Tracking the SARS-CoV-2 virus with genome sequencing

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A study published in *Cell Reports* shows how next generation genetic sequencing can track mutations in the SARS-CoV-2 virus, which can in effect help with transmission tracing, diagnostic testing accuracy and vaccine effectiveness.

"Once you have the virus' genetic sequence with next generation sequencing (NGS), then you can start asking more questions," said Dirk Dittmer, Ph.D., professor of microbiology and immunology at the UNC School of Medicine, and senior author of the study. "Where have we seen this exact sequence before? Did it come from a different state or country? When did this patient travel there and who else may have it?"

Dittmer says this type of virus monitoring is also important in diagnostic testing. Much of the testing developed to diagnose COVID-19 looks for one portion of the gene sequence that causes the novel coronavirus. If that sequence mutates, the test is no longer accurate and results will be affected. Dittmer says that within their study, his team did find variations in the virus' genetic sequence, but fortunately none of the variations were located in the portion of the virus targeted in common diagnostic testing.

"We are concerned about future mutations though," Dittmer said. "It is inherent in a virus' nature to mutate. Changes in other areas of the genetic sequence can not only disrupt testing, but hinder the effectiveness of vaccines."

That's why Dittmer's lab has been collaborating with multiple other labs at UNC-Chapel Hill to stay up to date on what, if any changes should be made to testing protocols and possible vaccine development. Dittmer's lab receives positive SARS-CoV-2 samples from the lab of Melissa Miller, Ph.D., director of UNC Medical Center Microbiology and Molecular Microbiology Laboratories, where UNC's COVID-19 diagnostic testing was developed and put in place March 16.

"Because we are only looking at one gene sequence for the virus, we have told the FDA that we will continually monitor for changes in this gene sequence so that we can be assured that our test is still reliable," said Miller, a co-author of the study. "NGS will help us do that."

Dittmer's recent study is the largest to focus on suburban and rural communities. Researchers were able to reconstruct the mutational landscape of cases seen at the UNC Medical Center in Chapel Hill, NC, a tertiary clinical care center. From March 30 through May 8, 175 samples from confirmed COVID-19-positive patients were analyzed.

Out of the samples tested, 57% carried the spike D614G variant noted in similar studies. The presence of this variant is associated with a higher genome copy number and its prevalence has expanded throughout the pandemic. The genetic variations found in these samples also support the hypotheses that the majority of cases in North Carolina originated from people traveling within the U.S. rather than internationally.

With a grant from the N.C. Policy Collaboratory based at UNC-Chapel Hill, Dittmer's lab will continue using NGS to track the SARS-CoV-2 virus through the remainder of 2020. The goal is to enroll every patient at UNC Hospitals with flu or respiratory symptoms for COVID-19 diagnostic testing. These samples will be sequenced and compiled to form a comprehensive profile of any virus that these patients carry, information that will continue to help a community of researchers in their fight against SARS-CoV-2 and potentially novel coronaviruses.

More information: Ryan P. McNamara et al. High-density amplicon sequencing identifies community spread and ongoing evolution of SARS-CoV-2 in the Southern United States, *Cell Reports* (2020). DOI: 10.1016/j.celrep.2020.108352

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https://phys.org/news/2020-10-tracking-sars-cov-virus-genome-sequencing.html