TESSy - The European Surveillance System

Gonococcal Antimicrobial Surveillance Reporting Protocol 2019

Euro-GASP

Surveillance data for 2018 and 2019

March 2019

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Introduction

The emergence of antimicrobial resistance (AMR) in *Neisseria gonorrhoeae* (NG) is a serious threat to the treatment and control of gonorrhoea. Numerous formerly effective therapeutic agents can no longer be used due to the emergence of resistance and subsequent rapid global spread. The development and spread of resistance to third generation cephalosporins in recent decades has further limited treatment options. The current European guideline recommends dual treatment with ceftriaxone and azithromycin to try to delay the development and/or spread of resistance against the last options for treatment.

One of the specific objectives for surveillance of sexually transmitted infections in Europe is "to detect and monitor the resistance patterns in gonococci, preferably by epidemiological characteristics, in Europe to contribute to the treatment guidelines of gonorrhoea and to ensure appropriate treatment by promoting the coordination of laboratory network on gonococci resistance testing, including quality assurance and training." In order to fulfil this objective, the European Gonococcal Antimicrobial Surveillance Programme (Euro-GASP) was launched in August 2009, and is currently outsourced to an international team lead by Public Health England and Örebro University Hospital (Sweden).

The current objectives and scope of Euro-GASP are:

- Support the ECDC in monitoring the susceptibility of *N. gonorrhoeae* isolates in the European Union/European Economic Area (EU/EEA) and EU enlargement countries by conducting surveillance for antimicrobial resistance in gonococci;
- Support EU/EEA Member States and EU enlargement countries in developing high quality antimicrobial susceptibility testing and molecular typing including whole genome sequencing (WGS);
- Support EU/EEA Member States in improving the quality of epidemiological data reported through Euro-GASP;
- Through an external quality assessment (EQA) scheme, assess the accuracy of quantitative *N. gonorrhoeae* antimicrobial susceptibility testing reported by participating laboratories and the comparability of results between laboratories in order to identify any training needed for targeted capacity building;
- Perform WGS of *N. gonorrhoeae* strains in order to inform about the geographic and temporal distribution patterns of public health relevant strains of *N. gonorrhoeae* in the EU/EEA region, including associations between genotype, antimicrobial resistance and patient characteristics;
- Provide training on STI laboratory diagnostics, *N. gonorrhoeae* susceptibility testing and molecular typing including WGS.

Sentinel surveillance has followed a hybrid centralized-decentralized model, with some countries performing susceptibility testing in their own laboratories, while others lacking capacity have sent isolates to hub laboratories.

This protocol presents the instructions for collecting gonococcal strains and reporting of AMR data in the European surveillance system (TESSy).

The Reporting Protocol is supplemented by the *Technical Annex*, which contains updated generic information for each data collection.

Likewise, the Surveillance Protocol will contain some of the generic information previously contained in the Reporting Protocols.

How to use this document

This Reporting Protocol provides information for laboratories participating in Euro-GASP and reporting countries' data managers in three main sections:

- Information on the *European Gonococcal Antimicrobial Surveillance Programme*.
- *Reporting to TESSy* – contains guidelines on how to prepare data for submission to TESSy, deadlines, subject-specific information (e.g. new changes to metadata), and links to further information.
- *Annex 1* – contains:
    - A history of metadata changes for the subject(s) covered by this Reporting Protocol.
    - The metadata set for the subject(s) covered by this Reporting Protocol.
- *Annex 2* – contains subject-specific material relevant for distribution with the Reporting Protocol, including:
    - Contact information
    - Testing protocols
- *Annex 3* – contains information related to the protocol for implementation of Euro-GASP at a national level

Finding further information

 Paragraphs denoted by the information icon tell where you can find further information.

Updated links to all the schedules, documentation and training materials mentioned in this Reporting Protocol are included in the *Technical Annex*, including:

- Metadata sets and history.
- Tutorials for data transformation using respectively Excel and Access.
- TESSy user documentation.
- CSV and XML transport protocols.

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Framework for European Gonococcal Antimicrobial Surveillance Programme: isolates collected in 2018 and 2019

Isolate collection

Submitted isolates

Each country should aim to collect 110 gonococcal isolates each year, with the overall aim to retrieve and test 100 isolates (200 isolates in some countries, see below). Countries participating in centralised testing should collect a minimum number of 10 isolates per year for a shipment to be organised. If less than 10 isolates are available then multiple years can be combined and the results added to ECDC surveillance atlas for those years, even if the reports for those years have been published.

For countries performing decentralised testing where 100 isolates likely represent less than 10% of the total number of cases of gonorrhoea (Belgium, Denmark, France, Germany, Hungary, Ireland, the Netherlands, Spain, Sweden and the United Kingdom), up to 200 isolates should be collected in order to provide a more representative sample. If more than 200 isolates are reported in TESSy, the first two hundred isolates by date of diagnosis may be selected for analysis if a justification to include the additional isolates is not available.

Selection criteria

Isolates should be selected from consecutive patients and from patients representing different patient groups and geographical regions within the country to reflect the distribution of gonorrhoea cases in that country, if known. Consecutive isolate selection may not be possible if particular patient groups/regions are selected or if isolates with corresponding epidemiological data are selected in place of isolates with no data. Care should be taken to avoid selection bias.

Multiple isolates from a single patient should be considered as a single episode of infection if the isolates were recovered within a period of ≤4 weeks, and only one isolate should be submitted, according to the hierarchy below. Where more than one isolate is collected from a patient, then a hierarchy of desired isolates for collection would be:

Males - 1. Pharyngeal 2. Rectal 3. Urethral 4. Other

Females – 1. Pharyngeal 2. Cervical 3. Other anogenital (High vaginal swab (HVS)/rectal/urethral) 4. Other

Given the current view that cephalosporin resistance emerged through interaction between commensal *Neisseria* species and *N. gonorrhoeae* in the pharynx and the fact that cephalosporins and most other antimicrobials have a lower efficacy in the pharynx, pharyngeal samples (where available) should be selected first as cephalosporin resistance is most likely to develop at this site.

Submission of isolates for centralised testing

Each participating laboratory will be provided with cryopreservative beads to store gonococcal isolates (see Annex 1) until collection by courier once annually.

Schedule of isolate collection 2018/2019

The collection dates are between September and November. Countries with low collection numbers should use isolates from throughout the year. In addition, isolates outside of the September-November collection period may be submitted if this enables a more representative isolate set from patients to be submitted (i.e. isolates representing different patient groups and geographical regions within the country to reflect the distribution of gonorrhoea cases in that country).

Data collection

It is the aim of this surveillance system to link *N. gonorrhoeae* susceptibility data with basic epidemiological data to get an overview of risk groups and to target prevention measures. All data from the AMR susceptibility testing should be submitted to TESSy. The set of variables and validation rules are described in the section *GONOAMR metadata set*. This section also includes the variables which are part of the "Datasource". Instructions on data reporting can be found in the section Reporting to TESSy.

Epidemiological information

A set of variables is collected as part of the enhanced STI surveillance and submitted by the national STI surveillance contact points in each country. It is suggested that the same source of epidemiological information is used for the GONOAMR surveillance database where it is possible to link the epidemiological information with the microbiological information in case-based formats.

The method of obtaining epidemiological data could be implemented as follows:

1. The STI microbiology contact points who are submitting or testing isolates for AMR surveillance, will contact the national contact points for STI surveillance, who will already have collated this information, and request the information. This will require a patient identifier – at national level - to link the information. However, the patient identifier should not be sent to TESSy, it should be used for internal purposes only.
2. If the information submitted by the national contact points for STI surveillance cannot be linked with gonococcal isolates and associated antimicrobial susceptibility data (e.g. if the data for STI surveillance are aggregate, or there is no shared patient identifier between the epidemiological and microbiological data), the national contact points for STI microbiology would enter the available epidemiological data that were possible for the laboratory to retrieve (either data submitted with the isolate or data requested from place of sample collection).

In both instances the epidemiological and microbiology data will be submitted by the national STI contact point (either microbiologist or epidemiologist or data managers) in TESSy.

Please note that the submission of AMR results should not be delayed by missing epidemiological data; AMR results should be uploaded as soon as they become available and the data can be replaced by complete data at a later stage.

Centralised testing

Where centralised testing is being carried out, the hub will send results back to member states' laboratories. Epidemiological and AMR data should then be entered in TESSy by member states. This could be done by the microbiology or epidemiological focal point as discussed above. As a quality control process, the hub will be able to check with the TESSy helpdesk on whether all cases tested have been reported through TESSy so further follow-up can be organised with individual laboratory/epidemiological contacts.

Susceptibility testing

Centralised testing

For countries participating through centralised testing, all isolates sent to the hub will be tested for susceptibility to the following panel of therapeutically relevant antimicrobials. Further details on the testing methodology can be found in *Annex 2*.

- Ciprofloxacin (agar dilution breakpoint technique or MIC gradient strip testing)
- Azithromycin (MIC gradient strip testing)
- Cefixime (MIC gradient strip testing)
- Ceftriaxone (MIC gradient strip testing)

- β-lactamase test (nitrocefin test) for detection of high-level penicillin resistance

In addition, gentamicin and spectinomycin should be tested for isolates **collected** in 2019 if possible as 2019 is a "snapshot" year[1].

Laboratories participating through centralised testing will be supported to move to decentralised testing through training, including country visits and twinning activities where necessary.

Decentralised testing

Laboratories from individual countries meeting the criteria described below will perform their own susceptibility testing and enter their results directly into TESSy. Even though antimicrobial susceptibility testing methods may vary, it is important that the breakpoints are harmonised and breakpoints used in Euro-GASP are adhered to (*Annex 2*).

Selection criteria for decentralised testing

To ensure the data quality is maintained for decentralised testing, the criteria for selecting individual laboratories to use their own methods to test the agreed core antimicrobial panel would include:

- Laboratories should perform consistently well in the EQA (no more than 5% of MIC results should differ by more than two doubling dilutions of the modal MICs). EQA results not fulfilling these criteria can result in exclusion of national data for one or several years.
- Laboratories should have a good comparability (at least 90% concordance between resistance category and no more than 5% of MIC results should differ by more than two doubling dilutions) between the laboratories own national or regional susceptibility testing data and susceptibility data generated by centralised susceptibility testing.

If laboratories participating in decentralised testing wish to include data from gonococcal isolates that have undergone antimicrobial susceptibility testing in other laboratories, the decentralised laboratory needs to ensure that all submitting laboratories additionally pass the decentralised criteria stated above. Details of these additional laboratories should be provided to the hub.

If laboratories significantly change their susceptibility testing methods i.e. changing from agar dilution to MIC gradient strip testing, then the Euro-GASP hub should be notified. Local validation data can be submitted to Euro-GASP for review, however this is not mandatory and decentralised laboratories are expected to use appropriate control strains (see Annex 2) so any potential issues are identified and to ensure consistency in the longitudinal data.

Procedure for decentralised testing

Laboratories identified as suitable candidates for participating in decentralised testing are required to:

- Submit MIC data and corresponding resistance category assigned, that has been generated using MIC gradient strip testing, the agar dilution method or the agar dilution breakpoint method.
- Use appropriate gonococcal control strains (see *Annex 2*) (previously supplied by ECDC via the EQAs, also available at NCTC) and internal quality control (IQC) data should ideally be submitted annually to the Euro-GASP hub for quality assurance purposes. The MICs of the control strains should be within the modal MIC ranges and the Euro-GASP hub can help in troubleshooting if deviations from these MIC ranges are noted.

[1] Gentamicin and spectinomycin are no longer routinely tested annually as neither spectinomycin nor gentamicin is routinely used for treatment of gonorrhoea. Spectinomycin is also difficult to acquire. However, a snapshot of the current antibiotic susceptibility situation is performed every third year using an extended panel of antibiotics, including spectinomycin and gentamicin. This is not mandatory. The last "snapshot" year was 2016 and 2019 is therefore a "snapshot" year.

- Test a core group of antimicrobials, ideally as close as possible to the core panel tested by the centralised approach, but as an absolute minimum to include ceftriaxone, cefixime and azithromycin:
    - Ceftriaxone
    - Cefixime
    - Azithromycin
    - Ciprofloxacin
    - ß-lactamase/penicillinase activity
- Submit susceptibility data to TESSy in a timely fashion.

In the short-term it is anticipated that data should be submitted from one laboratory per country. If multiple testing sites exist within a country then there should be local organisation of data collection and data should be submitted by the (main) national STI laboratory contact.

Confirmation of resistant isolates

The susceptibility testing and *N. gonorrhoeae* species identification should be repeated for all isolates that are resistant to ceftriaxone (MICs>0.125 mg/L), on isolates that show elevated resistance to cefixime (MICs>0.25 mg/L), and all isolates showing high-level resistance to azithromycin (MICs≥256 mg/L). Those isolates are also recommended to be sent to the Reference Laboratory Hub (London/Örebro) for further verification and whole genome sequencing (including determination of NG-MAST ST, MLST ST, NG-STAR ST and genetic resistance determinants). If necessary, a Material Transfer Agreement (MTA) can be signed by the ECDC/Reference Laboratory Hub and the owner of the isolates.

National protocol

Each country reporting susceptibility data should provide the following additional information on how surveillance for *N. gonorrhoeae* is implemented at national level. This information is critical in interpreting data and in ensuring accurate linking of laboratory and epidemiological data. The National Protocol template, including data to be provided, is available in *Annex 3.*

Gonococcal susceptibility data analysis

Collated data will be analysed for a brief Euro-GASP report will be analysed for emerging trends in AMR. All susceptibility category data will be available on-line here: https://atlas.ecdc.europa.eu/public/index.aspx. The following analyses are currently performed and a selection included in the surveillance report. Additional analyses might be included in the report based on emerging trends:

1. Summary of isolates tested and percentage of epidemiological data completeness for each country (table).
2. Patient characteristics reported for Euro-GASP gonococcal isolates (table).
3. Patient age distribution by gender and sexual orientation (table).
4. Overall incidence of resistance for each included antimicrobial for each testing year (line graph).
5. Resistance to cefixime, azithromycin and ciprofloxacin, beta-lactamase production, by country with trends over time (table).
6. Map of proportion of isolates with cefixime resistance by country.
7. MIC distribution by year for cefixime (bar graph).
8. Percentage of isolates with cefixime resistance by gender and sexual orientation (line graph).
9. MIC distribution by year for ceftriaxone (bar graph).

10. Map of proportion of isolates with azithromycin ECOFF > 1 mg/L by country.
11. MIC distribution by year for azithromycin (bar graph).
12. Percentage of isolates with azithromycin ECOFF > 1 mg/L by gender and sexual orientation (line graph).
13. Ciprofloxacin resistance by gender and sexual orientation (described in text).
14. Summary of diagnostic tests used (supplementary table).
15. Percentage of known treatments used (supplementary table).

Reporting to TESSy

This section provides both an overview of the TESSy reporting process and tips on where you can find useful information.

The overall process is:

1. *Familiarise yourself with the data collection deadlines*.
2. *Prepare (export and transform) your data*.
3. *Check that your data complies with the metadata*.
4. *Check that your data source profile is up-to-date*.
5. *Submit your file(s) to TESSy*.
6. *Finalise and approve your submission*.

Checking the data collection schedule

An updated link to the current data collections schedule is provided in the *Technical Annex*.

The deadline for reporting isolates collected in 2018 is 31 May 2019. The aim is to produce a report on 2018 data before the end of 2019. Please note that if epidemiological data is not available by the collection deadline, this can still be uploaded to TESSy at a later stage. It is important that schedules are respected to achieve the updated timeframes. Countries not reporting in time will be excluded from the 2018 report.

Any emerging AMR issues which need to be disseminated rapidly can also be reported via EPIS STI (Epidemic Intelligence Service for STI).

Preparing data

After you have exported the data from your national database, you need to ensure that the data are in a format that TESSy can accept. This applies both to the type of file submitted to TESSy (only CSV and XML files can be submitted) and to the format of the data in certain fields.

Tutorials covering how you can transform your data to the correct TESSy format using Excel or Access are available on the TESSy documents website. Information on the file formats is available in the CSV Transport Protocol and XML Transport Protocol.

Checking metadata

The TESSy metadata define the fields and data formats that are valid as input to TESSy for a given subject.

As requirements to the data to be shared among TESSy users change, the data changes needed to support the new requirements are identified and agreed upon between the National Surveillance Contact Points, the Network Coordination Groups and ECDC's Disease Experts, and then implemented as changes to the TESSy metadata.

In order to ensure that your data can be saved correctly in TESSy, you therefore need to check that your data are correctly formatted according to the most recent metadata set.

Changes to the metadata for the subject of this Reporting Protocol are described in:

- *Changes to current metadata* – changes since the last Reporting Protocol.
- *Annex 1 Metadata change history* – all preceding changes.

It is especially important to focus on:

- **Field formats**

  Many fields require that data are formatted in a specific way. For example, dates must be in the YYYY-MM-DD format; dates in the DD/MM/YYYY format will be rejected.

- **Coded values**

  Some fields only permit the use of specific values (coded values). For example, **M**, **F**, **UNK**, or **Other** are the coded values for *Gender* and any other value in a *Gender* field will be rejected.

The metadata file contains all the definitions and rules you need to comply with to format your data correctly for every subject (usually a disease). The file can be downloaded as an Excel file from the TESSy documents website.

By filtering the fields in the file by subject, you can see the fields required for your subject and the rules applying to these fields.

The *Technical Annex* provides an overview of how you work with the metadata file, and the TESSy user documentation provides in-depth details on metadata.

Checking your data source profile

Before submitting your file(s), please review the profile for your data source(s) in TESSy (go to **Data Sources**), and update the information, if necessary.

Complete and up-to-date data source information for each subject is important for improving interpretation of data - each surveillance system has different features that need to be taken into account when comparing data at an international level.

If your data source information is out-of-date and you do not have access rights to update it, please request your National Focal Point for Surveillance or National Coordinator to do so.

In-depth information on the data source variables is available in the TESSy user documentation.

Submitting your data

Data is submitted through the TESSy web interface (go to **Upload**).

The *Technical Annex* provides an overview of how you submit files to TESSy, and the TESSy user documentation provides in-depth descriptions of all the upload methods.

Finalising your submission

The compliance of your data with the validation rules in the metadata is checked automatically during the data upload process.

The result of your upload – i.e. rejected or validated – is displayed immediately after the conclusion of the check in the **Validation details** webpage. Please review the result carefully:

- If your file has been rejected, there will be a message explaining each instance of non-compliance with the metadata that you need to correct.
- If your file has been validated, there might be warnings and remarks relating to possible data quality issues or to potential overwriting of existing records that you should consider.

When your file has been validated and you are satisfied that all corrections have been made, please ensure prompt approval – unapproved uploads can block for the approval of other uploads.

The TESSy user documentation provides information on reviewing validation results and adjusting reporting periods to avoid overwriting existing records.

Changes in current GONOAMR metadata

The 2018 changes are summarised in Annex 1: Table 4: Summary of implemented general changes (applicable to several record types)

The previous metadata changes are described in *Annex 1*.

Information on changes to the metadata for other subjects is available on the TESSy documentation website.

In 2019 additional validation rules have been introduced and applied to RecordType 8:

- The variables AZMSIR, CROSIR, CIPSIR, CFMSIR and SPTSIR have been made mandatory, however UNK is allowed. Reporting of the SIR variables is essential to allow for appropriate analysis and display of the data in the surveillance atlas
- For the variables CROSIR, CIPSIR, CFMSIR and SPTSIR and respective ResultSign variables, a warning is given if SIR is "I" and ResultSign is not "=". For variables AZMSIR, CROSIR, CIPSIR, CFMSIR and SPTSIR if SIR is "R" and ResultSign is "<" and if SIR is "S" and ResultSign is ">". This has been introduced as some errors with the ResultSign variables have been noticed.
- For variable AZMSIR the ECOFF at 1 mg/L should be used for "R", <=1 mg/L should be "S". Please note that the ECOFF is not to be used for recording resistance and susceptibility, but for distinguishing between isolates with acquired resistance mechanisms (MIC > 1 mg/L).

Annex 1 GONOAMR metadata

This section describes:

GONOAMR metadata set

Table 1: Description of the variables to be collected for the European Gonococcal Antimicrobial Surveillance Programme.

Note: Changes from previous versions are highlighted.

Variable	Variable description	Coding	Validation rules
RecordId	Unique identifier for each record within and across the national surveillance system – Member State selected and generated. A unique identifier must be used for all years; repeat use of a specific identifier will replace the contents of the original entry. We suggest to include the isolate year in the RecordId to avoid overwriting data.	Text	Mandatory
RecordType	RecordType corresponding to the Subject	GONOAMR	Mandatory
RecordTypeVersion	Version of the RecordType used. **This should be reported as 8**. If you use different RecordType versions the data may be rejected.	8	
Status	Default if left out: NEW/UPDATE. If set to DELETE, the record with the given RecordId will be deleted from the TESSy database (or better stated, invalidated). If set to NEW/UPDATE or left empty, the record is newly entered into the database.	Status of reporting NEW/UPDATE or DELETE (inactivate).	
Subject	Subject corresponding to the RecordType	GONOAMR	Mandatory
ReportingCountry	The country reporting the record.	ISO coded value list	Mandatory
DataSource	The data source for AMR NG (laboratory) that the record originates from.	Coded value list; codes maintained by each Member State in the Data Source editing interface in TESSy	Mandatory
DateUsedForStatistics	Date the specimen was taken from the patient, alternatively use date received in laboratory	Preferred format: yyyy-mm-dd	Mandatory
Gender	Gender of the infected person	F = Female M = Male O = Other UNK = UNK	Mandatory
Age	Age in years of patient as reported in the national system	0-120, UNK	Mandatory

Variable	Variable description	Coding	Validation rules
PlaceOfResidence	Place of residence of patient, NUTS level 0-3 (region)	NUTS code 0-3. Available from the TESSy metadataset (sheet "coded value lists"; coded value list "NUTS")	
ClinicalServiceType	Type of clinical service where patient was first seen	ANC - ANC COMB - Combined service DV - Dermatology-venereology clinic ED - Hospital Emergency Dept FPC - Family Planning Clinic GP - General Practitioner GYN - Gynaecology clinic ID - Infectious disease clinic OPC - Other primary care STI - Dedicated STI clinic URO - Urology YTH - Youth clinics O - Other UNK – Unknown	
ClinicLocation	Clinic location	Free text address using the format: Street, Number, Postcode, City. As a minimum please report City.	
ClinicCoordinates	Clinic coordinates	Latitude and Longitude of the STI clinic where the case was tested. Latitude and Longitude in this order. Format: NN.NN, NN.NN	
CountryOfBirthGONOAMR	Country of birth of patient	ISO coded value list (Country), UNK	
ProbableCountryOfInfection	Probable country(ies) of infection, country(ies) visited during the incubation period of the reported disease. Repeatable field.	ISO coded value list, UNK	
Transmission	Mode of transmission	HETERO = Heterosexual contact MSM = MSM/homo or bisexual male MTCT = Mother-to-child transmission O = Other UNK = Unknown	Error if Transmission = MSM and Gender = F Error if Transmission = MSM, Gender is not Male or Other
SiteOfInfection	Site of Infection	AR = Ano-Rectal GEN = Genital PH = Pharyngeal O = Other UNK = Unknown	
PrevGono	Existing evidence about previous gonorrhoea	Y = Yes N = No UNK =Unknown	

Variable	Variable description	Coding	Validation rules
HIVStatus	HIV Status of patient at time of diagnosis	POS = Positive POSKNOWN = Known HIV positive POSNEW = New HIV diagnosis NEG = Negative UNK = Unknown	
ConcurrentSTI	Concurrent STI	CHLAM = Chlamydia HEPB = Hepatitis B HEPC = Hepatitis C HERP = Genital herpes LGV = LGV SYPH = Syphilis WARTS = Genital warts MYCO = Mycoplasma genitalium NO = No concurrent STI UNK = Unknown	
ResultPor[2]	*porB* allele number generated from a 490 nucleotide *porB* sequence submitted to the NG-MAST website (http://www.ng-mast.net)	Number	number should be >=1 and an integer
ResultTbpB[2]	*tbpB* allele number generated from a 390 nucleotide *tbpB* sequence submitted to the NG-MAST website (http://www.ng-mast.net)	Number	number should be >=1 and an integer
ResultSeqType[2]	NG-MAST sequence type. A combination of the *porB* and *tbpB* allele numbers, obtained by submission to the NG-MAST website (http://www.ng-mast.net)	Number	number should be >=1 and an integer
Genogroup[2]	NG-MAST genogroup as defined in molecular typing surveys	'G' and number e.g. G1407	
DiagnosticTest	Diagnostic test used Note: this is a repeatable field and multiple columns with this variable name can be included.	CULT = culture (including methods used to identify *N. gonorrhoeae* from culture, such as MALDI-TOF, API and Phadebact) MICRO = microscopy N/A = Not applicable NUCLACID = detection of nucleic acid O = Other UNK = Unknown	

[2] To upload only for years when whole genome sequencing studies are implemented

Variable	Variable description	Coding	Validation rules
TreatmentUsed	Treatment used Note: this is a repeatable field and multiple columns with this variable name can be included.	AZM = Azithromycin CFM = Cefixime CIP = Ciprofloxacin CRO = Ceftriaxone CROAZM = Ceftriaxone and Azithromycin GEN = Gentamicin O = Other SPT = Spectinomycin CFMAZM = Cefixime and Azithromycin DOX = Doxycycline PEN = Penicillin CRO_250mg_AZM_1g = Ceftriaxone 250mg and Azithromycin 1g CRO_250mg_AZM_2g = Ceftriaxone 250mg and Azithromycin 2g CRO_500mg_AZM_1g = Ceftriaxone 500mg and Azithromycin 1g CRO_500mg_AZM_2g= Ceftriaxone 500mg and Azithromycin 2g CRO_1g_AZM_1g = Ceftriaxone 1g and Azithromycin 1g CRO_1g_AZM_2g = Ceftriaxone 1g and Azithromycin 2g CRO_250mg = Ceftriaxone 250mg CRO_500mg = Ceftriaxone 500mg CRO_1g = Ceftriaxone 1g AZM_1g = Azithromycin 1g AZM_2g = Azithromycin 2g CFM_400mg_AZM_1g = Cefixime 400mg and Azithromycin 1g CFM_400mg_AZM_2g = Cefixime 400mg and Azithromycin 2g CFM_400mg = Cefixime 400mg UNK = Unknown	
PenicillinaseActivityGONO	Penicillinase activity	POS = Positive NEG = Negative UNK = Unknown	
AZMResultSign	Sign	< Less than <= Less than or equal = Equal > Greater than	
CFMResultSign	Sign		
CIPResultSign	Sign		
CROResultSign	Sign		
GENResultSign	Sign		
SPTResultSign	Sign		
AZMResultValue	Value	Number	Error if TestMethod = Etest/MIC and ResultValue is not
CFMResultValue	Value		
CIPResultValue	Value		

Variable	Variable description	Coding	Validation rules
CROResultValue	Value		reported
GENResultValue	Value		
SPTResultValue	Value		
AZMSIR	Final interpretation result	S = Susceptible I = Intermediate susceptibility R = Resistant UNK = Unknown	Mandatory, UNK allowed. Error if ResultValue is reported and SIR is not reported or is reported as "UNK"
CFMSIR	Final interpretation result		
CIPSIR	Final interpretation result		
CROSIR	Final interpretation result		
GENSIR	Final interpretation result		
SPTSIR	Final interpretation result		
AZMTestMethod	Test method	ETEST = MIC gradient strip test MIC = MIC BKP = Breakpoint	
CFMTestMethod	Test method		
CIPTestMethod	Test method		
CROTestMethod	Test method		
GENTestMethod	Test method		
SPTTestMethod	Test method		

Table 2: Validation rules

Variables in rule	Severity	Validation rule	Validation message
Gender, Transmission	Error	If Gender is not 'M' or 'Other' and Transmission is 'MSM'	If MSM transmission is reported, gender should be 'M' or 'Other'
Gender, Transmission	Error	If Gender is 'F' and Transmission is 'MSM'	Females cannot have Transmission = MSM.
CIPResultValue, CIPSIR	Error	If CIPResultValue > 0.03 and CIPResultValue <= 0.06 and CIPSIR is not 'I'	If CIPResultValue > 0.03 and CIPResultValue <= 0.06, CIPSIR must be I.
CIPResultValue, CIPSIR	Error	If CIPResultValue > 0.06 and CIPSIR is not 'R'	If CIPResultValue > 0.06, CIPSIR must be R.
CIPResultValue, CIPSIR	Error	If CIPResultValue <= 0.03 and CIPSIR is not 'S'	If CIPResultValue <= 0.03, CIPSIR must be S.
SPTResultValue, SPTSIR	Error	If SPTResultValue > 64 and SPTSIR is not 'R'	If SPTResultValue > 64, SPTSIR must be R.
SPTResultValue, SPTSIR	Error	If SPTResultValue <= 64 and SPTSIR is not 'S'	If SPTResultValue <= 64, SPTSIR must be S.
AZMResultValue, AZMSIR	Error	If AZMResultValue > 1 and AZMSIR is not 'R'	If AZMResultValue > 1, AZMSIR must be R (ECOFF).
AZMResultValue, AZMSIR	Error	If AZMResultValue<= 1.0 and AZMSIR is not 'S'	If AZMResultValue <= 1.0, AZMSIR must be S.
CFMResultValue, CFMSIR	Error	If CFMResultValue>0.125 and CFMSIR is not 'R'	If CFMResultValue > 0.125, CFMSIR must be R.
CFMResultValue, CFMSIR	Error	If CFMResultValue<=0.125 and CFMSIR is not 'S'	If CFMResultValue <= 0.125, CFMSIR must be S.
CROResultValue, CROSIR	Error	If CROResultValue>0.125 and CROSIR is not 'R'	If CROResultValue > 0.125, CROSIR must be R.
CROResultValue, CROSIR	Error	If CROResultValue<=0.125 and CROSIR is not 'S'	IF CROResultValue <= 0.125, CROSIR must be S.
GENSIR	Error	If GENSIR is not 'UNK'	There are no resistance breakpoints defined for gentamicin: GENSIR must be UNK.
GENResultSign, GENResultValue	Error	If GENResultSign is reported and GENResultValue is not reported	If GENResultSign is reported, then GENResultValue should be reported.
CIPResultSign, CIPResultValue	Error	If CIPResultSign is reported and CIPResultValue is not reported	If CIPResultSign is reported, then CIPResultValue should be reported.
SPTResultSign, SPTResultValue	Error	If SPTResultSign is reported and SPTResultValue is not reported	If SPTResultSign is reported, then SPTResultValue should be reported.

Variables in rule	Severity	Validation rule	Validation message
AZMResultSign, AZMResultValue	Error	If AZMResultSign is reported and AZMResultValue is not reported	If AZMResultSign is reported, then AZMResultValue should be reported.
CFMResultSign, CFMResultValue	Error	If CFMResultSign is reported and CFMResultValue is not reported	If CFMResultSign is reported, then CFMResultValue should be reported.
CROResultSign, CROResultValue	Error	If CROResultSign is reported and CROResultValue is not reported	If CROResultSign is reported, then CROResultValue should be reported.
GENResultSign, GENResultValue	Error	If GENResultValue is reported and GENResultSign is not reported	If GENResultValue is reported, then GENResultSign should be reported.
CIPResultSign, CIPResultValue	Error	If CIPResultValue is reported and CIPResultSign is not reported	If CIPResultValue is reported, then CIPResultSign should be reported.
SPTResultSign, SPTResultValue	Error	If SPTResultValue is reported and SPTResultSign is not reported	If SPTResultValue is reported, then SPTResultSign should be reported.
AZMResultSign, AZMResultValue	Error	If AZMResultValue is reported and AZMResultSign is not reported	If AZMResultValue is reported, then AZMResultSign should be reported.
CFMResultSign, CFMResultValue	Error	If CFMResultValue is reported and CFMResultSign is not reported	If CFMResultValue is reported, then CFMResultSign should be reported.
CROResultSign, CROResultValue	Error	If CROResultValue is reported and CROResultSign is not reported	If CROResultValue is reported, then CROResultSign should be reported.
GENResultValue, GENSIR	Error	If GENResultValue is not reported and GENSIR is 'UNK'	If GENSIR is unknown(UNK), then GENResultValue must be known.
CIPResultValue, CIPSIR	Error	If CIPResultValue is not reported and CIPSIR is 'UNK'	If CIPSIR is unknown(UNK), then CIPResultValue must be known.
SPTResultValue, SPTSIR	Error	If SPTResultValue is not reported and SPTSIR is 'UNK'	If SPTSIR is unknown(UNK), then SPTResultValue must be known.
AZMResultValue, AZMSIR	Error	If AZMResultValue is not reported and AZMSIR is 'UNK'	If AZMSIR is unknown(UNK), then AZMResultValue must be known.
CFMResultValue, CFMSIR	Error	If CFMResultValue is not reported and CFMSIR is 'UNK'	If CFMSIR is unknown(UNK), then CFMResultValue must be known.
CROResultValue, CROSIR	Error	If CROResultValue is not reported and CROSIR is 'UNK'	If CROSIR is unknown(UNK), then CROResultValue must be known.
CFMResultValue	Warning	If CFMResultValue is > 0.25	Please note that the cefixime MIC reported is > 0.25: according to the Euro-GASP reporting protocol, the MIC should be repeated and identification confirmed.
CROResultValue	Warning	If CROResultValue is > 0.125	Please note that the ceftriaxone MIC reported is > 0.125: according to the Euro-GASP reporting protocol, the MIC should be repeated and identification confirmed.
AZMResultSign, AZMSIR	Error	if AZMResultSign='<' and AZMSIR='R'	If the AZMResultSign is "<" or "<=" then AZMSIR should not be reported as "R"
CFMResultSign, CFMSIR	Error	if CFMResultSign='<' and CFMSIR='R'	If the CFMResultSign is "<" or "<=" then CFMSIR should not be reported as "R"
CIPResultSign, CIPSIR	Error	if CIPResultSign='<' and CIPSIR='R'	If the CIPResultSign is "<" or "<=" then CIPSIR should not be reported as "R"
CROResultSign, CROSIR	Error	if CROResultSign='<' and CROSIR='R'	If the CROResultSign is "<" or "<=" then CROSIR should not be reported as "R"
SPTResultSign, SPTSIR	Error	if SPTResultSign='<' and SPTSIR='R'	If the SPTResultSign is "<" or "<=" then SPTSIR should not be reported as "R"
CFMResultSign, CFMSIR	Error	if CFMResultSign='<=' and CFMSIR='R'	If the CFMResultSign is "<" or "<=" then CFMSIR should not be reported as "R"
CIPResultSign, CIPSIR	Error	if CIPResultSign='<=' and CIPSIR='R'	If the CIPResultSign is "<" or "<=" then CIPSIR should not be reported as "R"

Variables in rule	Severity	Validation rule	Validation message
CROResultSign, CROSIR	Error	if CROResultSign='<=' and CROSIR='R'	If the CROResultSign is "<" or "<=" then CROSIR should not be reported as "R"
SPTResultSign, SPTSIR	Error	if SPTResultSign='<=' and SPTSIR='R'	If the SPTResultSign is "<" or "<=" then SPTSIR should not be reported as "R"
AZMResultSign, AZMSIR	Error	if AZMResultSign='<=' and AZMSIR='R'	If the AZMResultSign is "<" or "<=" then AZMSIR should not be reported as "R"
AZMResultSign, AZMSIR	Error	if AZMResultSign='>' and AZMSIR='S'	If theAZMResultSign is ">" or ">=" then AZMSIR should not be reported as "S"
CFMResultSign, CFMSIR	Error	if CFMResultSign='>' and CFMSIR='S'	If the CFMResultSign is ">" or ">=" then CFMSIR should not be reported as "S"
CIPResultSign, CIPSIR	Error	if CIPResultSign='>' and CIPSIR='S'	If the CIPResultSign is ">" or ">=" then CIPSIR should not be reported as "S"
CROResultSign, CROSIR	Error	if CROResultSign='>' and CROSIR='S'	If the CROResultSign is ">" or ">=" then CROSIR should not be reported as "S"
SPTResultSign, SPTSIR	Error	if SPTResultSign='>' and SPTSIR='S'	If the SPTResultSign is ">" or ">=" then SPTSIR should not be reported as "S"
AZMResultSign, AZMSIR	Error	if AZMResultSign='>=' and AZMSIR='S'	If the AZMResultSign is ">" or ">=" then AZMSIR should not be reported as "S"
CFMResultSign, CFMSIR	Error	if CFMResultSign='>=' and CFMSIR='S'	If the CFMResultSign is ">" or ">=" then CFMSIR should not be reported as "S"
CIPResultSign, CIPSIR	Error	if CIPResultSign='>=' and CIPSIR='S'	If the CIPResultSign is ">" or ">=" then CIPSIR should not be reported as "S"
CROResultSign, CROSIR	Error	if CROResultSign='>=' and CROSIR='S'	If the CROResultSign is ">" or ">=" then CROSIR should not be reported as "S"
SPTResultSign, SPTSIR	Error	if SPTResultSign='>=' and SPTSIR='S'	If the SPTResultSign is ">" or ">=" then SPTSIR should not be reported as "S"
AZMResultSign, AZMTestMethod	Warning	if AZMResultSign '>=' and AZMTestMethod = MIC	Please note that in case the highest tested concentration shows growth, you should report AZMResultValue =[the highest tested concentration] and AZMResultSign=">".
CFMResultSign, CFMTestMethod	Warning	if CFMResultSign '>=' and CFMTestMethod = MIC	Please note that in case the highest tested concentration shows growth, you should report CFMResultValue =[the highest tested concentration] and CFMResultSign=">".
CIPResultSign, CIPTestMethod	Warning	if CIPResultSign '>=' and CIPTestMethod = MIC	Please note that in case the highest tested concentration shows growth, you should report CIPResultValue =[the highest tested concentration] and CIPResultSign=">".
CROResultSign, CROTestMethod	Warning	if CROResultSign '>=' and CROTestMethod = MIC	Please note that in case the highest tested concentration shows growth, you should report CROResultValue =[the highest tested concentration] and CROResultSign=">"..
GENResultSign, GENTestMethod	Warning	if GENResultSign '>=' and GENTestMethod = MIC	Please note that in case the highest tested concentration shows growth, you should report GENResultValue =[the highest tested concentration] and GENResultSign=">".

Variables in rule	Severity	Validation rule	Validation message
SPTResultSign, SPTTestMethod	Warning	if SPTResultSign '>=' and SPTTestMethod = MIC	Please note that in case the highest tested concentration shows growth, you should report SPTResultValue =[the highest tested concentration] and SPTResultSign=">".
AZMResultSign, AZMTestMethod	Warning	if AZMResultSign '>=' and AZMTestMethod =ETEST	Please note that in case the highest tested concentration shows growth, you should report AZMResultValue =[the highest tested concentration] and AZMResultSign=">"..
CFMResultSign, CFMTestMethod	Warning	if CFMResultSign '>=' and CFMTestMethod = ETEST	Please note that in case the highest tested concentration shows growth, you should report CFMResultValue =[the highest tested concentration] and CFMResultSign=">".
CIPResultSign, CIPTestMethod	Warning	if CIPResultSign '>=' and CIPTestMethod = ETEST	Please note that in case the highest tested concentration shows growth, you should report CIPResultValue =[the highest tested concentration] and CIPResultSign=">".
CROResultSign, CROTestMethod	Warning	if CROResultSign '>=' and CROTestMethod = ETEST	Please note that in case the highest tested concentration shows growth, you should report CROResultValue =[the highest tested concentration] and CROResultSign=">".
GENResultSign, GENTestMethod	Warning	if GENResultSign '>=' and GENTestMethod = ETEST	Please note that in case the highest tested concentration shows growth, you should report GENResultValue =[the highest tested concentration] and GENResultSign=">"..
SPTResultSign, SPTTestMethod	Warning	if SPTResultSign '>=' and SPTTestMethod =ETEST	Please note that in case the highest tested concentration shows growth, you should report SPTResultValue =[the highest tested concentration] and SPTResultSign=">".
AZMResultValue, AZMTestMethod	Error	If AZMTestMethod = Etest/MIC then AZMResultValue must be reported	If a method which produces an MIC is used then the resulting MIC should be reported
CFMResultValue, CFMTestMethod	Error	If CFMTestMethod = Etest/MIC then CFMResultValue must be reported	If a method which produces an MIC is used then the resulting MIC should be reported
CIPResultValue, CIPTestMethod	Error	If CIPTestMethod = Etest/MIC then CIPResultValue must be reported	If a method which produces an MIC is used then the resulting MIC should be reported
CROResultValue, CROTestMethod	Error	If CROTestMethod = Etest/MIC then CROResultValue must be reported	If a method which produces an MIC is used then the resulting MIC should be reported
GENResultValue, GENTestMethod	Error	If GENTestMethod = Etest/MIC then ResultValue must be reported	If a method which produces an MIC is used then the resulting MIC should be reported
SPTResultValue, SPTTestMethod	Error	If SPTTestMethod = Etest/MIC then ResultValue must be reported	If a method which produces an MIC is used then the resulting MIC should be reported
CIPSIR, CIPResultValue	Error	If CIPResultValue is reported and CIPSIR is not reported or is reported as "UNK"	If an MIC is reported then the interpretation according to EUCAST guidelines should be reported
AZMSIR, AZMResultValue	Error	If AZMResultValue is reported and AZMSIR is not reported or is reported as "UNK"	If an MIC is reported then the interpretation according to EUCAST guidelines should be reported

Variables in rule	Severity	Validation rule	Validation message
SPTSIR, SPTResultValue	Error	If SPTResultValue is reported and SPTSIR is not reported or is reported as "UNK"	If an MIC is reported then the interpretation according to EUCAST guidelines should be reported
CFMSIR, CFMResultValue	Error	If CFMResultValue is reported and CFMSIR is not reported or is reported as "UNK"	If an MIC is reported then the interpretation according to EUCAST guidelines should be reported
CROSIR, CROResultValue	Error	If CROResultValue is reported and CROSIR is not reported or is reported as "UNK"	If an MIC is reported then the interpretation according to EUCAST guidelines should be reported
CROSIR; CIPSIR; CFMSIR; SPTSIR and respective *ResultSign variables	Warning	if SIR is "I" and ResultSign is not "="	If the SIR value is "I" then the ResultSign should usually be reported as "="
AZMSIR; CROSIR; CIPSIR; CFMSIR; SPTSIR and respective *ResultSign variables	Warning	if SIR is "R" and ResultSign is "<"	If the SIR value is "R" then the ResultSign should usually not be "<"
AZMSIR; CROSIR; CIPSIR; CFMSIR; SPTSIR and respective *ResultSign variables	Warning	if SIR is "S" and ResultSign is ">"	If the SIR value is "S" then the ResultSign should usually not be ">"
AZMSIR	Error	if SIR is "I"	No clinical breakpoints for azithromycin available, ECOFF > 1 mg/L

Table 3: Euro-GASP data source variables

Variable	Variable description	Coding	Validation rule
Subject mnemonic	Mnemonic of country data source	Coded value list	
Subject name	Name of country data source	Coded value list	
Comment	Short description of the surveillance system for the disease. Important details for the analysis.	Text	
Coverage	Coverage of the surveillance system	NAT = National REG = Regional LOC = Local UNK = Unknown	Mandatory
Comprehensive	Comprehensive: Reporting is based on cases occurring within the whole population of the geographical area where the surveillance system is set up (national, regional, etc.). Sentinel: Reporting is based on a selected group of physicians/hospitals/laboratories/or other institutions' notifications and/or cases occurring within a selected group of population defined by age group, gender, exposure or other selection criteria. Other: Reporting is based on a part of the population or group of physicians (or other institutions) which is not specified, for example reporting of some laboratories with no selection criteria.	Comp = Comprehensive O = Other Sent = Sentinel UNK = Unknown	Mandatory
StartSurvSys	Start year for data collection in the surveillance system.	YYYY	

Variable	Variable description	Coding	Validation rule
InternalQualityControl	WHO-recommended strains used for quality control procedures.	WHOCS = WHO control strains OTH = Other control strains used NT = Not tested UNK = Unknown	

GONOAMR metadata change history

Metadata changes prior to 2014 can be found on the TESSy documents website.

GONOAMR metadata change history

Table 4: Summary of implemented general changes (applicable to several record types)

Year	Subject	Description
2019	**GONOAMR**	The variables AZMSIR, CROSIR, CIPSIR, CFMSIR and SPTSIR have been made mandatory, however UNK is allowed. Reporting of the SIR variables is essential to allow for appropriate analysis and display of the data in the surveillance atlas For the variables CROSIR, CIPSIR, CFMSIR and SPTSIR and respective ResultSign variables, a warning is given if SIR is "I" and ResultSign is not "=". For variables AZMSIR, CROSIR, CIPSIR, CFMSIR and SPTSIR, if SIR is "R" and ResultSign is "<" and if SIR is "S" and ResultSign is ">". This has been introduced as some errors with the ResultSign variables have been noticed. For variable AZMSIR the ECOFF at 1 mg/L should be used for "R", <=1 mg/L should be "S". Please note that the ECOFF is not to be used for recording resistance and susceptibility, but for distinguishing between isolates with acquired resistance mechanisms (MIC > 1 mg/L)
2018	**GONOAMR**	New optional variables have been added (ClinicLocation, ClinicCoordinates) to collect alternative information on the clinic location in order to better understand the source of isolates included in Euro-GASP. Update coded value lists for SiteOfInfectionSTI: removed NA (Not applicable) Add validation rules for: • Transmission and Gender • TestMethod and ResultValue Change coded value list for CountryOfBirth from Country_Incl_HistCountries to Country - previously included historical countries make analysis more difficult when historical countries have broken up (eg USSR). Update coded value lists for TreatmentUsed - addition of doses for the main antimicrobials used for treatment Add validation rules for SIR and ResultValue variables to reduce the likelihood of errors where countries report MIC values but not the interpretation of the result.
2017	**GONOAMR**	Ciprofloxacin breakpoints have been implemented to conform with EUCAST breakpoints (S≤0.03 mg/L, I=0.047-0.06 mg/L, R>0.06 mg/L) and a subsequent update of the validation rules for variables 'CIPResultValue' and 'CIPSIR'; Three additional treatment options were added to the variable 'TreatmentUsed'; CFMAZM = Cefixime and Azithromycin, DOX = Doxycycline, PEN = Penicillin A new variable 'Genogroup' was added to record the NG-MAST genogroups from the molecular

Year	Subject	Description
		typing surveys. These changes have been implemented through a new record type version GONOAMR.v7 and were previously agreed by the Euro-GASP network at the co-ordination meeting in Bratislava, March 2016.
2016	**GONOAMR**	Validation rules have been added to improve the quality of reported data and reduce errors. These include validation rules comparing ResultSign and SIR to reject combinations which are not logical and validation rules for ResultSign and ResultValue which do not allow the use of ResultSign '>='
2015	**GONOAMR**	Following discussions at the Euro-GASP co-ordination meeting in December 2013 and the STI Network Meeting in 2014, the structure of the metadata has been changed to a single level one. This means that only one file needs to be uploaded now. This file includes all the epidemiological and microbiological variables. In addition, the following changes have been made: • New variables to collect data on diagnostic tests used and treatment used (both repeatable fields) • Removing Ureaplasma from the list of possible co-infections (not considered an STI in many patients) • Specifying “Mycoplasma genitalium” as a possible co-infection (previously defined as “mycoplasma”) • Reporting of penicillinase activity is now through the PenicillinaseActivityGONO field, coded as “Pos”, “Neg” or “Unk”. • Updating of validation rules in the context of the new structure. These changes have been implemented through a new record type version GONOAMR.v5. All previous metadata versions have been deactivated. This means that only this format can be used for reporting.
2014	**All**	Update NUTS codes according to the NUTS Codes 2010 classification from EUROSTAT

Annex 2 GONOAMR-specific material

- Contact information:
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Procedure for saving gonococcal isolates

1. Label a cryovial with a study number using a permanent marker, or the labels provided.
2. Using a loop, gather as much growth as possible from a pure fresh culture and re-suspend in the microbank fluid.
3. Close the cryovial tightly and invert 5 times to mix up the organism with the fluid.
4. Using a fine-tip pastette remove as much liquid as possible, and close the cryovial tightly.
5. Place in the freezer (preferable -70°C, range -50°C to -80°C) in a designated box.
6. Record the data for that strain and study number.

Centralised testing protocol

1. Isolates are shipped frozen to Public Health England, London, UK or Örebro University Hospital, Örebro, Sweden
2. The isolates are stored at −70°C or in liquid nitrogen.
3. Isolates are transferred to non-selective agar (such as GCVIT with 1% Vitox (Oxoid)) and incubated for 18 to 24 hours at 36°C in humid 5% CO_2-enriched atmosphere.
4. The purity and the identity of the isolates are confirmed by Gram stain, oxidase and PCR or Maldi-TOF. A further sub-culture from a single colony (to avoid mixed infections) is grown.
5. If there is a high level of contamination, cultures are repeatedly transferred to selective agar.
6. Susceptibility testing is performed using the agar dilution breakpoint technique Etest for ciprofloxacin, azithromycin, spectinomycin and gentamicin (spectinomycin and gentamicin tested in snapshot years only; 2016 and 2019). Suspensions of cultures aged 18 to 24 hours are prepared equivalent to McFarland standard 0.5 (approximately 10^4 colony forming units (cfu)/µL) in sterile saline. Using a multipoint inoculator, suspensions are inoculated onto GC agar plates with 1% Vitox, containing a panel of antimicrobials at the following breakpoint concentrations:

Table 5: Concentrations (mg/L) of antimicrobials used for the agar dilution breakpoint technique

Antimicrobial	Intermediate	Resistant
Ciprofloxacin	0.03	0.06
Spectinomycin♯		64
Gentamicin♯ (no breakpoint determined yet)	1, 2, 4, 8, 16	

♯Testing in snapshot years; 2016 and 2019

7. The ceftriaxone and cefixime MICs are determined using Etests according to the manufacturer's instructions.
8. All isolates are tested for penicillinase production using the chromogenic reagent Nitrocefin.
9. The following control strains are tested on the poured agar dilution plates and each batch of Etests (Table 6):

- WHO G
- WHO K
- WHO M
- WHO P
- WHO O (for use when spectinomycin is being tested)

Table 6. WHO Control Strains for use in Euro-GASP – MICs and susceptibility categories (SCs) obtained from Euro-GASP data

		Azithromycin		Cefixime		Ceftriaxone		Ciprofloxacin		Gentamicin		Spectinomycin	
Strain	**β-lactamase**		**MIC**	**SC**	**MIC**	**SC**	**MIC**	**SC**	**MIC**	**SC**	**MIC**	**SC**	**MIC**
WHO G	NEG		0.25	S	≤0.016	S	0.008	R	0.125	UK	4	S	16
WHO K	NEG		0.25	R	0.25	S	0.064	R	>32	UK	4	S	16
WHO M	POS		0.5	S	≤0.016	S	0.008	R	2	UK	4	S	16
WHO O	POS		0.25	S	0.016	S	0.016	S	0.008	UK	4	R	>1024
WHO P	NEG		4	S	≤0.016	S	0.004	S	0.004	UK	4	S	16

Notes: MIC data collated from the centralised/decentralised testing centres and the Euro-GASP EQAs to establish modal MICs and SCs. Decentralised laboratories should also establish their own local modal MIC data. Control strain MICs should be no more than one doubling dilution different to the MICs in the Table 6. The modal MICs in Table 6 may be updated when further data has been collected. Decentralised testing laboratories are ultimately responsible for their own QC data however QC data should be sent to the ECDC microbiologists regularly to ensure the data is within the expected limits.

10. Bacterial growth is recorded for the agar dilution plates and the MIC is recorded from the Etest plates. The category of resistance is determined using the following breakpoints:

Table 7. MIC breakpoints for specific antimicrobials

Antimicrobial	**MIC breakpoint (mg/L)**		
	R >	**I**	**S ≤**
Azithromycin	1*		1*
Cefixime	0.12*		0.12
Ceftriaxone	0.12*		0.12
Ciprofloxacin	0.06	0.06	0.03
Spectinomycin	64		64
Gentamicin	No breakpoints determined yet		

Note: European Committee on Antimicrobial Susceptibility Testing breakpoints are used (www.eucast.org/clinical_breakpoints).
**ECOFF used to detect isolates with antimicrobial resistance determinants, which are recorded as "R" in Euro-GASP*
***0.125 mg/L if Etest or other MIC gradient strip test is used*

11. Isolates that are contaminated in the original vial or are slow to grow are re-saved.

Annex 3 Protocol for Euro-GASP implementation at the national level

Each country referring gonococcal isolates or susceptibility data should provide the following additional information to implement Euro-GASP at national level. This information is critical in interpreting data and in ensuring accurate linking of laboratory and epidemiological data. Data to be provided includes:

- Sampling strategy – providing information on the geographical coverage of isolates submitted (complete, national, regional, local).
- Information on regions of the country covered (or place of residence)
- Describe the Data source and sampling frame: where the isolates come from (STI clinics, DV clinics, GPs, hospitals etc.); how are they sampled (consecutive patients; sampling)
- How is the AMR data linked to the epidemiological data (available with isolate submitted to the laboratory, data is requested from the isolate source, such as the STI clinic/GP surgery, data is requested from the epidemiologist)
- MIC range of testing method for each antimicrobial;
- Control strains tested for each media/reagent batch or for each antimicrobial tested;
- Institute/Laboratory/Person submitting the AMR and epidemiological AMR data in TESSy;
- Information on how the AMR data and epidemiological data is linked.

Please complete and return it to:

Email: *STIHIVHEP@ecdc.europa.eu* in copy to *michelle.cole@phe.gov.uk*

Table 8. Euro-GASP information form

1. Identifying information Name: Laboratory/Institute name: Date form completed:
2. Sampling strategy – Please provide information on the geographical coverage of isolates submitted (complete, national, regional, local)
3. Please provide information on regions of the country covered (or place of residence)
4. Please describe the source of the isolates (STI clinics, DV clinics, GPs, hospitals etc.)
5. How are the isolates sampled (consecutive, selective)?
6. How were the epidemiological data obtained (available with isolate submitted to the laboratory; data were requested from the isolate source, such as the STI clinic/GP surgery; data were requested from the epidemiologist)?
7. How are the AMR data and epidemiological data linked?
8. Institute/laboratory/person submitting the GC AMR data to TESSy.

9. Institute/laboratory/person submitting the epidemiological data to TESSy.

10. For laboratories performing decentralised testing, please provide the following antimicrobial information:

	Methodology (MIC gradient strip testing and manufacturer/Agar dilution/breakpoint)	Agar base (GC, chocolate, DST etc.)	MIC range (min – max)
Ceftriaxone			
Cefixime			
Azithromycin			
Ciprofloxacin			
Spectinomycin			
Gentamicin			
Beta-lactamase			

11. Please list the control strains tested for each media/reagent batch or for each antimicrobial tested.