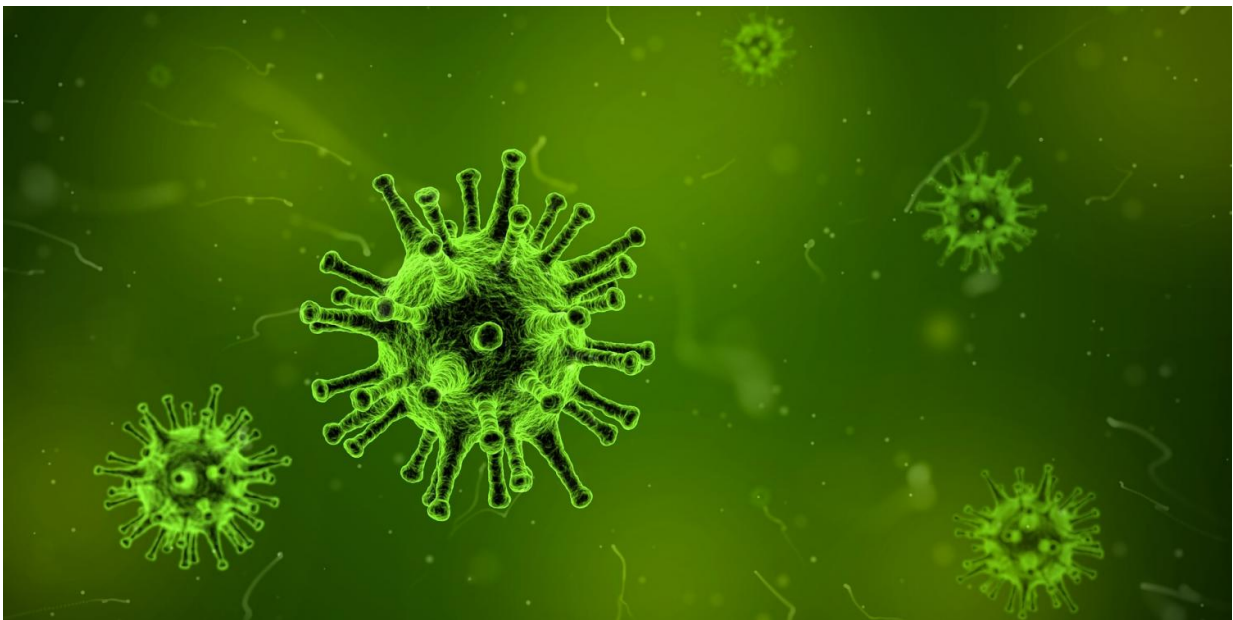


Researchers look to next generation genetic sequencing for deeper understanding of COVID-19

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It might be the future of diagnostic testing for common infections, and could prove to be a crucial tool for understanding and fighting novel viruses. Next generation genetic sequencing—or next generation sequencing (NGS) – is becoming more common in research, although it still isn't widely available. At the UNC School of Medicine, it is part of a research collaboration to better understand viral lung infections,

including COVID-19—the novel coronavirus sweeping the world.

"We can use NGS, which detects all viruses in a given sample from a patient, to make certain our current tests are working correctly to identify the COVID-19 [virus](#)," said Dirk Dittmer, Ph.D., director of the UNC Viral Genomics Core and member of the Lineberger Comprehensive Cancer Center.

NGS not only identifies all viruses present in a sample, but sequences, or decodes, the DNA of the viruses. Having the ability to sift through the genomic code of a virus gives insight into how old it is, where it came from, and if it is mutating.

"It's like taking a fingerprint of the virus," Dittmer said. "It allows us to explore a sample and take a deeper look at what we find. It could help us learn many things, including why some people get sick from the virus and others do not."

Standard diagnostic testing used to quickly detect influenza or respiratory infections looks only for a limited number of pre-determined viruses, and doesn't provide information beyond a positive or negative result. The same goes for testing developed to diagnose COVID-19. The [test](#) developed by UNC researchers looks for one portion of the virus' gene sequence that causes the novel coronavirus.

"Because we are only looking at one gene sequence for the virus, we must continually monitor for changes in this gene sequence so that we can be assured that our test is still reliable," said Melissa Miller, Ph.D., director of UNC Medical Center Microbiology and Molecular Microbiology Laboratories. "NGS will help us do that."

Miller and Dittmer are collaborating to keep the COVID-19 tests as accurate as possible. After UNC has gone through the FDA's process of

confirmation for their testing—getting the first five positive and first five negative results confirmed by North Carolina's laboratory of public health—the first positive 100 specimens will go to Dittmer's lab for further sequencing studies.

"It certainly helps the overall knowledge that we have of COVID-19 disease and coinfections of other viruses that might be there," Miller said.

Dittmer and William A. Fischer, MD, professor in the division of pulmonary diseases and critical care medicine, are corresponding authors on a study published this month in the journal of Influenza and Other Respiratory Viruses. The lead author of the study is Subhashini A. Sellers, MD, assistant professor in the division of pulmonary diseases and critical care medicine. The study's goal was to identify the burden of respiratory illness on people living with HIV. To make sure all viruses and bacteria were accounted for in the samples, Dittmer and his colleagues compared the sensitivity of NGS to standard diagnostic testing for corona viruses, influenza viruses and other infections in people living with HIV, who had respiratory symptoms.

"We used NGS because there is concern that people with HIV are susceptible to viruses not usually on the pathogen panel used in standard of care testing," said Sellers. "In our standard testing we found a strain of rhinovirus, but when it was genetically sequenced we saw it was more unique than the usual strains we see. NGS can help us track this kind of information, which is important in quickly detecting and tracing novel infections and community outbreaks."

"When it comes to [novel viruses](#), you can determine the genetic sequence of a virus and compare it to a database of all known viruses," Dittmer said. "By using [genetic sequencing](#), researchers previously found that the closest 'relative' of COVID-19 was a [coronavirus](#) found in bats."

Dittmer is working on a clinical trial using NGS to ensure COVID-19 testing is accurate on a larger scale. In the meantime, his lab will continue to collaborate with Dr. Miller.

Dittmer said, "This is an example of how having a great research environment at UNC SOM is allowing our community to come together and contribute to the greater [public health](#) effort."

More information: Subhashini A. Sellers et al. Burden of respiratory viral infection in persons with human immunodeficiency virus, *Influenza and Other Respiratory Viruses* (2020). [DOI: 10.1111/irv.12734](https://doi.org/10.1111/irv.12734)

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