TESSy - The European Surveillance System

Zoonotic influenza virus Reporting Protocol Version 2.2, May 2024

Contents

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 sets 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

An event of a human case infected with an influenza virus deriving from an animal source should be reported within 24 hours to EWRS which will cover the IHR notification for EU/EEA countries.

This reporting protocol describes the surveillance of the zoonotic influenza virus data in the EU/EEA and wider European Region.

Aggregate data on zoonotic influenza (number of tested H5, number tested H7, number detected H5 and number detected H7) can be uploaded to INFLZOOAGGR .

For the reporting of case-based data the record type INFLZOO should be used.

Aggregate data on number of tested and positive human cases enables the collection of denominator data as well as nominator data in case more human infections are occurring. For sporadic human infection a case-based reporting should be preferred to report information from people infected with a zoonotic influenza virus. The data aims to support situational risk assessment and trends over time.

Case-based and aggregate data can be uploaded retrospectively when more information becomes available.

Aim

To support the timely and complete reporting on number of samples tested, aggregate number of detected and of key information of zoonotic influenza cases in the EU/EEA and wider European Region.

Objectives

- To collect denominator data on number of tested people.
- To help assess the onset of the disease, confirmation of the subtype of infection and severity.
- To provide information on exposure, treatment and outcome.
- To provide additional contextual information to help understand the case identification.
- To analyse trends over time.

Changes from last version

Version 2.1: Inclusion of the aggregated record type INFLZOOAGGR and description of variables and coded value lists.

Version 2.2: Inclusion of additional species under INFLZOO variable on exposure to animal species

Reporting to TESSy

When, what and how to report

Deadline for reporting:

An event of a human infection with avian influenza virus should be reported within 24 hours to EWRS covering IHR for EU/EEA countries. If a suspected human case is under investigation, such information should be shared via EpiPulse with ECDC and other countries for awareness. Data for monitoring the event and assess trends should be reported to TESSy at least in the subsequent week following identification and confirmation.

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 data formats that are valid as 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.

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-Www** format (e.g 2021-W01); dates in any other format will be rejected.

- **Coded values**

  Some fields only permit the use of specific values (coded values). If any other value is used in the field, the upload 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.

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 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 you 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.
- 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 – Zoonotic influenza virus metadata

Revisions of the zoonotic influenza virus metadata set

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

Zoonotic influenza virus record types and metadata sets

Current record type versions

Table 1 shows the record type versions to be used when reporting zoonotic influenza virus case based (Record type: INFLZOO) or aggregated (Record-type: INFLZOOAGGR) data to TESSy.

Table 1: Zoonotic influenza virus record type versions

Record type	Type of data	Record type version
INFLZOO	Case-based	1
INFLZOOAGGR	Aggregated	1

INFLZOO metadata record type version 1

Common TESSy variables

Record identifier (mandatory)

Field: RecordId

Coding: Text (max 80 characters)

The record identifier is provided by the Member State. Enter a value that is unique for every record in the dataset with the format NUTS2 or countryregion_Www of cases (e.g. BE23_W23).

Record type (mandatory)

Field: RecordType

Coding: INFLZOO

The record type defines the structure and the format of the data reported.

Record type version

Field: RecordTypeVersion

Coding: 1

The version of the record type defines the current structure of the data reported. The current version

of the INFLZOO record type is 1. This variable is not mandatory as TESSy concludes the record type version from the metadataset indicated by default. However, the variable RecordTypeVersion can override this default.

Subject (mandatory)

Field: Subject
Coding: INFLZOO

The subject describes the data to be reported.

Data source (mandatory)

Field: DataSource
Coding: Pre-assigned as CountryCode-INFLZOO to each country; can be modified by National Coordinator

The data source (surveillance system) that the record originates from.

Status (mandatory)

Field: Status
Coding: NEW/UPDATE/DELETE

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-Www

The week reported cases were diagnosed.

Epidemiological variables

Date of onset (mandatory)

Field: DateOfOnset
Coding: yyyy-mm-dd, UNK

Date of onset of disease. Not applicable in asymptomatic cases. If not applicable, please use 'Unk'

Date of notification (mandatory)

Field: DateOfNotification

Coding: yyyy-mm-dd

UNK

Date when the case is notified the first time to the place of notification

Place of notification

Field: PlaceOfNotification

Coding: NUTS/GAUL

Place of the first notification of the case to a regional authority. Select the most detailed NUTS level possible. Region should be provided at the NUTS 2 level. If the region is not in 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(EU/EEA) or GAUL(non-EU/EEA) level possible

Imported

Field: Imported

Coding: N = No
Y = Yes
UNK = Unknown

Patient travelled outside the reporting country in the 14 days prior to symptom onset

Probable country of infection (repeatable)

Field: ProbableCountryOfInfection

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

Country(ies) visited in the 2 weeks prior to onset of illness. If there is more than one country N/A should be used in the empty repeated fields.

EpiPulse ID (mandatory)

Field: EpiPulseID

Coding: TEXT

Link to EpiPulse through outbreak ID

Case classification

Field: Classification

Coding: CONF = Confirmed
POSS = Possible
PROB = Probable

UNK = Unknown

Case classification according to EU case definition or national definition

Laboratory method (repeatable)

Field: LabMethod

Coding:
ANTIGEN = Antigen detection
GENOSEQ = Genotyping/Sequencing
ISOV = Isolation of virus
NEU = Neutralisation
NUC = NAAT by RT-PCR, other or not specified
O = Other, please specify
SCONV = Seroconversion or fourfold titre rise
SIGG = NCOV specific IgG-antibodies
SIGM = NCOV specific IgM-antibodies
SIGMG = NCOV specific IgM- and IgG antibodies
UNK = Unknown

Laboratory method used to make diagnosis

Surveillance system

Field: SurvSys

Coding:
N = Non-sentinel patient
S = Sentinel patient
Unk = Unknown

Surveillance system, sentinel or non-sentinel

Setting

Field: Setting

Coding:
C = Community
H = Hospital
I = Investigation of outbreak
NA = Not applicable
OTH = other
UNK = Unknown

Specification of the setting of diagnosis or case identification

Gender

Field: Gender

Coding:
F = Female
M = Male
O = Other (e.g., transsexual)
UNK = Unknown

Gender of the reported case.

Age (mandatory)

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.

Virus Type (mandatory)
Field: VirusType
Coding: A = type A influenza virus
B = type B influenza virus
C = type C influenza virus
D= type D influenza virus
Virus type

Virus HA subtype (mandatory)
Field: HA Subtype
Coding: H1 = A(H1)
H2 = A(H2)
H3 = A(H3)
H4 = A(H4)
H5 = A(H5)
H6 = A(H6)
H7 = A(H7)
H8 = A(H8)
H9 = A(H9)
H10 = A(H10)
H11 = A(H11)
H12 = A(H12)
H13 = A(H13)
H14 = A(H14)
H15 = A(H15)
H16 = A(H16)
H17 = A(H17)
H18 = A(H18)
O = Other
UNK = Unknown

Virus HA subtype

Virus NA subtype (mandatory)
Field: NA Subtype
Coding: N1 = A(HxN1)
N2 = A(HxN2)
N3 = A(HxN3)
N4 = A(HxN4)
N5 = A(HxN5)
N6 = A(HxN6)
N7 = A(HxN7)
N8 = A(HxN8)
N9 = A(HxN9)
N10 = A(HxN10)
N11 = A(HxN11)
O = Other
UNK = Unknown

Virus NA subtype

Pathogen or subtype - Other
Field: TypeOther
Coding: TEXT

Details of pathogen or subtype, if coded as 'other', but is known.

Exposure to animal species (repeatable)
Field: AnimalExposure
Coding: A = avian (all species) if details or species unknown
B = bat
C = chicken or other domesticated birds (poultry, turkey,…)
F = ferret or mink
G = goat
P = pig
R = cattle
S = seal
W = wild bird
O = other
Unk = Unknown
Exposure of the human case infected with a zoonotic flu virus to an animal

Exposure to animal species, other species, describe
Field: AnimalExposureOther
Coding: TEXT

Exposure of the human case infected with a zoonotic flu virus to an animal species not listed

Viral coinfection (repeatable)
Field: ViralCoinfection
Coding: SARSCOV2 = SARS-CoV-2
INFL = seasonal influenza virus
O = Other respiratory viral pathogen, please specify
OTHCOR = Other coronavirus
RSV = RSV (Respiratory syncytial virus)
UNK = Unknown
Presence of viral co-infection

Viral coinfection - Other
Field: ViralCoinfectionOther
Coding: TEXT

Other viral coinfection not found in the list of possible values

Clinical Presentation (repeatable)
Field: ClinicalPresentation
Coding: ASY = Asymptomatic
CONJ = Conjunctival injection
COUGH = Dry or productive cough
DIARR = Diarrhoea
FEVER = History of fever/chills
HEAD = Headache

IRR = Irritability/confusion
O = Other, please specify
PAIN = Pain
PAINABDO = Pain - abdominal
PAINCHEST = Pain - chest
PAINJOINT = Pain - joint
PAINMUSC = Pain - muscular
PAINOTH = Pain - other
RUNOS = Runny nose
SBREATH = Shortness of breath
SORETHR = Sore throat
UNK = Unknown
VOMIT = Nausea/vomiting
WEAK = General weakness

Clinical symptoms on onset

Clinical presentation – Other

Field: ClinicalPresentationsOther
Coding: Text
UNK = Unknown

Other reported clinical symptoms not found in the list of possible values

Influenza Vaccination

Field: InfluenzaVaccination
Coding: N = No
Y = Yes
UNK = Unknown

Current seasonal influenza vaccination

Date of Vaccination

Field: DateOfVacc
Coding: yyyy-mm-dd,
UNK

Date of vaccination

Occupation

Field: Occupation
Coding: HCW = HealthCareWorker
VET = Veterinarian
CUL = Culler
COF = Commercial farmer
BYF = Backyard or hobby farmer
RIN = Bird ringer
OTH = other
UNK = unknown

Information on the occupation of the case

Occupation– Other

Field: OccupationOther
Coding: TEXT

Information on the occupation of the case not listed

Precondition (repeatable field, mandatory)

Field: Precondition
Coding: ASPL = Asplenia
ASTH = Asthma
CANC = Cancer, malignancy
CARDIACDIS = Cardiac disorder, excluding hypertension
DIAB = Diabetes
HIV = HIV/other immune deficiency
HYPERT = Hypertension
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, please specify
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 = Current smoking
TB = Tuberculosis
UNK = Unknown precondition

Patient's underlying condition or conditions

Precondition –other

Field: PreconditionOther
Coding: Text
Details of underlying conditions, if Precondition is coded as 'other', but is known.

Hospitalisation (mandatory)

Field: Hospitalisation

Coding: N = No
UNK = Unknown
Y = Yes

Hospitalisation in the 4 weeks after onset of illness.

Date of Hospitalisation (mandatory)

Field: DateOfHospitalisation
Coding: *yyyy-mm-dd*

UNK= Unknown

If not applicable, please use 'UNK'. Date of Hospitalisation

Intensive care (mandatory)

Field: IntensiveCare

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).

Date of admission to ICU or HDU

Field: DateOfICUHDU

Coding: yyyy-mm-dd

Date of admission to intensive care unit or high dependency unit

Number of days in ICU or HDU

Field: NumberDaysICUHDU

Coding: Numerical
NA = Not applicable
UNK = Unknown

Total number of days patient spent in IDU or HDU

Complications (repeatable)

Field: Complications

Coding: AKI = Acute renal/kidney injury
ARDS = Acute respiratory distress syndrome
BRONCH = Bronchiolitis
ENCEPH = Encephalitis
HEARTFAIL = Heart failure
MULTIFAIL = Multi-organ failure
MYOCARD = Myocarditis
NONE = None
O = Other (please specify separately)
OTHBAC = Other secondary bacterial infection
PNEU = Bacterial pneumonia (secondary)
SEPSIS = Sepsis/Multi-organ failure
STILLBIRTH = Still birth as pregnancy outcome in a case
UNK = Unknown

Complications at any time

Respiratory support (mandatory, repeatable)

Field: RespSupport
Coding: ECMO = Extracorporeal membrane oxygenation
N = No
NOTAVAIL = No respiratory support available
NOTNEC = No respiratory support necessary
O = Other, please specify
OXYGEN = Oxygen therapy
UNK = Unknown
VENT = Ventilator including non-invasive positive pressure ventilation

Level of respiratory support given to patient.

Respiratory support - Other

Field: RespSupportOther
Coding: Text
UNK = Unknown

Other respiratory support not found in the list of possible values.

Outcome (mandatory)

Field: Outcome
Coding: ALIVE = Alive, recovered, cured
DIEDINFLZOO = zoonotic influenza was main or contributing cause of death
DIEDOTHER = Death not related to influenza infection
DIEDUNK = Cause of death unknown
STILLTREATMENT = Still on medical treatment (not recovered)
UNK = Unknown outcome

Information on the outcome of the case in the 4 weeks after onset of illness

Date of hospital discharge

Field: DateOfDischarge
Coding: yyyy-mm-dd
UNK= Unknown

Date of hospital discharge

Date of death

Field: DateOfDeath
Coding: yyyy-mm-dd
UNK= Unknown

Date of death (exact date only)

Cause of death

Field: CauseOfDeath
Coding: INFLMAIN = The main cause of death was influenza
INFLUNDER = The underlying cause of death was influenza
NOTINFL = Cause of death not influenza related.

SECBACT = The cause of death was a secondary bacterial infection acquired in hospital
UNK = Cause of death was unknown

Cause of Death

Drug Used Prophylaxis (mandatory)

Field: DrugUsedProphylaxis

Coding: NONE = None
AMA = Amantadine
BALO = Baloxavir Marboxil
O = Other (or combinations with other)
OSEL = Oseltamivir
OSELZANA = Oseltamivir and Zanamivir
UNK = Unknown
ZANA = Zanamivir

Antivirals used as prophylaxis in the 14 days before onset of illness

Drug Used Treatment (mandatory)

Field: DrugUsedTreatment

Coding: M2 = M2 inhibitors
NONE = None
BALO = Baloxavir Marboxil
O = Other (or combinations with other)
OSEL = Oseltamivir
OSELZANA = Oseltamivir and Zanamivir
UNK = Unknown
ZANA = Zanamivir

Antivirals used as prophylaxis in the 14 days before onset of illness

Starting date of Treatment (mandatory)

Field: DateOfTreatment

Coding: yyyy-mm-dd
UNK

Starting date for antiviral treatment of the case during illness phase

Resistance (mandatory, repeatable)

Field: Resistance

Coding: M2 = M2 inhibitors
NONE = None
O = Other
OSEL = Oseltamivir
UNK = Unknown
ZANA = Zanamivir
BALO = Baloxavir Marboxil

Resistance to antiviral treatment as assessed by virologists. Report whether resistance has been detected to any antivirals in the coded value list.

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.

M2 sequence aa resistance mutations

Field: M2AAMutations
Coding: TEXT
Listing of amino acid substitution in M2 associated with antiviral resistance (WHO table) separated by semi colon. Format for reporting composition ALL relevant amino acid positions: e.g. S31N.

NA sequence aa resistance mutations

Field: NAAAMutations
Coding: TEXT
Listing of amino acid substitution in NA associated with antiviral resistance (WHO table) separated by semi colon. Format for reporting composition ALL relevant amino acid positions: e.g. H275Y.

PA sequence aa resistance mutations

Field: PAAAMutations
Coding: TEXT
Listing of amino acid substitution in PA associated with antiviral resistance (WHO table) separated by semi colon. Format for reporting composition ALL relevant amino acid positions: e.g. I38T or I38M or I38F

Interpretation M2 Blocker Resistance Testing

Field: InterprM2BlockerResistTest
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.

Interpretation Baloxavir Marboxil Resistance Testing

Field: InterprBaloxavirResistTest
Coding: AARS = amino acid substitution in PA identified previously associated with reduced susceptibility for baloxavir
AANS = No amino acid substitution in PA previously associated with reduced susceptibility for baloxavir marboxil
AAINP = Amino Acid substitution Interpretation not possible
NA = Not applicable

Interpretation of Baloxavir Marboxil Resistance Testing.

Interpretation Oseltamivir Resistance Testing

Field: InterprOseltamivirResistTest

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 Oseltamivir Resistance Testing.

Interpretation Zanamivir Resistance Testing

Field: InterprZanamivirResistTest

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 Zanamivir Resistance Testing.

ISD: HA sequence number

Field: HAISD

Coding: TEXT

Accession number for sequence data HA, ISD or other.

ISD: NA sequence number

Field: NAISD

Coding: TEXT

Accession number for sequence data NA, ISD or other.

ISD: M2 sequence number

Field: M2ISD

Coding: TEXT

Accession number for sequence data M2, ISD or other.

ISD: PA sequence number

Field: PAISD

Coding: TEXT

Accession number for sequence data PA, ISD or other.

ISD: HA sequence number

Field: HAISD

Coding: TEXT

Accession number for sequence data HA, ISD or other.

Wgs ENA identifier

Field: WgsEnaId

Coding: Text

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.

Wgs Sequence RA identifier (repeatable)

Field: WgsSequenceId

Coding: Text

Sequence identifier for whole genome or 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 WgsEnaId variable

Comment

Field: Comment

Coding: Text

Free comment on data, suggestion to fill in conclusion here.

INFLZOOAGGR metadata record type version 1

Common TESSy variables

Record ID

Field: RecordId

Coding: Text

The record identifier is provided by the Member State. It must be unique within the national respiratory virus diseases surveillance system and anonymous.

Record type

Field: RecordType

Coding: CV

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: NUM

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.

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

Field: Subject

Coding: CV

The subject describes the data to be reported.

Status

Field: Status

Coding: CV

Coded value list: [Statuses]: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.

Data Source

Field: DataSource

Coding: CV

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.

Reporting Country

Field: ReportingCountry

Coding: CV
Coded value list: [Countries](see the coded values list)

This variable identifies the country reporting the case.

Date used for statistics

Field: DateUsedForStatisticsWeek

Coding: DATE

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 it is preferably the date the sampling and/or testing has been performed or case was notified to the national health authorities (notification date).

Pathogen:

Field: Pathogen

Coding: CV

Coded value list: PathogenRESPI:
INFL = Influenza virus
MERS = MERS-CoV
O = Other
RSV = Respiratory syncytial virus
SARSCOV2 = SARS-CoV-2

Pathogen associated with tests or detections. 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

Influenza virus HA subtype

Field: HASubtype

Coding: CV

Coded value list:InfluenzaVirusHASubType

H1 = A(H1)
H10 = A(H10)
H11 = A(H11)
H12 = A(H12)
H13 = A(H13)
H14 = A(H14)
H15 = A(H15)
H16 = A(H16)
H17 = A(H17)
H18 = A(H18)
H2 = A(H2)
H3 = A(H3)
H4 = A(H4)
H5 = A(H5)
H6 = A(H6)
H7 = A(H7)

H8 = A(H8)
H9 = A(H9)
O = Other
UNK = Unknown

Influenza virus NA subtype
Field: NASubtype:
Coding: CV
Coded value list: InfluenzaVirusNASubType
N1 = A(HxN1)
N10 = A(HxN10)
N11 = A(HxN11)
N2 = A(HxN2)
N3 = A(HxN3)
N4 = A(HxN4)
N5 = A(HxN5)
N6 = A(HxN6)
N7 = A(HxN7)
N8 = A(HxN8)
N9 = A(HxN9)
O = Other
UNK = Unknown

Number tested
Field: NumTested
Coding: NUM
The number of samples tested per week

Number detected
Field: NumDetected
Coding: NUM
The number of samples testing positive per week

Comment
Field: Comment
Coding: Text
Free comment on data, suggestion to fill in conclusion here.