

New York City's coronavirus outbreak spread from more European sources than first reported

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Colorized scanning electron micrograph of a dying cell (blue) heavily infected with SARS-CoV-2 (yellow), the virus that causes COVID-19. Credit: NIAID Integrated Research Facility, Fort Detrick, Maryland.

The COVID-19 pandemic started earlier than previously thought in New York City and Long Island by dozens of people infected mostly with

strains from Europe. A new analysis also shows that most of the spread was within the community, as opposed to coming from people who had traveled.

Previous testing had detected the first case of the virus on March 3 before infections exploded throughout the metropolitan area, leading to 260,600 positive cases by mid-May.

Led by NYU Grossman School of Medicine researchers, the new study used [gene testing](#) to trace the origins of SARS-CoV-2, the [pandemic virus](#), throughout the New York City region in the spring. It showed that the virus first took root in late February, seeded by at least 109 different sources that burst into chains of infection, rather than from a single "patient zero."

Notably, the study authors say, more than 40 percent of people who tested positive had no known contact with another infected person before they contracted the virus.

"Our findings show that New York's early screening test methods missed the onset and roots of the outbreak by several days at the minimum," says study co-lead author Matthew Maurano, Ph.D., an assistant professor in the Department of Pathology at NYU Langone Health. "The work strongly suggests that to nip future outbreaks in the bud, we need a system of rapid, plentiful real-time genetic surveillance as well as traditional epidemiologic indicators."

The investigators also found that more than 95 percent of New Yorkers with COVID-19 had a strain of the virus with a mutation that may make it easier to transmit to others. This finding, Maurano says, helps explain why the virus spread so aggressively in New York, even when accounting for the city's [high population density](#).

In gene sequencing, researchers compare small snips of genetic code to identify mutations that are only found in a particular strain of the virus. These "flags," Maurano says, can then be used to track how the strain has spread over time, similarly to tests used to trace ancestry in people. Experts have previously used this technique to follow outbreaks of influenza, methicillin-resistant *Staphylococcus aureus* (MRSA), and Ebola, among other infections.

The new study, published online Oct. 22 in the journal *Genome Research*, is the largest effort to date to trace the COVID-19 pandemic using gene sequencing, according to Maurano.

For the study, the researchers collected viral genetic information on 864 nasal swabs taken from New Yorkers who had tested positive for COVID-19 between March 12 and May 10. Most of the people were from Manhattan, Brooklyn, and Nassau County on Long Island. Then, the investigators compared the gene sequences of the virus from these samples to those seen in the original strain isolated last winter from patients in Wuhan, China, where the pandemic is believed to have begun.

The study revealed that the genetic codes of the virus in New York more closely matched those of strains from Europe or other U.S. states rather than those from China, where the virus originated. In addition, some of the early chains of infection from person to person ran at least 50 people long.

"Our gene sequencing techniques allowed us to evaluate the precision of our screening tests," says senior study author Adriana Heguy, Ph.D., a professor in the Department of Pathology at NYU Langone. "Based on these results, it is clear that we need a system of plentiful testing that provides rapid results."

She notes that the sequences analyzed in the study accounted for just 10 percent of COVID-19 patients within a single hospital system in New York. The true scale of the community infection was therefore likely much higher, and the original introduction of the [virus](#) to New York City was possibly earlier.

Heguy says the team next plans to investigate whether the mutations uncovered by genetic testing could affect the [coronavirus](#) in other ways, such as causing new or more severe symptoms of COVID-19.

More information: Matthew T Maurano et al, Sequencing identifies multiple early introductions of SARS-CoV-2 to the New York City Region, *Genome Research* (2020). [DOI: 10.1101/gr.266676.120](https://doi.org/10.1101/gr.266676.120)

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