

September 16, 2020 | By Scott LaFee

How SARS-CoV-2 Went from Single Cases to Overwhelming Continents

Quick, effective interventions contained the first cases of novel coronavirus in North America and Europe, but insufficient testing and tracing created new transmission opportunities and spawned an pandemic

Early detection and intervention stanching the first known introductions of the SARS-CoV-2 virus into North America and Europe, validating the effectiveness of quick, comprehensive testing and contact tracing, reports a multi-institutional team of scientists in the September 10, 2020 online issue of [Science](#).

But subsequent introductions of the virus, carried by travelers, were less effectively monitored and managed — and the virus that causes COVID-19 soon took root, spreading across both continents and leading to a global pandemic that, at last count, has produced more than almost 30 million cases of COVID-19 and killed more than 934,000 people.

“We wanted to understand how and when the virus first took hold in the United States, dramatically upending the lives of everyone in this country,” said Joel Wertheim, PhD, associate professor in the Division of Infectious Diseases and Global Public Health at UC San Diego School of Medicine and a corresponding author on the study. “Pinpointing the timing of this introduction can reveal which early public health measures were effective and which failed to stop viral spread.”



Researchers say travelers were the initial cases of COVID-19 in the United States and Europe. These first cases were quickly contained, but inadequate public health measures spawned subsequent, overwhelming outbreaks and an eventual pandemic. Photo credit: [Pixabay](#).

The study combined genomic sequencing of SARS-CoV-2 samples from around the world, computer modeling of epidemics based on different datasets and variables, and analyses of travel records to reconstruct the global spread of the virus from its origins in Wuhan, China late last year.

The findings clarify early hypotheses about how the novel coronavirus emerged in North America and Europe, upend some popular but speculative notions and demonstrate the value and effectiveness of immediate, intensive testing and contact tracing in preventing viral outbreaks, both now and in the future.

Among the authors' conclusions:

- The earliest known cases of COVID-19 — a traveler from Wuhan, China to Seattle on January 15 and a German businessman returning home from Shanghai, China on Jan. 20 — were not linked to outbreaks that occurred several weeks later. Rather, in both cases, the diagnosed patients were effectively isolated and treated, with contact tracing limiting community exposure. Subsequent outbreaks in Washington and Germany involved viral strains genetically different from the two original cases.
- Evidence indicates the SARS-CoV-2 virus first entered the U.S. in significant fashion in early February, carried by travelers from China. The nationality of the index case or first identified case leading to the larger epidemic is not and cannot be known, in part because tens of thousands of U.S. citizens and visa holders continued to travel from China to the U.S. even after a travel ban was announced in late-January.
- Germany was not the originating site of the COVID-19 epidemic in Europe. Like the U.S., the dispersal route of the virus was China to Northern Italy and then to the rest of the continent. The early German case was not the source of the outbreak in Northern Italy. Italy was also the source for the later spread of the virus to New York City and other outbreaks in the U.S., carried again by travelers.
- Early efforts at containment, which featured aggressive testing, isolation of diagnosed persons, contact tracing and wide-scale adherence to measures, such as masking and social distancing, worked: The first cases did not lead to broader transmissions and larger outbreaks in February when the greater public health threat emerged. Researchers came to this conclusion by running multiple computer models of viral spread, based on differing data sets, and comparing the simulations to what happened in reality.

"By re-running the introduction of SARS-CoV-2 into the U.S. and Europe through simulations, we showed that it was very unlikely that the first documented viral introductions into these locales led to productive transmission clusters," said Wertheim. "Molecular epidemiological analyses are incredibly powerful for revealing transmissions patterns of SARS-CoV-2."

By employing multiple, diverse analytic tools, the authors say there is a better understanding of the short-term evolution and behavior of SARS-CoV-2. More importantly, they note the findings underscore the effectiveness of public health measures — testing, tracing, masking, distancing — if enacted quickly and broadly.

"We believe that those measures (in the first cases in Washington and Germany) resulted in a situation where the first sparks could successfully be stamped out, preventing further spread into the community," said first author Michael Worobey, PhD, professor of ecology and evolutionary biology at University of Arizona. "What this tells us is that the measures taken in those cases are highly effective and should serve as a blueprint for future responses to emerging diseases that have the potential to escalate into worldwide pandemics."

Co-authors of the study are Jonathan Pekar, UC San Diego; Brendan B. Larsen, University of Arizona; Martha I. Nelson, National Institutes of Health; Verity Hill and Andrew Rambaut, University of Edinburgh; Jeffrey B. Joy, University of British Columbia; Marc A. Suchard, UC Los Angeles; and Philippe Lemey, Rega Institute, Belgium.

Funding for this research came, in part, from the David and Lucile Packard Foundation, University of Arizona College of Science, Multinational Influenza Seasonal Mortality Study-Fogarty International Center, European Research Council, Wellcome Trust, National Institutes of Health (grants K01AI110181, AI135992, AI136056, U19 AI135995, T15LM011271), the Research Foundation-Flanders, the Canadian Institutes of Health Research Coronavirus Rapid Response Programme, the Genome Canada Bioinformatics and Computational Biology Programme, and the Biotechnology and Biological Sciences Research Council.

MEDIA CONTACT

Scott LaFee, 858-249-0456, slafee@ucsd.edu

UC San Diego's [Studio Ten 300](#) offers radio and television connections for media interviews with our faculty, which can be coordinated via studio@ucsd.edu. To connect with a UC San Diego faculty expert on relevant issues and trending news stories, visit <https://ucsdnews.ucsd.edu/media-resources/faculty-experts>.