

National SARS-CoV-2 Strain Surveillance (NS3) Frequently Asked Questions (FAQs)

Why is CDC organizing this?

There are multiple potential applications for routinely sequencing and characterizing SARS-CoV-2 clinical specimens as part of the public health response to the COVID-19 pandemic. These can broadly be grouped into three objectives:

1. Population-level molecular epidemiology/virus monitoring: By routinely acquiring sequences from a subset of COVID-19 cases, it is possible to monitor the spread of the virus across time and within populations.
2. Outbreak investigation: Sequence data can be a useful tool for characterizing clusters of COVID-19 cases and differentiating point source outbreaks from multiple introductions. They can also be used to characterize spread of the virus among individuals in settings where there is a high likelihood of transmission. Examples include healthcare settings, places of employment, long-term care facilities, schools, places of worship, shelters housing persons experiencing homelessness, and correctional and detention facilities.
3. Virus characterization: by routinely collecting standardized epidemiologic and clinical data, and linking these with associated virus sequences, sequencing can be a valuable tool to identify viral variants that might have different transmissibility, pathogenicity, clinical outcomes, vaccine or treatment resistance, or might be associated with potential “rare” events, such as re-infection.

While this current effort will focus on objectives 1 and 3 above, the creation of a national SARS-CoV-2 genomic surveillance system will support the additional objective (outbreak investigations).

What are we asking from state public health labs?

For National SARS-CoV-2 Strain Surveillance (NS3), we request all state laboratories provide on a biweekly basis: confirmed, deidentified, diagnostic specimens (with Ct values ≤ 28) and standardized metadata on a representative selection of COVID-19 cases. We are seeking specimens representing a variety of demographic and clinical characteristics and geographic locations. The selection of a diverse set of specimens will help ensure that a representative set of sequences is generated for national monitoring.

For enhanced surveillance activities starting in January 2021, we are requesting all state laboratories provide additional specimens, for a defined specified period of time (short-term, interim), to specifically address contemporary SARS-CoV-2 variants of interest. Variants of interest are identified through genomic analysis of circulating viruses. Criteria for selecting variants of interest for submission are outlined in Appendix 3, Section 2, which will be continually updated with changes communicated through updates to the guidance and through APHL.

What is our commitment to you?

For National SARS-CoV-2 Strain Surveillance (NS3), CDC will provide sequence results in a timely manner and provide routine national level analyses to monitor trends in transmission of the virus in the United States.

For enhanced surveillance activities starting in January 2021, CDC will provide results more rapidly and follow up directly with the state or territorial epidemiologist in the event of unexpected or unusual observations (e.g., sequence confirmation of a variant of interest). Finally, we will serve as an available resource for questions or further technical guidance on use of SARS-CoV-2 genomic data.

How many samples should I send and how often?

For NS3, we are requesting that states submit specimens every two weeks. We are asking each state to submit a minimum of 10 specimens every two weeks, plus additional specimens based on population size (see Appendix 2).

For enhanced surveillance activities starting in January 2021, we are requesting additional specimens that are suspect variants of interest (Appendix 3, Section 1). Each state should submit up to twenty (20) specimens representing SARS-CoV-2 Spike Gene Target Failure (SGTF – Appendix 3, Section 2-I) and up to twenty (20) specimens representing potential B.1.351 lineage specimens (Appendix 3, Section 2-II).

How should I select samples to send?

For NS3, we are asking states to purposively select a diverse set of specimens that represent multiple geographic locations not associated with a single outbreak event and, if possible, varying demographic characteristics and clinical outcomes. It is important that all specimens have a relatively low Ct value (≤ 28) and have been stored properly (for more information, see <https://www.cdc.gov/coronavirus/2019-ncov/lab/guidelines-clinical-specimens.html>).

For enhanced surveillance activities starting in January 2021, please see Appendix 3, Sections 1 and 2.

How do I send those samples?

Please see Appendix 1, for detailed sample submission information. Please ship specimens on every other MONDAY, if possible, in 1.5-2.0 mL cryovials. If this date is an observed holiday, please ship on the next available business day (Monday through Thursday). Include a printed sample manifest. Ship overnight using your usual courier such as FedEx or UPS to the following address:

ATTN: STATT Lab: Unit 66 TRL
Centers for Disease Control and
Prevention 1600 Clifton Road, NE
Atlanta, Georgia, 30333
Telephone:
404639-3931
Email: sarsseqshipping@cdc.gov

How will I get results?

Once genomic sequences are obtained and assessed for quality, the consensus sequence data will be uploaded and released into GenBank and GISAID with a minimum set of metadata. Raw sequence reads will be deposited into the Sequence Read Archive (SRA) at a later date, once quality assurances have been met and any human reads have been removed. CDC will also be available to assist states in accessing, viewing, and understanding sequencing results. The following metadata information will be included in all sequence data submissions: sample type, collection date, gender, age, and geolocation information including state. Race will not be reported to these public databases. Sequences will be named according to their geographical location, as per established conventions (e.g., SARS-CoV-2/human/USA/XX (state acronym)-CDC- xxxxxxxx (unique identifier)/2021). CDC is included in the name to reference that it was sequenced at CDC and not by the state public health laboratory or other entity. Note that NCBI and GISAID require slightly different naming conventions:

ICTV (NCBI) SARS-CoV-2/host/location/isolate/date
SARS-CoV-2/human/USA/XX-CDC-xxxxxxx2021

GISAID hCoV-19/location/isolate/date
hCoV-19/USA/XX-CDC-xxxxxxx2021