ECDC TECHNICAL REPORT

# COVID-19 surveillance guidance

## Transition from COVID-19 emergency surveillance to routine surveillance of respiratory pathogens

October 2021

# Key messages

Most European Union/European Economic Area (EU/EEA) countries have established comprehensive surveillance systems for COVID-19 with a large proportion reporting all positive cases regardless of indication for testing. Furthermore, testing policies have been different across countries, thus affecting data comparability at EU/EEA level. This guidance encourages countries to transition from emergency surveillance to more sustainable, objective-driven, surveillance systems according to the following key points:

- Systems should allow for integrated surveillance of COVID-19, influenza and other respiratory pathogens that are likely to co-circulate in the population.
- Current influenza surveillance systems are not sufficiently sensitive and representative to enable joint COVID-19 surveillance, thus countries should consider expanding the coverage of sentinel providers to improve sensitivity and to collect sufficient specimens for further characterisation.
- Countries should focus on reporting symptomatic cases, i.e. cases that have been tested because of experiencing COVID-19 compatible symptoms, as this will improve comparability.
- If comprehensive testing of all those presenting with symptoms is not feasible, a representative subset of symptomatic cases should be tested, preferably by PCR.
- A representative subset of SARS-CoV-2 positive specimens should be sequenced. Genomic surveillance of representative samples should be coupled with targeted comprehensive sampling in special settings or populations.
- Monitoring of vaccine effectiveness should be carried out through ad hoc studies, possibly embedded in surveillance systems.
- Countries should continue mortality monitoring and consider sero-epidemiological surveys among complementary systems which will help meet the main surveillance objectives.

# Background

In April 2020, ECDC published an updated strategy for COVID-19 surveillance at national and EU/EEA level [1], which was complemented by a document on COVID-19 testing strategies and objectives [2] and a guidance for representative and targeted genomic SARS-CoV-2 monitoring [3]. Although the main objectives of COVID-19 surveillance have not changed (i.e. to monitor disease incidence and severity, and to monitor viral changes), both the COVID-19 epidemic and surveillance approaches in the EU/EEA have changed for several reasons:

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First, surveillance systems have improved substantially, and most EU/EEA countries have reached high testing capacity. However, the impact of new testing policies (e.g. systematic screening of asymptomatic individuals outside of the healthcare system) was not fully anticipated, leading to a possible distortion of epidemiological indicators such as the test rate, the test positivity rate and eventually the case notification rate [4]. In addition, the high testing intensity (approximately 4 000 weekly tests per 100 000 population in the EU/EEA since April 2020) may not be sustainable in the long run, as testing is offered free of charge in most countries.

Second, in the context of a largely dominating variant of concern (VOC) such as SARS-CoV-2 Delta variant, more emphasis should be given to a targeted sampling approach to detect early signals of emergence or introductions of new variants that need to be rapidly assessed, aiming to make the best of limited sequencing resources, while maintaining representative community sampling. Information on the indication and setting where cases have been sampled for sequencing would be necessary to monitor representativeness of sampling and implement corrective actions if this is not achieved.

Last, the success of the vaccine rollout in many EU/EEA countries changed the overall epidemiology of COVID-19 with a higher incidence in younger age groups and fewer severe cases alongside a reduction of non-pharmaceutical interventions (NPI). Yet, since vaccines aim at preventing severe disease while infection among vaccinated individuals can occur, virus circulation in the population is likely to continue requiring a more consistent surveillance approach to correctly monitor trends and identify areas of increased transmission and change in infection-severity, and impact. Therefore, it is important to ensure that indications for testing do not differ between vaccinated and unvaccinated individuals.

This document proposes an updated COVID-19 surveillance guidance to help countries adapt their surveillance systems to the changing epidemics of COVID-19.

# Surveillance objectives

COVID-19 surveillance at EU/EEA level has three main objectives:

- Monitor COVID-19 incidence by time, place, and person, and describe severe cases, in order to guide public health measures, and understand their impact.
- Rapidly detect and monitor SARS-CoV-2 variants at an early stage of local circulation in order to rapidly assess their characteristics and to issue potential containment measures.
- Support monitoring of vaccine effectiveness to inform optimal vaccination programmes and strategies.

To achieve these objectives, surveillance systems should rely on both primary care (or other dedicated community-based settings where testing of suspect COVID-19 cases takes place) and secondary care systems. These systems could be complemented by additional surveillance systems or ad hoc studies/surveys depending on specific objectives (Table 1).

**Table 1. COVID-19 surveillance objectives and systems**

| Objective | Surveillance system | | |
|---|---|---|---|
| | Primary care/community-based setting | Hospitals | Other |
| **Monitor COVID-19 incidence by time, place, and person and describe severe cases** | | | |
| Monitor disease incidence | Yes | If population-based, multiplication factors can be used to estimate incidence | Periodic serosurveys (to monitor infection);<br>Point prevalence surveys;<br>Participatory surveillance methods;<br>Wastewater surveillance |
| Describe severe cases over time | No | Yes, better with severe acute respiratory infections (SARI) surveillance where suspect cases have equal chances of being tested | Ad hoc studies to assess risk factors for severity<br>Mortality surveillance, including excess mortality monitoring |
| **Detect and monitor viral changes** | | | |
| Rapidly detect variants, trigger their assessment, and monitor their spread and trends | Representative sample of specimens undergo sequencing and/or genotyping.<br>It may be necessary to sequence all samples if the number of cases is small. | Comprehensive sequencing is preferred to ensure detection of variants associated with increased transmission or severity, or with immune breakthrough infections. | Targeted sampling (e.g. outbreak with rapid spread). |
| **Support monitoring of vaccine effectiveness (VE)** | | | |
| Estimate and monitor VE | Yes, for VE against symptomatic infection | Yes, for VE against severe infection | Ad hoc studies to estimate VE in specific settings/populations and VE against infection. |

# Routine surveillance systems

Most EU/EEA Member States established comprehensive surveillance systems for COVID-19 during the pandemic. These systems have provided critical information for public health decision making. However, due to the large differences in testing strategies across countries and changes over time, the comparability of these systems and the utility of the data they generate are limited. With an important part of testing done outside of the healthcare system (e.g. rapid antigen tests (RAT) done at individual request without any clinical indication), data reported on confirmed cases may be biased in an unpredictable manner. For example, test results may not be representative of the wider population if testing is specially required for some specified activities, or if testing is associated with high out-of-pocket payment (and hence only affordable by those financially better off). In addition, it is likely that widespread testing, i.e. testing not undertaken for diagnostic purposes, will not remain feasible in the coming months.

It is therefore essential that COVID-19 surveillance relies on data sourced from healthcare providers. Since it may be challenging to include all primary care providers with assurance of high consistency and comparability of data (e.g. representativeness of cases, testing according to common criteria), it may be more efficient to rely on sentinel schemes based on syndromic surveillance similar to those in place for seasonal influenza surveillance. If high data consistency and comparability can be obtained with comprehensive surveillance, this remains an optimum option. The integration of COVID-19 into seasonal influenza surveillance may have an impact on the existing system, especially if some parameters are changed (e.g. testing strategy). It is important to assess and monitor the impact of these changes given that the COVID-19 pandemic may have also changed other parameters such as health-seeking behaviour. For example, it is possible that more people will stay at home to isolate themselves when having influenza-like illness in the post-COVID-19 era.

For secondary care surveillance, indication for testing is less problematic since most severe cases are likely to be tested. The main challenge here is to ensure high-quality data, especially in terms of completeness. Inclusion of all hospitals would be optimum, but it may be more efficient to rely on sentinel sites with well-defined denominator data.

The proposed COVID-19 surveillance system is described using published surveillance system descriptors (5).

## Primary care surveillance

### System design

To achieve the objectives described above, a sentinel approach would need a higher coverage of the population under surveillance compared with influenza surveillance, and both higher testing and sequencing intensity. The ECDC guidance for representative and targeted genomic SARS-CoV-2 monitoring [3] suggests to sequence at least 200-300 samples per week and country to detect a variant circulating with a 2.5% prevalence. In comparison, in a pre-pandemic influenza season (2018/19), there were approximately 1 500 weekly flu positive specimens at the peak of the season with 70% test positivity for the entire EU/EEA. In addition, sentinel surveillance of influenza in primary care is usually conducted by representative national networks of primary care practitioners covering less than 5% of the population and in most instances less than 2% [6, 7]. Such systems will be less sensitive in detecting both cases and variants compared with the current ones, based on comprehensive laboratory reports.

Furthermore, since testing for clinical purposes may happen in dedicated centres rather than in the regular primary healthcare system, such centres should be included in the surveillance schemes using the same approach as for the selection of the sentinel primary care sites. Ideally, surveillance of COVID-19 should be integrated within an enhanced (i.e. with both higher population coverage and testing intensity) surveillance system for seasonal influenza and other respiratory pathogens under a syndromic surveillance approach that would perform well for most pathogens (see case definition).

Sentinel schemes with known population denominators will allow the calculation of rates to monitor disease incidence. However, with different healthcare systems and health-seeking behaviours across countries, these rates may still not be comparable. Test positivity rates may then be a better indicator to compare disease transmission across countries, provided that only tests performed for clinical reasons (i.e. on suspect COVID-19 cases based on common criteria) are included.

ECDC recommends that only symptomatic persons should be included in the surveillance system, even if asymptomatic persons are tested for SARS-CoV-2.

## Population under surveillance

The population under surveillance is the general population, i.e. anyone likely to seek primary care if COVID-19 compatible symptoms develop. Such surveillance may be complemented by a scheme targeting vulnerable populations such as residents of care homes, but such surveillance would have to be carried out under a different scheme [8] (see also complementary surveillance systems).

## Data sources

If a sentinel approach is preferred, only primary care services participating in the scheme should provide data that are used for calculating incidence.

If a comprehensive approach is preferred, all primary care services prescribing tests or testing for SARS-CoV-2 on clinical indication should be included.

## Case definition

As part of syndromic surveillance, rates of influenza-like illness (ILI) and/or acute respiratory infection (ARI) should be reported [9]. A representative sample of these ILI/ARI cases should ideally be tested concurrently for influenza and SARS-CoV-2 viruses. Multiplex RT-PCR tests can be used to simultaneously test for SARS-CoV-2, influenza and other respiratory viruses. Before introducing a new testing method or a new assay, a validation and verification exercise should be carried out, to ensure that the laboratory testing system is performing adequately for the circulating viruses.

For surveillance purposes, a case of COVID-19 would be defined as follow:

- Clinical criteria: Acute respiratory infection (ARI) or influenza-like illness (ILI) [9]
- Laboratory criteria: Detection of SARS-CoV-2 nucleic acid or antigen in a clinical specimen
- Confirmed case: any person meeting the clinical criteria AND the laboratory criteria.

## Case detection policy

If countries only report symptomatic cases seeking care in primary care, the impact of testing policies on surveillance should be limited. However, since systematic testing in specific settings such as schools could lead to a higher number of children reported with very mild disease, it is important to document whether testing policies are in place. Although both rapid antigen tests (RAT) and PCR are accepted according to the ECDC case definition, PCR is the preferred method for testing sentinel samples. Ideally, there should be no pre-test (e.g. self-test or RAT) before prescribing PCR. The use of PCR as a confirmatory test introduces biases and artificially increases the predictive positive value and therefore the test positivity rate.

## Type of information reported

At a minimum, both basic clinical and laboratory information should be reported, e.g. rate of ARI and proportion positive for SARS-CoV-2 (Table 2). Additional clinical information (e.g. symptoms or vaccination status) would be required for advanced analyses, including vaccine impact/effectiveness studies. Further laboratory information (e.g. sequencing data) and epidemiological information (e.g. link to other cases) would help understand the impact of VOC. This additional information would only be possible with case-based reporting (Table 3).

### *Molecular typing data reported*

When the number of cases presenting to sentinel surveillance sites are low, ideally, all specimens originating from sentinel systems testing positive for SARS-CoV-2 should be sequenced, and all influenza-positive samples should be genotyped to determine their subtype/lineage. At least 10% of the influenza viruses, or all during times of low circulation, should be further genetically characterised (sequenced) and tested (phenotypically and/or genotypically) for antiviral resistance [6]. If it is not possible to sequence all SARS-CoV-2-positive specimens or if a comprehensive testing approach is followed, a representative sample could be selected for sequencing. Representative sampling can be complemented by targeted sampling [3]. Since it is impossible to predict in which group new SARS-CoV-2 variants will emerge, the system should allow changes in groups targeted for sequencing. Whole Genome Sequencing, or at least complete or partial S-gene sequencing, should be performed to confirm infection with a specific variant. For early detection and prevalence calculation of variants of concern, alternative methods have been developed, such as PCR-based diagnostic screening assays. When PCR-based assays are used, confirmatory sequencing of at least a subset of viruses should be performed to be able to use these assay results as indicators of community circulation of variants of concern [10].

Sequencing results should be reported according to the sampling category (representative or targeted) on a weekly basis to The European Surveillance System (TESSy). Sequences should be entered in GISAID or other public databases in a timely manner, i.e. ideally within one to two weeks from sample collection and linked to the reported cases (if data reported case-based). Raw data can be deposited in the COVID-19 data portal (www.covid19dataportal.org). For influenza, a subset of SARS-CoV-2 viruses, especially any newly emerged variants, should be selected for antigenic characterisation to identify antigenically drifted variants.

### *Follow-up data reported*

Follow-up data are usually difficult to collect. Nevertheless, if such information is accessible, it would be valuable to report the outcome (see type of information reported).

### Data format

Reporting of aggregate numbers of cases, possibly broken down by age, sex and/or other criteria would be sufficient to monitor COVID-19 incidence. However, any other analysis would require case-based data (e.g. assessment of severity of VOC by age group).

Monitoring of vaccine effectiveness/impact would also require case-based data.

During the transition period, it is possible to envisage case-based reporting of all laboratory confirmed COVID-19 cases and aggregate reporting of syndromic surveillance data.

### Geographical coverage

It is advised that the surveillance system cover the entire national territory. Given the known heterogeneity of COVID-19 transmission within countries, it would be desirable to report data at subnational level (e.g. NUTS 2).

### Temporal continuity

Since the seasonality of COVID-19 is not entirely clear and transmission has so far continued throughout the year in Europe, it is advisable to maintain surveillance all year round for the time being. This would also be consistent with general recommendations on pandemic preparedness. However, this may be challenging for countries planning to fully integrate COVID-19 with seasonal influenza surveillance for which surveillance is performed from week 40 to week 20 of the following year. Since influenza seasonality may have been disrupted by lockdowns, ECDC would advise countries to consider year-round surveillance for seasonal influenza for 2022.

### Frequency of reporting

Data should be reported weekly to ECDC.

## Secondary and tertiary care surveillance

### System design

To monitor trends of severe COVID-19, it is advisable to rely on SARI surveillance, using a common case definition and data collection methods as per ECDC protocol. Ideally this surveillance system should be comprehensive, but if not possible, sentinel hospitals should be representative of the population under surveillance, and the catchment population of each sentinel site should be known to accurately estimate incidence rates.

SARI surveillance systems should cover most common respiratory viruses and monitor severity of respiratory infections (through hospitalisation rates, but also admissions to ICU and fatal outcome), as well as the impact of vaccination and other determinants.

All SARI cases should be tested for SARS-CoV-2 and for influenza when influenza is known to be circulating, preferably by PCR. Multiplex RT-PCR tests can be used to simultaneously test for SARS-CoV-2, influenza and other respiratory viruses.

### Population under surveillance

The population under surveillance is the general population, i.e. anyone likely to be admitted to hospital for SARI.

### Data sources

Ideally all hospitals should participate in SARI surveillance. If only a fraction of hospitals are included, their catchment population should be estimated and reported. If only a subset of hospitalised cases are reported (e.g., cases only admitted on specific days of the week), additional information on the reporting fraction should be provided to estimate hospitalisation rates. Data should be collected as soon as possible after admission to hospital and diagnosis, to ensure timeliness. Electronic health records obtained from hospital discharge databases can be used, but these should be complemented by (or only used to complement) other clinical and laboratory data if the requirements stated in this document are not met.

### Case definition

Although the latest WHO SARI case definition (2014) is widely used (patient with an acute respiratory infection that requires hospitalisation AND history of fever or measured fever of ≥ 38 C° AND cough with an onset within the previous 10 days), it might not be sensitive enough to capture many COVID-19 cases that require hospitalisation. The broader ECDC/EU COVID-19 clinical criteria (www.ecdc.europa.eu/en/covid-19/surveillance/case-definition) can be used, provided that the available data allow for analyses to be performed also by the WHO case definition (i.e. it should include fever, cough, date of onset of disease, and date of hospitalisation). This is to ensure stability over time and comparability across countries, but also to support future discussions on updates to the SARI case definition.

Countries able to carry out register-based surveillance using the International Statistical Classification of Diseases (ICD) could also consider using this data source for SARI surveillance although such approach may pose other challenges related to coding.

## Type of information reported

At a minimum, basic demographic, clinical and laboratory information should be reported. Case-based reporting would allow analyses on the impact of vaccination and VOC, for example (Table 4 and 5).

### *Molecular typing data reported*

When the number of cases presenting to sentinel hospitals is low, ideally, all hospitalised patients testing positive for SARS-CoV-2 should be sequenced -At least 10% of the influenza viruses, or all during times of low circulation, should be further genetically characterised (sequenced) and tested (phenotypically and/or genotypically) for antiviral resistance. All influenza positive samples should be genotyped to determine their subtype/lineage.

If it is not possible to sequence all hospital sentinel specimens or if a comprehensive testing approach is used, a representative sample could be selected for SARS-CoV-2 sequencing. Representative sampling can be complemented by targeted sampling. Sequencing results should be reported according to the sampling category (representative or targeted) on a weekly basis to The European Surveillance System (TESSy) [3]. Sequences should be entered in GISAID or other public databases in a timely manner, i.e. ideally within one to two weeks from sample collection and linked to the reported cases (if data reported case-based). Raw data can be deposited in the COVID-19 data portal (www.covid19dataportal.org). A subset of viruses, especially any newly emerged variants, should be selected for antigenic characterisation to identify antigenically drifted variants.

### *Follow-up data reported*

Follow-up data, especially regarding the outcomes, should be collected and updated whenever possible.

## Data format

Case-based reporting is recommended. Data should be sufficient to clearly define cases (such as symptoms and laboratory findings, including sequencing/variant data whenever possible), exposures (such as vaccination status, age, sex and preconditions), and outcomes (such as length of hospital stay, admission to ICU and death associated with the SARI event) – see example of minimum metadata below (Table 4 and 5).

## Geographical coverage

It is advised that the surveillance system cover the entire national territory. Given the known heterogeneity of COVID-19 transmission within countries, it would be desirable to report data at subnational level (e.g. NUTS 2).

## Temporal continuity

SARI surveillance should be carried out throughout the year.

## Frequency of reporting

Data should be reported weekly to ECDC.

# Complementary surveillance systems

## Sero-epidemiological surveys

Well-designed sero-epidemiological studies can allow the estimation of incidence of SARS-CoV-2 infection in the population studied, providing a basis also to estimate severe disease and infection fatality rates, when that information is available in the same population. When standardised laboratory assays and epidemiological methods are used, these estimates can be highly comparable over time and across geographical regions. Longitudinal or repeated studies with the same sampling and common testing methodology are particularly useful in understanding the temporal evolution of the disease and population immunity.

Seroprevalence studies using a nationwide random sampling frame are the gold standard to effectively monitor the immunity levels in a population. However, these can be costly and resource intensive to set up and run on a regular basis. Alternative solutions can be seroprevalence studies using residual blood from samples taken for other purposes in different healthcare settings or from blood donors, stratified by age group and geographic area. Despite the inherent biases, such design may provide an easy and convenient sampling frame, available at repeated time intervals, requiring significantly reduced resources and effort.

Ongoing monitoring of both the natural and the vaccine-induced immunity in the region can provide a better understanding of the epidemiological situation, inform mathematical modelling forecasts, assess impact of vaccination programmes, and help guide the effective implementation of further control measures. Using tests that target specific proteins, can help us differentiate naturally-acquired from vaccine-induced immunity. Assays targeting the nucleoprotein (N) can be used as a proxy for acquiring antibodies after natural infection, whereas assays targeting the spike (S) can detect post-infection and vaccine-induced antibodies.

Most vaccines initially distributed in the EU/EEA were inducing antibodies to the S protein. However, nowadays all different types of vaccines are being used by the Member States, making interpretation of antibody tests more challenging. Including both types of antibody assays in the testing strategy may help interpreting changing seropositivity and immunity levels in the local community.

Additional collection of information on the vaccination status and type (or name) of vaccine received by each individual (if feasible depending on the sampling methodology used) may enable a more accurate description of the background infection and immunity situation.

## Point prevalence surveys and healthcare-associated COVID-19

Point prevalence surveys (PPS) can be useful in healthcare settings to assess the prevalence of healthcare-associated COVID-19 (HA-COVID-19). ECDC developed a definition of HA-COVID-19 (see surveillance definition of source of infection at www.ecdc.europa.eu/en/covid-19/surveillance/surveillance-definitions) which was added to the COVID-19 case-based surveillance but was only reported by one country. Therefore, current ECDC surveillance systems have been unable to assess and follow-up the burden of healthcare-associated transmission of COVID-19 in hospitals. Estimates based on the date of hospitalisation and date of reporting or disease onset suggest that approximately 20% of hospitalised COVID-19 cases are `probably' or `definitely' healthcare-associated. In long-term care facilities, where the large majority of COVID-19 is healthcare-associated by definition, a simple aggregate surveillance system (one record per country per week) has allowed follow-up of the most important indicators in about half of EU/EEA countries [8]. To assess HA-COVID-19 in acute care hospitals, PPS of healthcare-associated infections (HAIs) performed by staff trained in assessing HAIs can be a valid alternative. ECDC therefore added HA-COVID-19 in the third European PPS of HAIs and antimicrobial use which will be organised in 2022. The recommended sampling method for these surveys allows to estimate the total burden, risk factors and associated nosocomial pathogens of HA-COVID-19 by country based on a representative sample of hospitals.

## Participatory surveillance methods

Population-based systems outside the regular healthcare system can provide complimentary information to healthcare-based systems, particularly in capturing data on milder infections, and can be combined with self-testing as well as surveys on other social and behavioural aspects such as treatment, symptoms, testing, vaccination, and healthcare seeking behaviour as well as other social relevant determinants. Influenzanet (www.influenzanet.org) is an established network across EU/EEA countries that adapted the system to monitor influenza-like illness during the pandemic to also cover COVID-19 symptoms and will integrate self-swabbing in future. Data are integrated in the weekly joint WHO and ECDC COVID-19 and influenza (www.FluNewsEurope.org) bulletins.

In addition to the coordinated efforts by Influenzanet, there are a variety of similar initiatives in different EU/EEA countries with regards to symptom checking apps where data are used for syndromic surveillance. Some of these apps are run by public health authorities and others by researchers or other bodies.

During time periods when access to primary health care was limited, established hotlines, online symptom checking tools, or contact to primary care providers via telephone were used to collect information on symptoms and were integrated with syndromic surveillance reporting through the national reporting. Such systems were also in place for other symptoms to e.g. identify outbreaks or monitor trends or particular disease groups (gastroenteritis etc).

The utility of syndromic surveillance is likely enhanced if reported symptoms can be validated with testing data, allowing the identification of symptoms that are more predictive of COVID-19 than others.

## Mortality surveillance

Some COVID-19 related deaths may not occur in the healthcare system and may therefore not be captured by COVID-19 routine surveillance systems.

It is of the utmost importance that the number of deaths due to COVID-19 are reported to ECDC on a weekly basis (case-based or aggregated data). The case definition is unchanged: A COVID-19 death is defined for surveillance purposes as a death resulting from a clinically compatible illness in a probable or confirmed COVID-19 case, unless there is a clear alternative cause of death that cannot be related to COVID disease (e.g. trauma). There should be no period of complete recovery between the illness and death. A death due to COVID-19 may not be attributed to another disease (e.g. cancer) and should be counted independently of pre-existing conditions that are suspected of triggering a severe course of COVID-19.

Since some COVID-19 deaths may be misclassified and since the total death toll of the pandemic may exceed COVID-19 deaths (e.g. deaths caused by delayed care), it is important to monitor excess all-cause mortality. ECDC encourages all EU/EEA countries to participate in the EuroMOMO activities (https://www.euromomo.eu/).

## Wastewater surveillance

Wastewater surveillance of SARS-CoV-2 and its variants complements other forms of COVID-19 routine surveillance. While viral RNA concentrations in wastewater cannot be reliably extrapolated to estimates of absolute disease incidence, they do allow early detection of (re-)emergence of COVID-19 in previously COVID-free regions, monitoring of disease trends over time and assessing the effectiveness of response measures taken.

On 17 March 2021, the European Commission published a recommendation for Member States to establish national routine wastewater surveillance of SARS-CoV-2 and its variants by 1 October 2021. Each national system should include wastewater from large cities with over 150 000 inhabitants at least, preferably with a minimum sampling frequency of two per week. A technical annex specifies the methodological quality standards required for data comparability across Member States.

The Commission's Joint Research Centre is coordinating the network of national wastewater surveillance data providers and building an IT platform for data collection and visualisation as well as network communication and exchange of best practices.

# References


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# Annex

**Table 2. Example of metadata for reporting of aggregate data**

| Variable | Coding |
|---|---|
| Date used for statistics (week date) | yyyy-Www |
| Region of reporting | Country/NUTS1 or 2/GAUL1/Country specific |
| Rate of ARI (all ages) per 1 000 consultations | Numeric |
| Rate of ARI (<15yr) per 1 000 consultations | Numeric |
| Rate of ARI (15-24yr) per 1 000 consultations | Numeric |
| Rate of ARI (25-49yr) per 1 000 consultations | Numeric |
| Rate of ARI (50-64yr) per 1 000 consultations | Numeric |
| Rate of ARI (65-79yr) per 1 000 consultations | Numeric |
| Rate of ARI (80+yr) per 1 000 consultations | Numeric |
| Proportion of specimens positive for SARS-CoV-2 (all ages) | Numeric |
| Proportion of specimens positive for SARS-CoV-2 (<15yr) | Numeric |
| Proportion of specimens positive for SARS-CoV-2 (15-24yr) | Numeric |
| Proportion of specimens positive for SARS-CoV-2 (25-49yr) | Numeric |
| Proportion of specimens positive for SARS-CoV-2 (50-64yr) | Numeric |
| Proportion of specimens positive for SARS-CoV-2 (65-79yr) | Numeric |
| Proportion of specimens positive for SARS-CoV-2 (80+yr) | Numeric |
| Proportion of specimens positive for influenza virus (all ages) | Numeric |
| Proportion of specimens positive for influenza virus (<15yr) | Numeric |
| Proportion of specimens positive for influenza virus (15-24yr) | Numeric |
| Proportion of specimens positive for influenza virus (25-49yr) | Numeric |
| Proportion of specimens positive for influenza virus (50-64yr) | Numeric |
| Proportion of specimens positive for influenza virus (65-79yr) | Numeric |
| Proportion of specimens positive for influenza virus (80+yr) | Numeric |

**Table 3. Example of metadata for reporting of case-based data**

| Variable | Coding |
|---|---|
| Place of reporting | Country/NUTS1 or 2/GAUL1/Country specific |
| Date used for statistics | yyyy-mm-dd (preferred); yyyy-Www; yyyy-mm; yyyy |
| Age | Numerical (0-120) |
| Sex | F = Female; M = Male; O = Other; UNK = Unknown |
| Brand COVID-19 vaccination dose 1 | See COVID-19 reporting protocol |
| Brand COVID-19 vaccination dose 2 | See COVID-19 reporting protocol |
| Date vaccination dose 1 | yyyy-mm-dd (preferred); yyyy-Www |
| Date vaccination dose 1 | yyyy-mm-dd (preferred); yyyy-Www |
| Laboratory results for influenza | N = Negative<br>NT = Not tested<br>P = Positive<br>UNK = Tested, but result unknown |
| Influenza type and subtype | A = A, not subtyped<br>PanAH1 = A(H1)pdm09<br>PanAH1N1 = A(H1N1)pdm09<br>AH3 = A(H3), not N subtyped<br>AH3N2 = A(H3N2)<br>B = B, lineage not determined<br>BVic = B(Victoria)<br>BYam = B(Yamagata)<br>RSV = RSV<br>O = Other<br>UNK = Unknown<br>NA = Not applicable |
| Laboratory results for SARS-CoV-2 | N = Negative<br>NT = Not tested<br>P = Positive<br>UNDET = Undetermined/inconclusive<br>UNK = Tested, but result unknown |
| Virus variant of SARS-CoV-2 | See COVID-19 reporting protocol |
| Wgs Sequence RA identifier | Id. |
| Date of onset | Id. |
| Clinical symptoms | Id. |
| Precondition | Id. |
| Outcome | ALIVE = Alive, recovered, cured<br>HOSPITALISED = admitted to hospital<br>DIEDNCOV = COVID-19 was main or contributing cause of death<br>DIEDOTHER = Death not related to COVID-19 infection<br>DIEDUNK = Cause of death unknown<br>STILLTREATMENT = Still on medical treatment (not recovered)<br>UNK = Unknown outcome |
| Date of last follow-up (outcome) | yyyy-mm-dd |

**Table 4. Example of minimum metadata for reporting of SARI case-based data**

| Variable | Coding |
|---|---|
| Date used for statistics | yyyy-mm-dd (preferred); yyyy-Www |
| Region | Country/NUTS1 or 2/GAUL1/Country specific |
| Age | Numerical (0-120) |
| Sex | F = Female; M = Male; O = Other; UNK = Unknown |
| Date of onset of symptoms | yyyy-mm-dd (preferred); yyyy-Www |
| Fever | N = No; Y = Yes; UNK = Unknown |
| Cough | N = No; Y = Yes; UNK = Unknown |
| Other clinical symptoms | See COVID-19 reporting protocol |
| Preconditions | Id. |
| Previous SARS-CoV-2 infection | N = No; Y = Yes; UNK = Unknown |
| Date of previous SARS-CoV-2 infection | yyyy-mm-dd (preferred); yyyy-Www |
| Brand COVID-19 vaccination dose 1 | See COVID-19 reporting protocol |
| Brand COVID-19 vaccination dose 2 | See COVID-19 reporting protocol |
| Date vaccination dose 1 | yyyy-mm-dd (preferred); yyyy-Www |
| Date vaccination dose 2 | yyyy-mm-dd (preferred); yyyy-Www |
| Laboratory results for influenza | N = Negative<br>NT = Not tested<br>P = Positive<br>UNK = Tested, but result unknown |
| Influenza type and subtype | A = A, not subtyped<br>PanAH1 = A(H1)pdm09<br>PanAH1N1 = A(H1N1)pdm09<br>AH3 = A(H3), not N subtyped<br>AH3N2 = A(H3N2)<br>B = B, lineage not determined<br>BVic = B(Victoria)<br>BYam = B(Yamagata)<br>RSV = RSV<br>O = Other<br>UNK = Unknown<br>NA = Not applicable |
| Laboratory results for SARS-CoV-2 | N = Negative<br>NT = Not tested<br>P = Positive<br>UNDET = Undetermined/inconclusive<br>UNK = Tested, but result unknown |
| Virus variant of SARS-CoV-2 | See COVID-19 reporting protocol |
| Wgs Sequence RA identifier | Id. |
| Date of hospitalisation | yyyy-mm-dd (preferred); yyyy-Www |
| Admission to ICU | N = No; Y = Yes; UNK = Unknown |
| Outcome | DISCHARGED = Discharged from hospital, alive, recovered, cured<br>DIED = Patient deceased (as a consequence of the acute respiratory infection)<br>STILLTREATMENT = Still admitted or transferred (not recovered)<br>UNK = Unknown outcome |
| Date of last follow-up (outcome) | yyyy-mm-dd (preferred); yyyy-Www |

**Table 5. Example of minimum metadata for reporting of SARI aggregate data**

| Variable | Coding |
|---|---|
| Date used for statistics (week date) | yyyy-Www |
| Region | Country/NUTS1 or 2/GAUL1/Country specific |
| Number of hospital SARI admissions (all ages) | Numeric |
| Number of hospital SARI admissions age 0-4 | Numeric |
| Number of hospital SARI admissions age 5-14 | Numeric |
| Number of hospital SARI admissions age 15-29 | Numeric |
| Number of hospital SARI admissions age 30-64 | Numeric |
| Number of hospital SARI admissions age 65-79 | Numeric |
| Number of hospital SARI admissions age 80+ | Numeric |
| Number of SARI admissions to ICU (all ages) | Numeric |
| Number of SARI admissions to ICU age 0-4 | Numeric |
| Number of SARI admissions to ICU age 5-14 | Numeric |
| Number of SARI admissions to ICU age 15-29 | Numeric |
| Number of SARI admissions to ICU age 30-64 | Numeric |
| Number of SARI admissions to ICU age 65-79 | Numeric |
| Number of SARI admissions to ICU age 80+ | Numeric |
| Number of hospital SARI deaths (all ages) | Numeric |
| Number of hospital SARI deaths age 0-4 | Numeric |
| Number of hospital SARI deaths age 5-14 | Numeric |
| Number of hospital SARI deaths age 15-29 | Numeric |
| Number of hospital SARI deaths age 30-64 | Numeric |
| Number of hospital SARI deaths age 65-79 | Numeric |
| Number of hospital SARI deaths age 80+ | Numeric |
| Total population covered by the hospitals submitting SARI data (all ages) | Numeric |
| Population aged 0-4 covered by the hospitals submitting SARI data | Numeric |
| Population aged 5-14 covered by the hospitals submitting SARI data | Numeric |
| Population aged 15-29 covered by the hospitals submitting SARI data | Numeric |
| Population aged 30-64 covered by the hospitals submitting SARI data | Numeric |
| Population aged 65-79 covered by the hospitals submitting SARI data | Numeric |
| Population aged 80+ covered by the hospitals submitting SARI data | Numeric |
| Number of SARI cases positive for influenza (all ages) | Numeric |
| Number of SARI cases positive for influenza age 0-4 | Numeric |
| Number of SARI cases positive for influenza age 5-14 | Numeric |
| Number of SARI cases positive for influenza age 15-29 | Numeric |
| Number of SARI cases positive for influenza age 30-64 | Numeric |
| Number of SARI cases positive for influenza age 65-79 | Numeric |
| Number of SARI cases positive for influenza age 80+ | Numeric |
| Number of SARI cases positive for SARS-CoV-2 (all ages) | Numeric |
| Number of SARI cases positive for SARS-CoV-2 age 0-4 | Numeric |
| Number of SARI cases positive for SARS-CoV-2 age 5-14 | Numeric |
| Number of SARI cases positive for SARS-CoV-2 age 15-29 | Numeric |
| Number of SARI cases positive for SARS-CoV-2 age 30-64 | Numeric |
| Number of SARI cases positive for SARS-CoV-2 age 65-79 | Numeric |
| Number of SARI cases positive for SARS-CoV-2 age 80+ | Numeric |