

Children's Hospital Los Angeles conducts largest pediatric genomic COVID-19 study to date

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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.

When it comes to children, it is becoming clear that COVID-19 impacts them more than was initially realized. Yet there is relatively little

information about SARS-CoV-2, the virus that causes the disease, in pediatric populations. Scientists at Children's Hospital Los Angeles have just published the [largest pediatric COVID-19 study](#) to date, suggesting, for the first time, a possible link between specific viral mutations and severity of the disease.

COVID-19 is not a genetic disease, but genetics of the SARS-CoV-2 virus play an important role in its spread. Mutations—mistakes in the virus' genome as it replicates—can affect how the virus transmits, and may play a role in disease severity. Understanding these links is critical to battling this pandemic.

"SARS-CoV-2 is genetically unstable," says Xiaowu Gai, Ph.D., the Director of Bioinformatics at Children's Hospital Los Angeles. "We tend to refer to 'the virus,' but when we think about the viral genome it's not a static, single virus but really a collection of the genetic changes in all the viruses within an infected patient."

Most of the mutations the SARS-CoV-2 virus undergoes are insignificant or can even weaken it, according to Dr. Gai, however, some mutations could change the course of the pandemic. For example, a mutation called D614G in what is called the Spike protein of the virus may contribute to increased transmissibility from person to person. At the beginning of the pandemic, the D614G mutation represented a small percentage of SARS-CoV-2 samples, but it has since increased so much that this version of the virus has taken over.

Now, Dr. Gai says, nearly every sample they sequence has this mutation. "What we don't know is whether this mutation and other mutations affect how severe the disease ends up being in a patient," he says. "That's what we're trying to find out." And for good reason—if doctors could predict which patients are more likely to have severe disease, lifesaving treatments could be administered sooner.

But there are few [genetic studies](#) published, and when it comes to understanding how the virus affects children, the data are even thinner. "There is really a lack of pediatric genomic studies for SARS-CoV-2," says [Jennifer Dien Bard](#), Ph.D., Director of the Clinical Microbiology and Virology Laboratory at Children's Hospital Los Angeles. "We're trying to change that."

Drs. Gai and Dien Bard have worked within a multidisciplinary team in the Department of Pathology and Laboratory Medicine to genetically sequence every single COVID-19-positive sample they receive, putting CHLA at the forefront of pediatric viral genomic studies. Their efforts have resulted in the largest collection of clinically correlated pediatric genomic data published to date for SARS-CoV-2. Beyond sequencing the samples, the scientists are investigating how subgroups of the virus (called clades) could affect children differently.

"This study is very unique," says Dr. Dien Bard, "because in addition to having this large pool of genomic data, we're really looking at what it all means: How can we trace this virus? How do the genomics correlate with clinical outcomes? These kinds of studies just aren't out there yet, so we're trying to fill that need."

One of the trends to emerge from the study is that a certain grouping of [mutations](#), called clade 20C, were more commonly seen in patients with the most severe COVID-19 symptoms. This study is the first to examine these potential links.

"Larger studies will be required to confirm that one subgroup of SARS-CoV-2 leads to worse prognosis," says Dr. Gai, "but this study is a clear example highlighting the importance of examining the genetics of the [virus](#). These are the puzzle pieces that will help us get ahead of this pandemic."

More information: Utsav Pandey et al, High Prevalence of SARS-CoV-2 Genetic Variation and D614G Mutation in Pediatric Patients with COVID-19, *Open Forum Infectious Diseases* (2020). [DOI: 10.1093/ofid/ofaa551](https://doi.org/10.1093/ofid/ofaa551)

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