Centers for Disease Control and Prevention

COVID-19

CDC's Role in Tracking Variants

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What is CDC doing to track SARS-COV-2 variants?

In the United States, CDC tracks emerging variants through genomic surveillance with the following approaches:

Leading the National SARS-CoV-2 Strain Surveillance (NS3) system

Since November 2020, CDC regularly receives SARS-CoV-2 samples from state health departments and other public health agencies for sequencing, further characterization, and evaluation. On January 25, 2021, the NS3 system was scaled-up to process 750 samples per week. Notable strengths of this system are the regular collection of numerous representative specimens from across the country and characterization of viruses beyond what sequencing alone can provide.

NS3 Submission Guidance Documents

NS3 samples displayed as phylogenic trees

Published COVID-19 Sequences

Partnering with commercial diagnostic laboratories

CDC is contracting with large commercial diagnostic labs to sequence samples across the United States. CDC has commitments from these laboratories to sequence 20,000 samples per week, with the capacity to scale up in response to the nation's needs.

Collaborating with universities

CDC has contracts with seven universities to conduct genomic surveillance research in collaboration with public health agencies. The studies are meant to provide deeper insights into viral genomics and molecular epidemiology within the various regions across the country.

CDC awards nearly $14.5 million for SARS-CoV-2 Sequencing

Supporting state, territorial, local and tribal health departments

Since 2014, CDC's Advanced Molecular Detection Program has been integrating next-generation sequencing and bioinformatics capabilities into the U.S. public health system. Many state and local health departments have been applying these resources as part of their response to COVID-19. Public health departments support local investigations, conduct studies, and make genomic data available to public databases. To further support these efforts, on December 18, 2020, CDC released $15 million from COVID supplemental funds through the Epidemiology and Laboratory Capacity Program.

Leading the SARS-CoV-2 Sequencing for Public Health Emergency Response, Epidemiology, and Surveillance (SPHERES) consortium

(SPHERES) consortium

Since early in the pandemic, CDC has led a national consortium of laboratories sequencing SARS-CoV-2, known as SPHERES. The SPHERES consortium consists of more than 200 institutions, including academic centers, industry, non-governmental organizations, and public health agencies. The consortium also includes almost one thousand scientists from across the United States. Through this coordination, genomic data are made available through public databases for use by public health professionals, researchers, and industry.

Why is genomic surveillance important for public health?

Routine analysis of genetic sequence data enables CDC and its public health partners to identify and characterize variant viruses—either new ones identified in the U.S. or those already identified abroad—and to investigate how variants impact COVID-19 disease severity and the effectiveness of vaccines, treatment, and diagnostic tests.

Surveillance of emerging variants can help detect variants with:

- **Ability to spread more quickly in people**
- **Ability to cause either milder or more severe disease in people**
- **Ability to evade detection by specific diagnostic tests**
  Many commercial nucleic acid amplification tests (NAATs) that use reverse transcription polymerase chain reaction (RT-PCR) have multiple targets to detect the virus, such that even if a mutation impacts one of the targets, the other RT-PCR targets will still work. However, there are some tests that rely on only one target, and mutations may impact their ability to work. FDA is using public health sequencing data to monitor mutations and their impact on confidential/proprietary diagnostic test designs. CDC has a system to regularly check the primer and probe sites for both the diagnostic test and the Flu Sc2 multiplex test.
- **Decreased susceptibility to medical therapies that employ monoclonal antibodies**
  Such therapy involves specifically designed antibodies that target regions of the virus to block infection. Because these treatments are more specific than natural immune response-generated antibodies, they may be less effective against variants that emerge.
- **Ability to evade natural or vaccine-induced immunity**
  Both natural infection with and vaccination against SARS-CoV-2 produce a "polyclonal" antibody response that targets several parts of the spike protein. The virus would need to accumulate significant mutations in the spike protein to evade immunity induced by vaccines or by natural infection.

Among these possibilities, the ability to evade vaccine-induced immunity would be the most concerning. There is no definitive evidence yet that this is occurring, but scientists are closely evaluating this possibility.

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