



TESSy - The European Surveillance System

Integrated respiratory virus surveillance RESPISEVERE and RESPISURV data sets Reporting Protocol Version 1.2, 13 December 2022

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Summary of changes to current metadata

V1.2 (13 December 2022)

- Updated coded value list for the variable VirusVariantCOVID (for RESPISURV) for reporting of XBB (Pango lineage XBB and sub-lineages).

V1.1 (October 2022)

- New influenza strains added to coded value lists in AntigenicGroup and GeneticClade.
- BQ.1 (Pango lineage BQ.1 and sub-lineages) added to coded value list VirusVariantNCOV [27 October 2022]

How to use this document

This Reporting Protocol provides information for reporting countries' data managers in three main sections:

- [Reporting to TESSy](#) – contains guidelines on how to prepare data for submission to TESSy, deadlines for data submission, subject-specific information (e.g. new changes to metadata), and links to further information.
- [Annex](#) – contains:
 - The metadata set for the subject(s) covered by this Reporting Protocol.

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 [TESSy Technical Guidelines & Tools](#) (see the menu 'Technical Guidelines and Tools' when logged in TESSy), 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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Introduction

This Reporting Protocol describes integrated data collection for influenza, SARS-CoV-2, and potentially other respiratory viruses (such as RSV or new viruses of public health concern) in the EU/EEA and wider WHO European Region. It includes two integrated record-types:

1. **RESPISURV** for reporting of **case-based data by pathogen** for cases meeting one or more of the following criteria:
 - Positive cases presenting to primary care sentinel surveillance systems (where data are available in case-based format)
 - Cases that have been sequenced or genotyped (SARS-CoV-2) or (sub)typed/lineage determined (influenza) irrespective of disease severity
 - Data on severe cases (hospitalised, requiring respiratory support, ICU admission or fatal) that are not covered by existing SARI surveillance systems (and therefore reported into SARISURV), irrespective of whether variant/type/lineage is available

Data reported into RESPISURV should ideally link laboratory and case information including virus characterisation and antiviral resistance data. Unlinked data can be reported to INFLANTIVIR if not possible to report to RESPISURV for the season 2022/23, however double reporting should be minimized as much as possible.

2. **RESPISEVERE** for reporting of **age-disaggregated hospital and ICU indicators** (new admissions and numbers of current inpatients due to respiratory illness associated with the pathogen), aggregated by week, indicator, and pathogen.

Please note that:

1. All data collected are shared with the World Health Organisation – Regional Office for Europe (WHO/Europe) on a daily basis to fulfil Member States reporting requirements to WHO. Duplicate reporting is therefore not required.
2. If data have not been uploaded in TESSy and approved on time it will not be possible to include the data in weekly reports. If you are unable to meet this deadline, please contact the ECDC Influenza and other respiratory viruses surveillance team (ecdc.influenza@ecdc.europa.eu, covid.surveillance@ecdc.europa.eu, and copy tessy@ecdc.europa.eu).
3. Case-based data on human infections with zoonotic influenza viruses should be reported to **INFLZOO** metadata set and aggregated to **INFLVIRWAGGR**.
4. Aggregated data on number of tests and detections for influenza and RSV data from sentinel and non-sentinel sources should be reported to **INFLVIRWAAGR** dataset. Aggregated data on number of tests and detections for SARS-CoV-2 data from sentinel sources should be reported to **INFLVIRWAAGR** dataset and aggregated non-sentinel data reported to **NCOVAGGR** and **NCOVTEST**.
5. Aggregated and case-based data from SARI surveillance systems should be reported to **INFLSARIAGGR**, **SARISURV** and denominator data to **SARIDENOM**.
6. Case-based data from laboratory-based surveillance on influenza-confirmed patients in hospitals should continue to be reported to **INFLSARI**.
7. Testing and variant data for SARS-CoV-2 should be continued to be reported to **NCOVTEST** and **NCOVVARIANT**

Definitions

Case definition: Cases should be reported according to the current [EU case definition](#). Data on probable and possible cases are not collected.

Definition of a hospitalised case: A patient who has tested positive for COVID-19 (within 14 days prior to admission or during the current admission) presenting with severe symptoms/complications from COVID-19 that require admission to a hospital or ICU/HDU facility. Patients admitted to hospital for isolation purposes and not because of clinical need should not be counted as hospitalised cases where it is possible to make a distinction.

Definition of a case admitted to an intensive care unit (ICU) or a high dependency unit (HDU)¹: A patient who has tested positive for COVID-19 (within 14 days prior to admission or during the current admission) presenting with severe symptoms/complications from COVID-19 that require admission to an ICU/HDU facility.

For reporting the number of current hospital or ICU/HDU in-patients (to RESPISEVERE), COVID-19 cases in hospital or ICU/HDU should continue to be counted even after they test negative provided the current hospital or ICU/HDU stay is a consequence of the COVID-19 infection. Weekly counts are estimated based on the number in hospital or ICU/HDU as of Wednesday for the week of reporting.

Aim

To support the timely and complete reporting of key information for influenza, COVID-19, and potentially other respiratory virus infections (such as RSV or new viral diseases of public health concern).

Objectives

1. Monitor the intensity, geographical spread and temporal patterns of influenza, COVID-19, and other respiratory virus infections to inform mitigation measures.
2. Monitor severity, risk factors for severe disease, and assess the impact on healthcare systems of influenza, COVID-19, and other respiratory virus infections to inform mitigation measures.
3. Monitor changes and characteristics of circulating and emerging respiratory viruses, particularly virological changes of influenza viruses, SARS-CoV-2, and other respiratory viruses to inform treatment, drug, and vaccine development.
4. Describe the burden of disease associated with influenza, COVID-19, and other respiratory virus infections.

¹ *High dependency unit: a unit with capabilities for more intensive observation, treatment and nursing care than can be provided on a regular ward*

Reporting to TESSy

When, what and how to report

Deadline for reporting:

COVID-19: Tuesday 23:59 for NCOVAGGR, NCOVARIANT, NCOVTEST, RESPISEVERE, and RESPISURV. Thursday 10:00 for INFLVIRWAGGR and all SARI recordtypes. Further detail on reporting of COVID-19 can be found on the [ECDC website](#).

Influenza and RSV: Thursday 10:00 for all recordtypes. Further detail on reporting of Influenza can be found on the [ECDC website](#).

Preparing data

Data may be entered directly in TESSy for individual records ('Manually create a record'). For any batch reporting by file upload (CSV or XML format) please note that once the data has been exported from your national database it needs to be in a format that TESSy can accept (see 'checking metadata').

Checking metadata

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

To ensure data can be saved correctly in TESSy, please check the 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 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 [Tessy User Guide](#) provides an overview of how you work with the metadata file, and the TESSy user documentation provides in-depth details on metadata.

Submitting your data

Data are submitted through the TESSy web interface (go to **Upload**). Previously reported data can be found through the review tab (see below).



 The [Tessy User Guide](#) provides an overview of how you submit files to TESSy and 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 check in the **Validation details** webpage has completed. 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 the approval of other uploads.

- The TESSy user documentation provides information on reviewing validation results and adjusting reporting periods to avoid overwriting existing records.
- General training and guidance on reporting is available on the [TESSy website](#). A training video on reporting COVID-19 data is available in the [ECDC virtual academy](#).

TESSy HelpDesk

Email: TESSy@ecdc.europa.eu

Telephone number: **+46-(0)8-5860 1601**

Availability: 9:00 – 16:00 Stockholm time, Monday to Friday (except ECDC Holidays)

Annex – Integrated Respiratory viral disease metadata

Revisions of the integrated respiratory viral disease metadata sets RESPISURV and RESPISEVERE

The most recent metadata set is available from the TESSy website under technical guidelines and tools tab (as shown below).



Metadata sets

Current record type versions

Table 1 shows the record type versions to be used when reporting integrated respiratory viral disease (Record type: RESPI) data to TESSy.

Table 1: RESPI record type versions

Record type	Type of data	Record type version
RESPISURV	Case-based	1
RESPISEVERE	Case-based ²	1

RESPISEVERE metadata record type version 1

Common TESSy variables

Record id (mandatory)

Field: RecordId

Coding: Text (max 80 characters)

The record identifier is provided by the Member State. It must be:

- unique within the national respiratory virus diseases surveillance system
- anonymous.

² RESPISEVERE is a “case-based” record type as it allows multiple rows for the same week. However, the number of hospital/ICU/HDU admissions or current inpatients are reported in an aggregated way.

Record type (mandatory)

Field: RecordType

Coding: RESPISEVERE = Respiratory virus severity indicators

The record type defines the structure and the format of the data reported (case based reporting or aggregate reporting). The record types are defined by ECDC and are related to the subject. Only valid combinations of subject, record type and data source are accepted.

Record type version

Field: RecordTypeVersion

Coding: Numeric

The version of the record type defines the current structure of the data reported. If no RecordTypeVersion is provided in the batch, it is set automatically with current version of the Record type. The current version of the RESPISEVERE record type is 1.

This variable is not mandatory as TESSy concludes the record type version from the metadata set indicated by default. However, RecordTypeVersion is required when no metadata set is provided at upload or when a RecordTypeVersion, other than the current one, needs to be used.

Subject (mandatory)

Field: Subject

Coding: RESPISEVERE = Respiratory virus severity indicators

The subject describes the data to be reported.

Data source (mandatory)

Field: DataSource

Coding: Can be created/ modified by the National Coordinator

The data source specifies the source from which the data originates and is generated and revised/updated by the national contact point for surveillance in each Member State. If needed multiple data sources per country can be entered by different users to facilitate reporting.

Status (mandatory)

Field: Status

Coded value list name: [Statuses]

Coding: DELETE = Delete a previously reported record.

NEW/UPDATE = Report a new or update a previously reported record (default).

The field 'Status' is used for updating data; the default is NEW/UPDATE. By choosing DELETE the selected record (or batch of data) will remain in TESSy but be marked as inactive; this data can be used to reconstruct data for a given date in the past.

Reporting country (mandatory)

Field: ReportingCountry

Coded value list name: [Countries]

Coding: International organization for standardization (ISO) 3166-1-alpha-2, (two-letter code)

This variable identifies the country reporting the case.

Date used for statistics (mandatory)

Field: DateUsedForStatistics

Coding: yyyy-Www

The week for which the reported data refers. This is the date used by the national surveillance institute/organisation in reports and official statistics. The date used for statistics can vary from country to country but is preferably the date the case was notified to the national health authorities (notification date). For RESPISEVERE, the date should ideally be based on the date of admission to hospital or ICU for the week in which the Wednesday fell that was used for estimation of the number of current inpatients in hospital or ICU/HDU (see Indicator variable).

Epidemiological variables

Age 00-04

Field: Age00-04

Coding: Numeric

Number of patients for age group 0-4 years corresponding to the reported indicator, newly reported for week of reporting.

Age 05-14

Field: Age05-14

Coding: Numeric

Number of patients for age group 05-14 years corresponding to the reported indicator, newly reported for week of reporting.

Age 15-29

Field: Age15-29

Coding: Numeric

Number of patients for age group 15-29 years corresponding to the reported indicator, newly reported for week of reporting.

Age 15-64

Field: Age05-14

Coding: Numeric

Number of patients for age group 15-64 years corresponding to the reported indicator, newly reported for week of reporting. Please only use this reporting type if data are not report for 15-29 and 30-64 separately.

Age 30-64

Field: Age30-64

Coding: Numeric

Number of patients for age group 30-64 years corresponding to the reported indicator, newly reported for week of reporting.

Age 65+

Field: Age65-79

Coding: Numeric

Number of patients for age group 65+ years corresponding to the reported indicator, newly reported for week of reporting. Please only use this reporting type if data are not report for 65-79 and 80+ separately.

Age 65-79

Field: Age30-64

Coding: Numeric

Number of patients for age group 65-79 years corresponding to the reported indicator, newly reported for week of reporting.

Age 80+

Field: Age80+

Coding: Numeric

Number of patients for age group 80+ years corresponding to the reported indicator, newly reported for week of reporting.

Age UNK

Field: AgeUnk

Coding: Numeric

Number of patients with unknown age, newly reported for week of reporting.

Indicator (mandatory)

Field: Indicator

Coded value list name: Indicator

Coding: HOSAD = Weekly hospital admissions due to respiratory illness associated with the pathogen

HOSINPAT = Current inpatients in hospital due to respiratory illness associated with the pathogen as of Wednesday for the week of reporting

ICUAD = Weekly ICU admissions due to respiratory illness associated with the pathogen

ICUINPAT = Current inpatients in ICU/HDU due to respiratory illness associated with the pathogen as of Wednesday for the week of reporting

Selected indicator due to respiratory illness associated with the pathogen

Pathogen (mandatory)

Field: Pathogen

Coded value list name: PathogenRESPI

Coding: INFL = Influenza virus

MERS = MERS-CoV

RSV = Respiratory syncytial virus

SARSCOV2 = SARS-CoV-2

O = Other

Pathogen associated with severity indicator. If selecting Other, please specify which pathogen in Pathogen – Other.

Pathogen – Other

Field: PathogenOther

Coding: Text

Specified pathogen not captured in the coded values for Pathogen.

RESPISURV metadata

The RESPISURV metadata, **recordtype version 1** is used for case-based data by pathogen for cases meeting one or more of the following criteria: (1) Positive cases presenting to primary care sentinel surveillance systems (where data are available in case-based format); (2) Cases that have been sequenced or genotyped (SARS-CoV-2) or (sub)typed/lineage determined (influenza) irrespective of disease severity; (3) Data on severe cases (hospitalised, requiring respiratory support, ICU admission or fatal) that are not covered by existing SARI surveillance systems (and therefore reported into SARISURV), irrespective of whether variant/type/lineage is available.

Data reported into RESPISURV should ideally link laboratory and case information including virus characterisation and antiviral resistance data. Unlinked data can be reported, however double reporting should be minimized as much as possible. If not possible to report influenza virus characterisation data to RESPISURV, it is possible to continue reporting strain-based data to INFLANTIVIR for the season 2022/23.

Irrespective of case-based data reporting to RESPISURV, all countries should report aggregated data by week for COVID-19 and Influenza.

Common TESSy variables

Record id (mandatory)

Field: RecordId

Coding: Text (max 80 characters)

The record identifier is provided by the Member State. It must be:

- unique within the national respiratory virus diseases surveillance system
- anonymous.

Record type (mandatory)

Field: RecordType

Coding: RESPISURV = Respiratory virus surveillance

The record type defines the structure and the format of the data reported (case based reporting or aggregate reporting). The record types are defined by ECDC and are related to the subject. Only valid combinations of subject, record type and data source are accepted.

Record type version

Field: RecordTypeVersion

Coding: Numeric

The version of the record type defines the current structure of the data reported. If no RecordTypeVersion is provided in the batch, it is set automatically with current version of the Record type. The current version of the RESPISEVERE record type is 1.

This variable is not mandatory as TESSy concludes the record type version from the metadata set indicated by default. However, RecordTypeVersion is required when no metadata set is provided at upload or when a RecordTypeVersion, other than the current one, needs to be used.

Subject (mandatory)

Field: Subject

Coding: RESPISURV = Respiratory virus surveillance

The subject describes the data to be reported.

Data source (mandatory)

Field: DataSource

Coding: Can be created/ modified by the National Coordinator

The data source specifies the source from which the data originates and is generated and revised/updated by the national contact point for surveillance in each Member State. If needed multiple data sources per country can be entered by different users to facilitate reporting.

Status (mandatory)

Field: Status

Coded value list name: [Statuses]

Coding: DELETE = Delete a previously reported record.

NEW/UPDATE = Report a new or update a previously reported record (default).

The field 'Status' is used for updating data; the default is NEW/UPDATE. By choosing DELETE the selected record (or batch of data) will remain in TESSy but be marked as inactive; this data can be used to reconstruct data for a given date in the past.

Reporting country (mandatory)

Field: ReportingCountry

Coding: International organization for standardization (ISO) 3166-1-alpha-2, (two-letter code)

This variable identifies the country reporting the case.

Date used for statistics (mandatory)

Field: DateUsedForStatistics

Coding: yyyy-mm-dd (preferred)
 yyyy-Www

This is the date used by the national surveillance institute/organisation in reports and official statistics. The date used for statistics can vary from country to country but it is preferably the date the case was notified to the national health authorities (notification date). If date of notification is not available, then date of onset or date of sample collection can be used instead. Where date of onset and/or date of sample collection are available then please also report these fields separately as these are most useful for epidemiological analysis.

Epidemiological variables

Age

Field: Age

Coding: Numerical (0-120)
 UNK = Unknown

Age of patient in years as reported in the national system at the time of disease onset.

Age in months

Field: AgeMonth

Coding: Numerical (0-23)
 NA = Not applicable
 UNK = Unknown

Age of patient in months as reported in the national system for cases <2 years of age at the time of disease onset.

Brand of last received COVID-19 vaccination dose

Field: BrandLastCOVID19Dose

Coded value list name: VaccineCOVID

Coding:

AZ = Vaxzevria – AstraZeneca
BECNBG = Inactivated – Beijing CNBG
BHACOV = Covaxin – Bharat
CAN = CanSino -Convidecia
CHU = Chumakov - Covi-Vac
COM = Comirnaty – Pfizer/BioNTech
COMBA.1 = Comirnaty – Pfizer/BioNTech Original/Omicron BA.1
COMBA.4-5 = Comirnaty – Pfizer/BioNTech Original/Omicron BA.4-5
CVAC = Curevac - CVnCOV
HAYATVAC = Hayat VAC
JANSS = Ad26.COV 2.5 – Janssen
MOD = mRNA-1273 – Moderna
MODBA.1 = Spikevax Moderna bivalent Original/Omicron BA.1
MODBA.4-5 = Spikevax Moderna bivalent Original/Omicron BA.4-5
NVX = Novavax – Covovax
NVXD = Novavax – Nuvaxovid
QAZVAQ = QazCovid-In
SGSK = Sanofi GSK - Subunit
SIICOV = Covishield – SII
SIN = Coronavac – Sinovac

SPU = Sputnik V – Gamaleya
SPUL = Gamaleya - Sputnik-Light
SRCVB = EpiVacCorona – SRCVB
UNK = Unknown
VLA = COVID-19 Vaccine (inactivated, adjuvanted) Valneva – Valneva
WUCNBG = Inactivated – Wuhan CNBG
ZFUZ = Sino-Uzbek - ZF-UZ-VAC
ZIF = Anhui ZL – Zifivax

Brand/Type of last received COVID-19 vaccination dose

Coinfection

Field: Coinfection

Coded value list name: PathogenRESPI

Coding: INFL = Influenza virus

MERS = MERS-CoV

O = Other

RSV = Respiratory syncytial virus

SARSCOV2 = SARS-CoV-2

Viral pathogen detected at the same time point (i.e., in the same specimen or within a 14-day timeframe). For SARS-CoV-2 and influenza co-infections, the variables Pathogen and Coinfection should be used to indicate these two pathogens, with VirusVariantCOVID and InfluenzaTypeSubtype used to specify the SARS-CoV-2 variant and influenza (sub)type/lineage.

Coinfection – Other

Field: CoinfectionOther

Coding: Text

UNK = Unknown

Specified pathogen not captured in the coded values for Coinfection.

Complications

Field: Complications

Coded value list name: ComplicationsNCOV

Coding: AKI = Acute renal injury

ARDS = Acute respiratory distress syndrome

BRONCH = Bronchiolitis

ENCEPH = Encephalitis

HEARTFAIL = Heartfailure

MIS-C = Multisystem Inflammatory Syndrome in Children

MULTIFAIL = Multi-organ failure

MYOCARD = Myocarditis

NONE = None

O = Other (please specify separately)

OTHBAC = Other secondary bacterial infection

PNEU = Bacterial pneumonia (secondary)

SEPSIS = Sepsis

STILLBIRTH = Still birth as pregnancy outcome in a case

UNK = Unknown

Complication associated with illness. This variable can be repeated in the event of multiple complications.

Date last received COVID-19 vaccination dose

Field: DateLastVaccDose

Coding: yyyy-mm-dd
 UNK = Unknown

Date last received COVID-19 vaccination dose.

Date of admission to hospital

Field: DateOfHospitalisation

Coding: yyyy-mm-dd
 UNK = Unknown

Date of admission to hospital (exact date). If not applicable, please use 'UNK'.

Date of admission to Intensive Care Unit/High Dependency Unit

Field: DateOfICUHDU

Coding: yyyy-mm-dd
 UNK = Unknown

Date of admission to intensive care unit or high dependency unit (exact date). If not applicable, please use 'UNK'.

Date of death

Field: DateOfDeath

Coding: yyyy-mm-dd
 UNK = Unknown

Date of death (exact date). If not applicable, please use 'UNK'.

Date of hospital discharge

Field: DateOfDischarge

Coding: yyyy-mm-dd
 UNK = Unknown

Date of discharge from hospital (exact date). If not applicable, please use 'UNK'.

Date of onset of disease

Field: DateOfOnset

Coding: yyyy-mm-dd
 UNK = Unknown

Date of onset of symptoms (exact date). If not applicable, please use 'UNK'.

Drug Used for Prophylaxis

Field: DrugUsedProphylaxis

Coded value list name: DrugUsedRESPISURV

Coding: J05AB16 = Remdesivir
J05AC02 = Rimantadine
J05AH01 = Zanamivir
J05AH02 = Oseltamivir
J05AX25 = Baloxavir marboxil
N04BB01 = Amantadine
O = Other
UNK = Unknown

Antivirals used as prophylaxis in the 14 days before onset of illness. This variable can be repeated in the event of multiple drugs used.

Drug Used for Treatment

Field: DrugUsedTreatment

Coded value list name: DrugUsedRESPISURV

Coding: J05AB16 = Remdesivir
J05AC02 = Rimantadine
J05AH01 = Zanamivir
J05AH02 = Oseltamivir
J05AX25 = Baloxavir marboxil
N04BB01 = Amantadine
O = Other
UNK = Unknown

Antivirals used for treatment of the case during illness phase. This variable can be repeated in the event of multiple drugs used.

Gender

Field: Gender

Coded value list name: Gender

Coding: F = Female
M = Male
O = Other
UNK = Unknown

Gender of the reported case.

Health care worker

Field: HealthCareWorker

Coded value list name: YesNoUnk

Coding: N = No
UNK = Unknown
Y = Yes

Information on whether the case is a healthcare worker or not.

Hospitalisation

Field: Hospitalisation

Coded value list name: YesNoUnk

Coding: N = No

UNK = Unknown

Y = Yes

Admission to hospital.

Influenza type and subtype

Field: InfluenzaTypeSubtype

Coded value list: VirusTypeSARI

Coding: A = Influenza A, not sub-typed

PanAH1N1 = A(H1N1)pdm09

PanAH1 = A(H1)pdm09, not N-typed

AH3N2 = A(H3N2)

AH3 = A(H3), not N-typed

B = Influenza B no lineage

BVic = Influenza type B, Victoria lineage

BYam = Influenza type B, Yamagata lineage

UNK = Unknown or not applicable (where Pathogen is not Influenza)

Influenza type, subtype, or lineage to be reported where Influenza is reported for the variables Pathogen or Coinfection

Influenza vaccinated current season

Field: InfluenzaVaccinated

Coded value list name: YesNoUnk

Coding: N = No

UNK = Unknown

Y = Yes

Received influenza vaccination in the most recent influenza season.

Intensive care

Field: IntensiveCare

Coded value list name: YesNoUnk

Coding: N = No

UNK = Unknown

Y = Yes

Case required care in an intensive care unit or high dependency unit (unit with capabilities for more intensive observation, treatment and nursing care than can be provided on a regular ward).

Number of COVID-19 vaccination dose received

Field: NumberOfCovid19VaccDose

Coding: Numeric

Number of COVID-19 vaccination doses received.

Outcome

Field: Outcome

Coded value list name: OutcomeRESPI

Coding: ALIVE = Alive, recovered, cured, discharged from hospital

DIED = Died, as a result of viral respiratory infection

DIEDOTH = Died, other

STILLTREATMENT = Still on medical treatment related to viral respiratory infection (not recovered)

UNK = Unknown outcome

Outcome refers to the patient's vital status resulting from viral respiratory infection (indicated pathogen). If death occurred due to another disease or reason, 'DIEDOTHER' should be reported. If the patient is still ill at the time of reporting, code the outcome as 'STILLTREATMENT'. The outcome should be updated when the patient's final outcome is known.

Pathogen (mandatory)

Field: Pathogen

Coded value list name: PathogenRESPI

Coding: INFL = Influenza virus

MERS = MERS-CoV

O = Other

RSV = Respiratory syncytial virus

SARSCOV2 = SARS-CoV-2

This variable identifies the primary pathogen identified. If multiple pathogens were identified, please use the variable Coinfection to specify the second pathogen. For SARS-CoV-2 and influenza co-infections, the variables Pathogen and Coinfection should be used to indicate these two pathogens, with VirusVariantCOVID and InfluenzaTypeSubtype used to specify the SARS-CoV-2 variant and influenza (sub)type/lineage.

Pathogen - Other

Field: PathogenOther

Coding: Text

UNK = Unknown

Specified pathogen not captured in the coded values for Pathogen

Place of infection

Field: PlaceOfInfection

Coding: NUTS_GAUL

The probable place of infection should be provided at the NUTS 3 level. If the place of infection is not an EU/EEA country, then use GAUL nomenclature.

Place of residence

Field: PlaceOfResidence

Coding: NUTS_GAUL

Place of residence of patient at the time of disease onset. Select the most detailed NUTS for EU/EEA countries. If the residence of the case is not an EU/EEA country, then use GAUL nomenclature.

Precondition

Field: Precondition

Coded value list: Preconditions

Coding: ASPL = Asplenia

ASTH = Asthma

CANC = Cancer, malignancy

CARDIACDIS = Cardiac disorder, excluding hypertension

DIAB = Diabetes

HIV = HIV

HYPERT = Hypertension

IMMUNO = Immune deficiency

KIDNEY = Kidney-related condition, renal disease

LIVER = Liver-related condition, liver disease

LUNG = Chronic lung disease, excluding asthma

NEUROMUS = Neuromuscular disorder, chronic neurological

NONE = None

O = Other precondition

OBES = Obesity

PREG = Pregnancy, trimester is unknown

PREG1 = Pregnancy, 1st trim, the 1st trim is from week 1 to the end of week 12

PREG2 = Pregnancy, 2nd trim, the 2nd trim is from week 13 to the end of week 26

PREG3 = Pregnancy, 3rd trim, the 3rd trim is from week 27 to the end of the pregnancy

PREGPOST = Post-partum (<6 weeks)

SMOKE = Smoke

TB = Tuberculosis

UNK = Unknown precondition

Patient's underlying condition(s). This variable can be repeated in the event of multiple preconditions.

Primary care case definition

Field: CaseDefinitionPC

Coded value list: CaseDefinitionPCRESPISURV:

Coding: ARI = Acute respiratory infection

ILI = Influenza-like illness

OTH= Other

UNK = Unknown

Case definition used for cases detected through primary care sentinel surveillance.

Primary care case definition - Other

Field: CaseDefinitionPCOther

Coding: Text

UNK = Unknown

Specified case definition not captured in the coded values for Primary Care Case Definition.

Respiratory support

Field: RespSupport

Coded value list: RespSupportNCOV

Coding: ECMO = Extracorporeal membrane oxygenation

N = No

O = Other

OXYGEN = Oxygen therapy

UNK = Unknown

VENT = Ventilator including non-invasive pos pressure vent

Level of respiratory support given to patient

SARS-CoV-2 variant type

Field: VirusVariantCOVID

Coded value list: VirusVariantNCOV

Coding:

P.1 = P.1 variants (L18F, T20N, P26S, D138Y, R190S, K417T, E484K, N501Y, H655Y, T1027I, V1176F)

S_GENE_DELETION = Variant virus with deletion in S-gene (defined by mutation: del 69-70 or by negative S-gene RT-PCR)

VARIANT_OTHER = Variants not included in the coded value list, please specify

B.1.525 = B.1.525 (mutations: E484K, D614G, Q677H)

B.1.427/B.1.429 = B.1.427/B.1.429 (mutations: L452R, D614G)

B.1.617.2 = B.1.617.2 (mutations: L452R, T478K, D614G, P681R); B.1.617.2 and all of its sublineages including AY sublineages

B.1.621 = B.1.621 (mutations: R346K, E484K, N501Y, D614G, P681H)

B.1.351 = B.1.351 (defined by mutations: D80A, D215G, E484K, N501Y, A701V)

B.1.1.7 = B.1.1.7 (mutations: del69-70, del144, N501Y, A570D, D614G, P681H, T716I, S982A, D1118H)

C.37 = C.37 (mutations L452Q, F490S, D614G)

BA.1 = BA.1 or B.1.1.529 with mutations del69-70, ins214EPE, S371L, G496S, T547K

BA.2 = BA.2 or B.1.1.529 with mutations V213G, T376A, R408S

BA.2.75 = BA.2 sub-lineage with mutations D339H, G446S, N460K, and R493Q in the RBD, and mutations K147E, W152R, F157L, I210V, and G257S in the N-terminal domain of the Spike protein

BA.2+L452X = BA.2 and any of its sub-lineages with mutations at position 452 of the Spike protein

BA.3 = BA.3 or B.1.1.529 with mutations del69-70, ORF1a:A3657V, ORF3a:T22V

BA.4 = BA.4 or B.1.1.529 with mutations L452R, F486V, del69-70, NSP7b: L11F, N:P151S, ORF1a: Δ141-143

BA.5 = BA.5 or B.1.1.529 with mutations L452R, F486V, del69-70

BQ.1 = Pango lineage BQ.1 and sub-lineages

XBB = Pango lineage XBB and sub-lineages

UNK = Sequence information unknown or not available

COVID-19 case with a variant virus of SARS-CoV-2 according to a mutation pattern of specific concern identified by sequence analysis or by a specific RT-PCR pattern. Each virus should only be reported once, using the most specific variant available, to avoid double reporting. If several apply, choose the most specific variant (highest number of matching mutations). The mapping of sublineages published at https://www.ecdc.europa.eu/sites/default/files/documents/PathogenVariant_public_mappings.csv should be used to determine how to assign specific sublineages to items in the coded value list above. Additional information about which specific sublineages have been mapped may optionally be provided in addition in VirusVariantCOVIDOther. Variants not included in the coded value list and/or which cannot be mapped to variants in the coded value list should be reported using

VARIANT_OTHER with more details provided in VirusVariantCOVIDOther. If typing results are inconclusive, report UNK.

SARS-CoV-2 variant type - Other

Field: VirusVariantCOVIDOther

Coding: Text

UNK = Unknown

Specified variant type not captured in the coded values for VirusVariantCOVID variable as indicated in VARIANT_OTHER response for VirusVariantCOVID variable.

Sequencing category

Field: SequencingCategory

Coded value list: SequencingCategoryRESPISURV

Coding: REPRESENTINEL = Representative, based on specimens from sentinel (primary care or SARI) surveillance

REPNONSENTINEL = Representative, based on a carefully selected subset of non-sentinel specimens

TARGETED = Targeted

UNK = Unknown

Sequencing category should be completed for samples where variant/subtype/type is known. Representative can be reported where the intention is to estimate the distribution of circulating variant/subtype/type in the population, based on samples taken in sentinel sites (REPRESENTINEL) and/or from a carefully selected (representative) subset of non-sentinel specimens (REPNONSENTINEL), where this is needed to increase the volume of representative sequencing or genotyping to the desired detection threshold. Targeted sequencing can be reported for unusual events or clinical presentations, travel, outbreaks, etc.

Refer to <https://www.ecdc.europa.eu/en/publications-data/operational-considerations-respiratory-virus-surveillance-europe> for more details.

Surveillance system

Field: SurvSystem

Coded value list: SurvSystem

Coding: NONSTL = Non-sentinel

REG = Registry

STL = Sentinel

UNK = Unknown

Type of surveillance system through which the case was notified.

Laboratory variables

Antigenic group

Field: AntigenicGroup

Coded value list: AntigenicGroupINFL

Coding:

agAH1/Guangdong-Maonan/SWL1536/2019 = A(H1) A/Guangdong-Maonan/SWL1536/2019 (H1N1)-like

agAH1/Norway/25089/2022 = A(H1) A/Norway/25089/2022 (H1N1)-like

agAH1/Sydney/5/2021 = A(H1) A/Sydney/5/2021 (H1N1)-like

agAH1/Victoria/2570/2019 = A(H1) A/Victoria/2570/2019 (H1N1)-like

agAH1NOCAT = A(H1)pdm09 not attributed to category
 agAH3/Cambodia/e0826360/2020 = A(H3) A/Cambodia/e0826360/2020-like
 agAH3/Darwin/9/2021 = A(H3) A/Darwin/9/2021-like
 agAH3/Denmark/3264/2019 = A(H3) A/Denmark/3264/2019 (H3N2)-like
 agAH3/Kansas/14/2017 = A(H3) A/Kansas/14/2017 (H3N2)-like
 agAH3NOCAT = A(H3) not attributed to category
 agBVictB/Austria/1359417/2021 = B/Austria/1359417/2021-like (BVictoria/2/87 (V1A.3a.2)-lineage)
 agBVictB/Brisbane/60/2008 = B/Brisbane/60/2008-like (B/Victoria/2/87 lineage)
 agBVictB/Cote d'Ivoire/948/2020 = B/Cote d'Ivoire/948/2020-like (BVictoria/2/87 (V1A.3a.1)-lineage)
 agBVictB/Netherlands/11267/2022 = B/Netherlands/11267/2022 (BVictoria/2/87 (V1A.3)-lineage)
 agBVictB/Washington/02/2019 = B/Washington/02/2019-like (BVictoria/2/87 (V1A.3)-lineage)
 agBVictNOCAT = B(Vic) lineage not attributed to category
 agBYamB/Phuket/3073/2013 = B/Phuket/3073/2013-like (B/Yamagata/16/88 (Y3)-lineage)
 agBYamNOCAT = B(Yam) lineage not attributed to category
 Coded list of reference strains for influenza virus Antigenic group.

Date of sample collection

Field: DateOfSampleCollection

Coding: yyyy-mm-dd

UNK = Unknown

Date of collection of sample used for laboratory confirmation of the pathogen (exact date). If not available date of testing can be used (exact date). If not applicable, please use 'UNK'.

ENA identifier

Field: EnaId

Coding: Text

UNK = Unknown

European Nucleotide Archive (ENA) run identifier, based on which the sequence read data can be retrieved. Starts with ERR or SRR, i.e., not the sample or experiment which ERS/ERX or SRS/SRX.

Genetic clade

Field: GeneticClade

Coded value list: GeneticCladeINFL

Coding:

genAH1/Guangdong-Maonan/SWL1536/2019 = A(H1)pdm09 group 6B.1A.5a.1 representative A/Guangdong-Maonan/SWL1536/2019
 genAH1/India/Pun-NIV312851/2021 = A(H1)pdm09 group 6B.1A.5a.2 representative A/India/Pun-NIV312851/2021
 genAH1/Norway/25089/2022 = A(H1)pdm09 group 6B.1A.5a.2 representative A/Norway/25089/2022
 genAH1/Slovenia/1489/2019 = A(H1)pdm09 group 6B.1A.7 repr, A/ Slovenia/1489/2019
 genAH1/Sydney/5/2021 = A(H1)pdm09 group 6B.1A.5a.2 representative A/Sydney/5/2021

genAH1/Victoria/2570/2019 = A(H1)pdm09 group 6B.1A.5a.2 representative
 A/Victoria/2570/2019
 genAH1NOClade = A(H1)pdm09 not attributed to clade
 genAH1SubgroupNotListed = A(H1)pdm09 attributed to recognised group in the guidance
 but not listed here
 genAH3/Bangladesh/4005/2020 = A(H3) group 3C.2a1b.2a.2 repr,
 A/Bangladesh/4005/2020
 genAH3/Cambodia/e0826360/2020 = A(H3) group 3C.2a1b.2a.1 repr,
 A/Cambodia/e0826360/2020
 genAH3/Darwin/9/2021 = A(H3) group 3C.2a1b.2a.2 representative A/Darwin/9/2021
 genAH3/Denmark/3264/2019 = A(H3) group 3C.2a1b.1a representative
 A/Denmark/3264/2019
 genAH3/Hong Kong/2671/2019 = A(H3) group 3C.2a1b.1b representative A/ Hong
 Kong/2671/2019
 genAH3/Kansas/14/2017 = A(H3) group 3C.3a1 repr, A/ Kansas/14/2017
 genAH3/Slovenia/8720/2022 = A(H3) group 3C.2a1b.2a.2 representative
 A/Slovenia/8720/2022
 genAH3NOClade = A(H3) not attributed to clade
 genAH3SubgroupNotListed = A(H3) attributed to recognised group in current guidance but
 not listed here
 genBvicB/Austria/1359417/2021 = B(Vic)-lineage clade V1A.3a.2 repr,
 B/Austria/1359417/2021
 genBvicB/Cote d'Ivoire/948/2020 = B(Vic)-lineage clade V1A.3a.1 repr, B/Cote
 d'Ivoire/948/2020
 genBvicB/Netherlands/11267/2022 = B(Vic)-lineage clade V1A.3 representative
 B/Netherlands/11267/2022
 genBvicB/Washington/02/2019 = B(Vic)-lineage clade V1A.3 repr, B/Washington/02/2019
 genBvicCladeB/Brisbane/60/2008 = B(Vic)-lineage clade V1A representative
 B/Brisbane/60/2008
 genBvicNOClade = B(Vic) lineage not attributed to clade
 genBvicSubgroupNotListed = B(Vic) attributed to recognised group in current guidance
 but not listed here
 genBYamB/Phuket/3073/2013 = B(Yam)-lineage clade Y3 representative
 B/Phuket/3073/2013
 genBYamNOClade = B(Yam) lineage not attributed to clade
 genBYamSubgroupNotListed = B(Yam) attributed to recognised group in current guidance
 but not listed here

Coded list of reference strains for Genetic clade for influenza viruses.

HA sequence aa resistance mutations

Field: HAAAMutations

Coding: Text

Listing of amino acid substitution in HA, separated by semi colon. Format for reporting composition
 ALL relevant amino acid positions: e.g. E190D for influenza viruses.

InterpretationM2BlockerResistanceTesting

Field: InterpretationM2BlockerResistanceTesting

Coded value list: InterpretationResistanceTest

Coding: AAHRI = Amino acid substitution previously associated with highly reduced inhibition
 AAINP = Genotypic interpretation not possible

AANI = No amino acid substitution prev assoc. with (highly)reduced inhibition
AARI = Amino acid substitution previously associated with reduced inhibition
HRI = Highly reduced inhibition
NA = Not applicable
NI = Normal inhibition
RI = Reduced inhibition

Interpretation of M2BlockerResistanceTesting for influenza viruses.

InterpretationOseltamivirResistanceTesting

Field: InterpretationOseltamivirResistanceTesting

Coded value list: InterpretationResistanceTest

Coding: AAHRI = Amino acid substitution previously associated with highly reduced inhibition
AAINP = Genotypic interpretation not possible
AANI = No amino acid substitution prev assoc. with (highly)reduced inhibition
AARI = Amino acid substitution previously associated with reduced inhibition
HRI = Highly reduced inhibition
NA = Not applicable
NI = Normal inhibition
RI = Reduced inhibition

Interpretation of OseltamivirResistanceTesting for influenza viruses.

InterpretationPABlockerResistanceTesting

Field: InterpretationPABlockerResistanceTesting

Coded value list: InterpPABlockerResistanceTest

Coding: AAINP = Amino Acid substitution Interpretation not possible
AANS = No amino acid substitution in PA previously associated with reduced suscept
AARS = Amino acid substitution in PA previously associated with reduced susceptibility
NA = Not applicable

Interpretation of PABlockerResistanceTesting for influenza viruses.

InterpretationZanamivirResistanceTesting

Field: InterpretationZanamivirResistanceTesting

Coded value list: InterpretationResistanceTest

Coding: AAHRI = Amino acid substitution previously associated with highly reduced inhibition
AAINP = Genotypic interpretation not possible
AANI = No amino acid substitution prev assoc. with (highly)reduced inhibition
AARI = Amino acid substitution previously associated with reduced inhibition
HRI = Highly reduced inhibition
NA = Not applicable
NI = Normal inhibition
RI = Reduced inhibition

Interpretation of ZanamivirResistanceTesting for influenza viruses.

M2 sequence aa resistance mutations

Field: M2AAMutations

Coding: Text

UNK = Unknown

Listing of amino acid substitution in M2 separated by semi colon. Format for reporting composition ALL relevant amino acid positions: e.g. S31N for influenza viruses.

NA sequence aa resistance mutations

Field: NAAAMutations

Coding: Text

UNK = Unknown

Listing of amino acid substitution in NA separated by semi colon. Format for reporting composition ALL relevant amino acid positions: e.g. H275Y for influenza viruses.

PA sequence aa resistance mutations

Field: PAAAMutations

Coding: Text

UNK = Unknown

Listing of amino acid substitution in PA separated by semi colon. Format for reporting composition ALL relevant amino acid positions: e.g. I38T or I38M or I38 for influenza viruses.

Strain id

Field: StrainID

Coding: Text

UNK = Unknown

The name of the virus - For influenza: [A|B]/[country|region|city]/[number]/[year] (e.g. A/California/7/2009). For SARS-CoV-2: hCoV-19/[country|region|city]/[number]/[year] (e.g. hCoV-19/Sweden/23/2022). For RSV HRSV/[A|B][X]/[state/province/city.country name]/[number]/[year] (e.g. HRSV/A/Copenhagen.Denmark/54/2022).

NOTE: Please add StrainID if you have reported the variables AntigenicGroup, GeneticClade or VirusVariantCOVID to be able to link epi and lab data, especially if you are reporting those from two separate data sources.

Sequence identifier

Field: SequenceId

Coding: Text

UNK = Unknown

Sequence identifier for whole genome or whole or partial gene sequence, based on which the sequence read data can be retrieved from external database such as GISAID, GenBank or other db (except ENA). GISAID isolate sequence accession number should be reported in format EPI_ISL_402123, GenBank MK334047.1. Please report ENAId in EnaId variable.