregated tables supporting the results presented in the main body of the report.

Detailed results for non-culture meningococcal samples

Table A3.1. Pathogen calls for NC1

Reported pathogen result	n	Denominator	%
N. meningitidis	22	32	68.8
Negative	10	32	31.3

Table A3.2. Serogroup calls for NC1

Reported serogroup result	n	% among typed submissions (n=18)	% among all responders (n=32)
B	13	72.2	40.6
None of the above	3	16.7	9.4
X	2	11.1	6.3

Table A3.3. Pathogen calls for NC4

Reported pathogen result	n	Denominator	%
N. meningitidis	26	32	81.2
Negative	6	32	18.8

Table A3.4. Serogroup calls for NC4

Reported serogroup result	n	% among typed submissions (n=19)	% among all responders (n=32)
W	14	73.7	43.8
X	2	10.5	6.3
B	1	5.3	3.1
C	1	5.3	3.1
None of the above	1	5.3	3.1

Table A3.5. Summary indicators for meningococcal non-culture samples

Sample	Interpretable pathogen responses, n	Correct pathogen identification, n (%)	Serogroup reported, n	Correct serogroup among all responders, n (%)	Correct serogroup among typed submissions, n (%)	Species Ct median (IQR)	Serogroup Ct median (IQR)
NC1	32	22 (68.8)	18	13 (40.6)	13 (72.2)	34.0 (33.1–34.9)	35.7 (35.0–36.0)
NC4	32	26 (81.2)	19	14 (43.8)	14 (73.7)	32.7 (30.9–34.3)	34.0 (30.4–35.7)

Detailed results for cultured meningococcal isolates

Table A3.6. Serogroup calls for isolate N1

Reported serogroup result	n	% among all responders (n=25)
W	23	92.0
C	1	4.0
None of the above	1	4.0

Table A3.7. Serogroup calls for isolate N2

Reported serogroup result	n	% among typed submissions (n=23)	% among all responders (n=25)
Y	22	95.7	88.0
None of the above	1	4.3	4.0

Table A3.8. Summary indicators for meningococcal cultured isolates

Isolate	Responses, n	Correct species identification, n (%)	Serogroup reported, n	Correct serogroup among all responders, n (%)	Correct serogroup among typed submissions, n (%)	MIC testing uptake, n (%)	WGS uptake, n (%)
N1	25	25 (100)	25	23 (92.0)	23 (92.0)	23 (92.0)	16 (64.0)
N2	25	25 (100)	23	22 (88.0)	22 (95.7)	23 (92.0)	16 (64.0)

Supplementary AST tables

Table A3.9. Participant modal MICs for selected antibiotics

Isolate	Antibiotic	Numeric MICs available, n	Participant modal MIC
N1	Penicillin G	18	1.0
N1	Amoxicillin	10	1.0
N1	Cefotaxime	20	0.032
N1	Ceftriaxone	12	0.004
N1	Ciprofloxacin	22	0.064
N1	Rifampicin	22	0.016
N2	Penicillin G	18	8.0
N2	Amoxicillin	11	4.0
N2	Cefotaxime	19	0.016
N2	Ceftriaxone	13	0.002
N2	Ciprofloxacin	22	0.004
N2	Rifampicin	22	0.016

Table A3.10. Concordance within one doubling dilution of the participant modal MIC

Isolate	Antibiotic	Numeric MICs available, n	Concordant results, n	Concordance, %
N1	Penicillin G	18	16	88.9
N1	Amoxicillin	10	9	90.0
N1	Cefotaxime	20	18	90.0
N1	Ceftriaxone	12	7	58.3
N1	Ciprofloxacin	22	19	86.4
N1	Rifampicin	22	12	54.5
N2	Penicillin G	18	12	66.7
N2	Amoxicillin	11	7	63.6
N2	Cefotaxime	19	16	84.2
N2	Ceftriaxone	13	8	61.5
N2	Ciprofloxacin	22	19	86.4
N2	Rifampicin	22	15	68.2

Table A3.11. Selected EUCAST v16.0 phenotype summary for informative meningococcal AST combinations

Isolate	Informative combination	Result basis	n with interpretable result	Expected phenotype	Expected phenotype recognised, n/N (%)	EUCAST S, n/N (%)	EUCAST I, n/N (%)	EUCAST R, n/N (%)
N1	Ciprofloxacin resistance	Numeric ciprofloxacin MIC	22	Resistant	19/22 (86.4%)	3/22 (13.6%)	0/22 (0.0%)	19/22 (86.4%)

Table A3.12. Cefinase/beta-lactamase results for meningococcal isolate N2

Isolate	Expected result	Reported result	n	Denominator	%
N2	Positive	Yes	10	25	40.0
N2	Positive	No	2	25	8.0
N2	Positive	Untested	10	25	40.0
N2	Positive	Missing	3	25	12.0
N2	Positive	Expected result recognised among all isolate responders	10	25	40.0
N2	Positive	Expected result recognised among Yes/No results	10	12	83.3

Supplementary WGS tables

Table A3.13. Completeness of reported WGS outputs for meningococcal isolates (pooled N1 and N2 submissions)

Reported WGS output	Reported, n	WGS-positive submissions, n	Completeness, %
Clonal complex (cc)	32	32	100.0
Sequence type (st)	32	32	100.0
PorA VR1	32	32	100.0
PorA VR2	32	32	100.0
FetA	32	32	100.0
LINcode	16	32	50.0
penA	28	32	87.5
rpoB	26	32	81.3
gyrA	28	32	87.5

Table A3.14. Isolate-specific completeness of reported WGS outputs

Isolate	WGS-positive submissions, n	cc	st	VR1	VR2	FetA	LINcode	penA	rpoB	gyrA
N1	16	16/16 (100)	16/16 (100)	16/16 (100)	16/16 (100)	16/16 (100)	8/16 (50.0)	14/16 (87.5)	13/16 (81.3)	14/16 (87.5)
N2	16	16/16 (100)	16/16 (100)	16/16 (100)	16/16 (100)	16/16 (100)	8/16 (50.0)	14/16 (87.5)	13/16 (81.3)	14/16 (87.5)

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