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Tracking the Coronavirus Epidemic From Wuhan to the World

Scientists and public health officials worldwide collaborate to understand COVID-19 and slow its spread.

February 27, 2020 By Susan Keown

With more than 77,000 confirmed cases in China and more than 2,000 elsewhere in the world, according to the World Health Organization, the viral disease known as COVID-19 has killed more than 2,600 people, disrupted global travel and forced governments and other organizations to take extreme measures to limit its global spread, from evacuations to mass quarantines.

Outbreaks now are occurring in South Korea, Italy and Iran, heightening concern that travelers infected but not severely ill may be carrying the virus from affected regions and sparking new outbreaks at their destinations.

The Centers for Disease Control and Prevention is working to contain the novel coronavirus behind COVID-19 and preparing for its “not if but when” community spread within the U.S. The CDC is evaluating community control methods — building off its strategies to mitigate pandemic flu — and asking the nation to anticipate “severe” disruptions to daily life, said Nancy Messonnier, MD, director of CDC’s National Center for Immunization and Respiratory Diseases, in a Feb. 25 press call.

Meanwhile, scientists are racing to understand this new threat, including how the virus is evolving and passing from person to person, to inform ongoing public health efforts and vaccine development.

Among the scientists on the front lines of that research effort are infectious-disease experts at Fred Hutchinson Cancer Research Center, such as Trevor Bedford, PhD, a computational biologist who studies how viruses evolve and spread. Bedford is gaining insights about the virus that causes COVID-19 (called SARS-CoV-2, and formerly known as 2019-nCoV) that he hopes will help save lives from this new viral respiratory illness.

As he has been analyzing the spreading virus, Bedford has been sharing what he’s learned so far with the public via media interviews, his team’s open-source platform for real-time tracking of viral evolution — Nextstrain.org — and his Twitter feed (follow Bedford at @trvrb).

On Feb. 13, Bedford told a gathering of international science reporters at the annual meeting of the American Association for the Advancement of Science in Seattle that his latest calculations show that by Feb. 8 as many as 200,000 people may have been infected, with about 15% of them experiencing severe symptoms.

An expert in building family trees of virus evolution, Bedford said that models that use genome sequencing to build family trees of the new virus are consistent with models developed by Imperial College London and others mapping the current scope of the outbreak. That model estimates that the case fatality of COVID-19 is about 1%. (Note that only a subset of infected people will be considered a "case.")

"The thing that is scary about this is that it does seem to be transmissible, and it does seem to be severe," he said.

Here are more highlights of what he and other experts have learned so far — and the critical questions they're still pursuing:

When did the virus emerge and how is it spreading?

Analyses by Bedford and others of the genetic sequences of some of the first human cases showed that the virus had remarkable lack of genetic diversity from person to person after it first emerged.

At first, there was not enough data to clarify what this meant — was the virus jumping repeatedly to humans from animals or, more dangerously, spreading rapidly between people after an initial jump from animals? "The DNA can't distinguish those two scenarios. Only epidemiological data or DNA from the reservoir animal can," Bedford told WIRED on Jan. 22. Figuring this out "would be the big epidemiological goal for everyone at the moment," he told the journal Nature the same week.

"If it's not contained shortly, I think we are looking at a pandemic," Bedford told STAT News on Jan. 27 — although he cautioned that it was impossible to say how serious one would be.

This research by Bedford and other virus-trackers is possible because of rapid genetic sequencing of infected people — unfeasible or even impossible not too many years ago — and a global commitment to sharing these genetic data freely with the worldwide research community. As of Feb. 25, Nextstrain already had 119 novel coronavirus genomes.

Typically, scientists "don't really talk externally that much because you're trying to get your best science so it can't be scooped," Bedford told the CBC, Canada's national public broadcaster, on Feb. 1. "You only really talk about things once it's all been published. This is flipping that around entirely where people are just being completely open with what they know."

He outlined the speed at which genomic information has been flowing:

"Basically, a week after registering that there's this new thing, the amazing scientists in China have a genome for the novel virus that had never been seen before. Then, after the first genome was released on a Friday afternoon, we had five more Sunday morning. And now, nine days later, we're up to 24," Bedford explained on the public radio show Science Friday on Jan. 24. "That first genome has been amazing for people developing rapid tests to be able to actually confirm cases, and these subsequent genomes are being very useful to understand basic epidemiological questions."

Because of the rapidly emerging nature of the disease, "adding a few key samples can change the story significantly," Bedford told the journal Nature on Jan. 28.

That is, in fact, what happened. With access to additional genetic sequences from more infected people, Bedford and Nextstrain teammates wrote on a report on their site on Jan. 30 that the disease's low mutation rate is the result of person-to-person spread since its initial jump, or jumps, from unknown animals to people in November or early December 2019.

In their Jan. 30 report, the team also wrote:

- While the virus has started to pick up mutations as it spreads between people — as this type of virus naturally does — these mutations don't appear to be linked with changes in the virus' behavior.
- Although data are too preliminary for firm conclusions, the new virus appears to be less likely to kill those with confirmed cases than its coronavirus cousin, SARS.

This report on Nextstrain.org describes the latest data on the spread and evolution of SARS-CoV-2 across the world. The map shows the number and location of viral sequences they analyze from cases around the world as the virus traveled out of China.Genomic analysis of nCoV spread. Situation report 2020-01-30. Author: Trevor Bedford, Richard Neher, James Hadfield, Emma Hodcroft, Misja Ilcisin, Nicola Müller. https://nextstrain.org/narratives/ncov/sit-rep/2020-01-30

According to the WHO, the data so far suggest that it takes about five days (with estimates ranging from one to 14 days) to develop symptoms of COVID-19 after catching the virus.

Bedford wrote on Twitter on Jan. 30 that the key question at that point for understanding the disease's transmission is how many people get infected with the virus without getting diagnosable symptoms of the disease.

> A few thoughts on where we stand on #COVID19.
> 1. It appears there aren't massive undercounts of cases in China (https://t.co/MRXH6eu9Bb). This fits as with both my own phylodynamic analyses (https://t.co/fMUyNJdxJ6) and those of @erikmvolz (https://t.co/F0bbvNMdxg). 1/6
> — Trevor Bedford (@trvrb) February 26, 2020

Based on estimates of the virus' spread through a community and the amount of time it would take health officials to detect a cluster of cases, Bedford told the Washington Post on Feb. 21 he expected health officials to know by mid-March whether COVID-19 is becoming widespread enough to be classified as a pandemic.

This story in Science from Jan. 31 looks in depth at work by Bedford and other scientists to uncover the novel virus' origins by mapping coronavirus genomes.

Who is most at risk of COVID-19?

So far, people who have been coming down with the most severe cases of COVID-19 are almost always older people and people with underlying health conditions, according to the CDC's Jan. 30 media briefing.

Is there a vaccine or other treatment?

There is no available vaccine, but multiple research efforts are underway to develop candidates. The first of these experimental vaccines was shipped on Feb. 24 to National Institutes of Health researchers, who are expected to begin human testing in April, the Wall Street Journal reported.

Although there are no drugs specifically for the virus that causes COVID-19, the WHO advises that patients who are hospitalized with confirmed cases of infection be treated with therapies to overcome particular symptoms of illness.

Could the novel coronavirus have been genetically engineered in a lab?

At the AAAS annual meeting on Feb. 13, Bedford fielded a number of questions from the international press corps about stories circulating that the virus causing COVID-19 might have been genetically engineered. “If you look for evidence of genetic engineering, you can find none whatsoever. It is completely consistent with natural evolution,” Bedford said.

In a Feb. 20 Twitter thread, Bedford summarized the evidence supporting a natural, rather than laboratory, origin for the virus:

> I’ve written before that #COVID19 has no evidence of genetic engineering and the “bioweapon” theory has no grounds. See, for example https://t.co/aR5NfTJzYq. In this thread I wanted to directly address the theory of escape from lab in Wuhan. 1/21
>
> — Trevor Bedford (@trvrb) February 20, 2020

Fred Hutch News Service writer Sabin Russell contributed reporting for this story.

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