Next-Generation Sequencing for SARS-CoV2 (COVID-19)

The Department of General Services' Division of Consolidated Laboratory Services (DCLS) is one of the first public health labs in the nation to use genetic technology to help public health officials better understand and track the scope of the COVID-19 pandemic in the commonwealth to strengthen prevention and response efforts.

DCLS is using next-generation sequencing to genetically decode some Virginia samples that contain the novel coronavirus, SARS-CoV-2, which causes COVID-19. Looking at this genetic fingerprint can help public health officials track in real-time how the virus is changing and provide insights into how it is being transmitted throughout Virginia.

DCLS is working alongside the U.S. Centers for Disease Control and Prevention (CDC) and international public health and university partners using specialized lab equipment and computer software to piece together the genetic makeup of the viruses collected from Virginians with confirmed cases of COVID-19 disease. DCLS is working collaboratively to create a library that stores this data from positive samples tested not only at its lab, but also those tested at private facilities, healthcare systems and universities.

HOW IT WORKS

Genome sequencing is a process used to determine the complete sequence of a particular organism's genome, which is the complete set of genetic material present in a cell or organism. SARS-CoV-2 genetic information is stored in the form of RNA, or ribonucleic acid, which is replicated in cells during infection.

The SARS-CoV-2 virus is made up of approximately 30,000 building blocks of genetic material called nucleotides; humans, by comparison, have over 3 billion. Soon after the virus first appeared in China, scientists were able to apply sequencing technologies to determine the full sequence of nucleotides that comprise the viral RNA genome. This information allowed for the development of diagnostic tests that looked specifically for segments of the coronavirus genome.

DCLS is using next-generation sequencing to genetically decode virus samples from Virginia residents. This sequence will be essentially the same in a single human sample, but as the virus makes copies of itself as it travels from one person to another it sometimes incurs small genetic changes called mutations. These mutations offer clues to where the virus most recently came from _ for instance, whether all positive cases in a nursing home or other setting potentially came from the same source or multiple sources.

Through the use of phylogenetic trees, diagrams similar to family trees showing the evolutionary relationships between different strains, scientists can determine how the virus has spread from one part of the world, nation or state to the next. They also can study how the mutations correlate with disease and which strains are associated with outbreaks while others appear to die out due to quarantine measures.

BENEFITS OF NEXT-GENERATION SEQUENCING OF COVID-19 CASES

By comparing the genetic sequence of the virus, public health officials can:

- More accurately track COVID-19 outbreaks
- Track how the virus is evolving and gain a clearer understanding of how the virus is being transmitted throughout the state
- Understand how different strains of the virus may correlate with illness severity
- Gauge the success of quarantining and social-distancing efforts
- Inform future efforts in vaccine and drug development

Continued tracking can help identify:

- How the coronavirus accrues changes over time
- Vaccine efficacy, once available, as the virus evolves
- Early warning signs that more infectious or lethal mutations have emerged
- Introductions of new viral variants into Virginia