



A nasal specimen is tested for SARS-CoV-2 at the University of Washington, Seattle. Scientists sequence the viral genomes from positive samples. GATES NOTES LLC

Science's extensive COVID-19 coverage is free to all readers. To support our nonprofit science journalism, please **make a tax-deductible gift today.**

Got a tip?

How to contact the news team

Advertisement

U.S. rushes to fill void in viral sequencing as worrisome coronavirus variants spread

By [Meredith Wadman](#) | Feb. 9, 2021 , 4:10 PM

Science's COVID-19 reporting is supported by the Heising-Simons Foundation.

Since May 2020, Jeffrey Milbrandt has had his systems fine-tuned to sequence 1000 coronavirus samples a week. The director of a major sequencing center at Washington University in St. Louis (WashU), Milbrandt knew months ago that the United States urgently needed to identify and track emerging variants of SARS-CoV-2, the pandemic coronavirus already spreading across the nation.

But to date, fewer than 100 coronavirus samples have made it to his sequencers at the McDonnell Genome Institute, and the United States remains nearly blind to several coronavirus strains that have recently upended the course of the pandemic. "We have it all worked out but there's not a lot of takers," Milbrandt says of his

center's sequencing abilities. "We are getting more inquiries from the press than from people who need the information. ... Some of us have pipelines available—they are just not being utilized."



Related

South Africa suspends use of AstraZeneca's COVID-19 vaccine after it fails to clearly stop virus variant



Danish scientists see tough times ahead as they watch more contagious COVID-19 virus surge



'A question of choices.' Pfizer vaccine leader on confronting new coronavirus variants



[See all of our coverage of the coronavirus outbreak](#)

The Centers for Disease Control and Prevention (CDC) plans to rapidly change that by coordinating a national surveillance system for coronavirus variants. Scientists and public health experts welcome the plan.

"The hardware is set up, the people are trained, the infrastructure is in place," says genome scientist Chris Mason of Weill Cornell Medicine. "It's just a big question: Who's gonna pay for it?"

Given the magnitude of the problem, some scientists worry that current plans don't go far enough. That WashU, one of the flagship centers that sequenced the human genome 2 decades ago, is idling in neutral is just one sign of the massive challenge the Biden administration faces as it tries to keep up with the virus. The latest bit of bad news on that front came on 7 February, when a team of U.S. scientists posted worrisome findings.

Their sequencing identified 212 instances of a highly contagious variant, B.1.1.7, from samples collected in the United States in December and January. They calculated

Advertisement

Latest News

Trending

that the variant is doubling in relative frequency in the United States every 10 days and is 35% to 46% more transmissible than the original virus. (Preliminary studies from the United Kingdom, where the variant was first identified, also suggest it may be more lethal.) In Florida, the variant accounted for about 4.5% of new cases by late January. Knowing what variants are present and where can be vital for policymakers. For example, skyrocketing levels of B.1.1.7 in England spurred strict winter lockdowns.

The United States is a sequencing superpower, but as of 7 February it ranks 36th in the world in sequencing SARS-CoV-2, according to data compiled by *The Washington Post*. To date, the United States is sequencing the genomes of just 0.36% of confirmed cases, with state rates ranging from 0.02% to 2.6%, according to *Science's* analysis of public databases (see map, left). The dismal showing is “totally unacceptable,” White House COVID-19 Coordinator Jeffrey Zients said at a recent press briefing. In contrast, Denmark, a leader in monitoring variants, has **sequenced more than half of positive cases**.

But scaling up variant surveillance involves many players, and sequencing itself isn't the rate-limiting step, says Duncan MacCannell, chief scientist of the CDC program that handles genomic surveillance of coronavirus. “If [we] had a straightforward way to connect the sequencing capacity at Washington University with samples and data, we would likely be using them.”

A White House document circulating in Washington, D.C., last week calls for spending \$340 million to sequence 5% of samples from confirmed COVID-19 cases, which would be about 39,000 genomes per week at current infection rates. But some scientists support a \$2 billion request to sequence up to 15% of cases, introduced in a bill last week by Senator Tammy Baldwin (D-WI).

Other scientists say current efforts need to ramp up faster. “The Biden administration is doing a lot, but ... it is not yet sufficient,” says Rob Knight, a sequencing expert

1. Major nutrition study aims to learn which diet best suits your genes and gut

2. How do the leading COVID-19 vaccines work? Science explains

3. Ancient human species made ‘last stand’ 100,000 years ago on Indonesian island

4. Rivers could generate thousands of nuclear power plants worth of energy, thanks to a new ‘blue’ membrane

5. Substance found in Antarctic ice may solve a martian mystery

Most Read

1. Substance found in Antarctic ice may solve a martian mystery

2. How do wombats poop cubes? Scientists get to the bottom of the mystery

3. Suspicions grow that nanoparticles in Pfizer's COVID-19 vaccine trigger rare allergic reactions

4. The cloak-and-dagger tale behind this year's most anticipated result in particle physics

5. More people are getting COVID-19 twice, suggesting immunity wanes quickly in some

Sifter

It is not a flower. It is a fungus!

By Sofia Moutinho | Feb. 4, 2021



Watch blue whales try to dodge ships in Patagonia

By Sofia Moutinho | Feb. 3, 2021



In biblical times, purple was the new black

By Sofia Moutinho | Jan. 29, 2021



Nine hikers mysteriously perished

at the University of California, San Diego (UCSD), and a co-author on the preprint on B.1.1.7 in the United States. "Far more sequencing needs to be done to understand the emergence and spread of new variants [and] to design new targeted probes to detect these variants cheaply and easily without sequencing every sample."

in the Russian mountains in 1959. Scientists may now know why

By Sofia Moutinho | Jan. 28, 2021



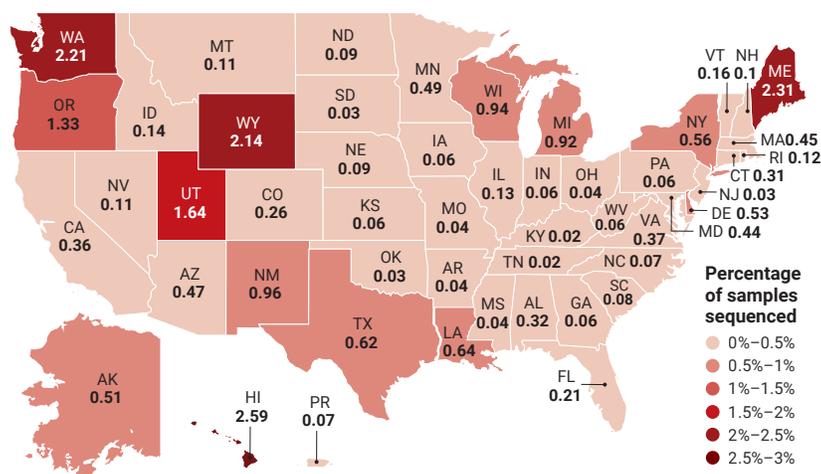
Mice feel for each other

By Sofia Moutinho | Jan. 15, 2021



More Sifter

Rare and uneven sequencing of coronavirus samples leaves the United States all but blind to emerging viral strains. Scientists are calling for sequencing at least 5% of positive cases nationally, a target not currently reached by any state.



(MAP) K. FRANKLIN/SCIENCE; (DATA) GISAID; JOHNS HOPKINS CORONAVIRUS RESOURCE CENTER

Sequencing all 30,000 bases of SARS-CoV-2's RNA genome allows researchers to detect misspellings, deletions, and other mutations that could give the virus new capabilities, such as spreading more easily, making people sicker, or evading vaccines. Two variants first identified in South Africa and Brazil, for example, may escape vaccine-induced antibodies. Like B.1.1.7, both have now been found in the United States, albeit only in a handful of cases.

CDC is responsible for SARS-CoV-2 surveillance, but it must work with a patchwork of state and local public health agencies. And until December, it had limited funding for sequencing as troubles with diagnostic testing consumed attention and the Trump administration

showed little interest. “Things were on a low slow burn for a while,” says Scott Becker, CEO of the Association of Public Health Laboratories.

Early last fall, CDC awarded small sequencing contracts to seven academic centers. For example, scientists at UCSD and Scripps Research got \$2.5 million to sequence samples in California and Mexico. Other small surveillance efforts moved ahead without CDC help. A group at Cedars-Sinai Medical Center, for example, last month identified a new variant spreading in California that contains a mutation that may help the virus invade cells more easily.

Then in late December, after the United Kingdom sounded the alarm over B.1.1.7, CDC finally got the go-ahead to support more sequencing. By 1 February, the agency had launched coronavirus-sequencing contracts worth a combined \$12.54 million with Illumina, its collaborator Helix, and medical testing giants LabCorp and Quest Diagnostics. They have committed to analyzing 6000 virus genomes per week by midmonth, CDC Director Rochelle Walensky said last week. Combined with sequences coming from academic centers and state public health labs, the United States will soon be sequencing “up to threefold more” samples than today, Walensky predicted on 8 February.

CDC is looking to expand its contracts with companies like LabCorp and Quest, MacCannell says. They “give us the ability to sample from their testing network, which combined spans the entire country. ... It has been a fantastic way of turning the lights on in parts of the country where we didn’t have a lot of data.”

Such partnerships are essential to a coordinated, national, virus-surveillance system, says Patrick Ayscue, a senior biosecurity fellow at the Chan Zuckerberg Biohub, which is playing a major role in coronavirus sequencing in California. “One of the primary bottlenecks in the U.S. is getting that sample onto a sequencer and then those

data back to people who can interpret that information and act on it.”

Engaging huge diagnostic labs like Quest and LabCorp along with public health labs in every state will help avoid “genomic deserts,” says Phil Febbo, chief medical officer at Illumina. For instance, not enough sequencing is being done now in majority Black communities in some southern states, says James Lillard, an immunologist at the Morehouse School of Medicine.

CDC has also begun to require that state and local public health labs submit, collectively, 750 sequences each week, Walensky noted in late January. But such labs have been both underfunded and swamped during the pandemic. At the Utah Public Health Laboratory—one of the most sophisticated and best equipped of the state labs—a shortage of pipette tips drove sequencing rates down from 600 per week in mid-January to 100 last week, says Kelly Oakeson, the lab’s chief sequencing scientist.

Other scientists say CDC’s goal is too low. “Seven hundred and fifty surveillance strains a week is nothing,” says Lea Starita, a genome scientist at the University of Washington, Seattle, and the Seattle Flu Study. Combined with the 6000 viral genomes CDC expects to receive weekly from the companies, that would allow sequencing of just 0.9% of the current weekly average of nearly 800,000 COVID-19 cases.

Many scientists support the 5% goal, including those on a white paper sent on 14 January to the presidential transition team by a coalition of 14 academic labs, companies, and others. They estimated that their group, if given funding today, could actually do much more—over 60,000 genomes per day within 10 weeks. Febbo estimates that would cost \$500 million in 2021.

Other scientists are bullish on the idea of aiming higher than 5% of genomes. David O’Connor, a viral sequencing expert at the University of Wisconsin, Madison, says he and colleague Tom Friedrich, working with local

stakeholders to track university-to-community transmission, have already achieved that 5% benchmark in Dane county, funded by a \$1.3 million CDC contract issued last fall. "If you can do that in a county like ours ... if you professionalize it and coordinate it ... you can absolutely get to 15%. It just takes resources and will."

Posted in: [Health](#), [Coronavirus](#)

doi:10.1126/science.abh0104



Meredith Wadman

[Email Meredith](#)

[Twitter](#)

More from News

South Africa suspends use of AstraZeneca's COVID-19 vaccine after it fails to clearly stop virus variant



Lizards may be protecting people from Lyme disease in the southeastern United States



Danish scientists see tough times ahead as they watch more contagious COVID-19 virus surge



Read the Latest Issue of *Science*

5 February 2021

Vol 371, Issue 6529



GENETICS

Genomes arising

ECOLOGY

Species? Climate? Cost? Ambitious goal means trade-offs

LATIN AMERICAN NEWS

Science bill rankles Mexican research community

ECOLOGY

Study shows winners, losers as desert warms

MEDICINE/DISEASES

Table of Contents

NIH's 'precision nutrition' bet aims for individualized diets

ASTRONOMY

Speedy robots gather spectra for sky surveys

© 2021 American Association for the Advancement of Science. All rights Reserved. AAAS is a partner of HINARI, AGORA, OARE, CHORUS, CLOCKSS, CrossRef and COUNTER.

Terms of Service

Privacy Policy

Contact AAAS