

Enrichment NGS emerges as surveillance tool for coronavirus

By Samantha Black, PhD, ScienceBoard.net Editor in Chief



January 29, 2020 -- As coronavirus continues to grow as a global health concern, researchers urgently seek efficient methods to predict and mitigate emerging coronavirus strains. An international team of researchers believes that targeted next-generation sequencing (NGS) may be a valuable tool for monitoring both current and future outbreaks of coronavirus. The research was published in [mSphere](#) on January 29.

Coronaviruses of bat origin have caused two pandemics in the last century, including the severe acute respiratory syndrome (SARS) coronavirus and Middle East respiratory syndrome (MERS) coronavirus. The most recent coronavirus outbreak, named 2019-nCoV, began causing illness in Wuhan, China, in late 2019 and has now spread to the U.S., with the first documented case diagnosed on January 21.

One of the tools for monitoring the spread of coronaviruses is next-generation sequencing. In the current study, researchers explored if whole-genome sequencing is necessary to characterize coronavirus, especially viruses that originate in bats. Their goal was to develop an efficient and cost-effective pipeline to identify and characterize bat coronavirus for future surveillance.

Researchers used an emerging NGS strategy called enrichment, in which NGS is enriched with probes, also known as baits -- small pieces of genetic material that bind to viral DNA. The baits were designed from 90 representative coronavirus genomes.

The researchers found that enrichment NGS not only decreases the amount of data requiring analysis but can also produce full-length genome coverage in both laboratory and clinical samples. In the study, the approximate cost per enrichment NGS was only \$60 and can be reduced further with the use of multiplexing.

In the context of surveillance studies, targeted enrichment is a valuable tool to triage samples for further processing. One limitation of this enrichment NGS pipeline is that it is only designed to identify known coronaviruses. Therefore, the authors suggest that the bait library will need to be frequently updated to be effective.

"Coronaviruses, especially those that are bat-borne, remain an important source of emerging infectious diseases," said Lin-Fa Wang, PhD, director of the Programme in Emerging Infectious Diseases at Duke-NUS Medical School in Singapore in a statement.

During times that are free of outbreaks, researchers can build up-to-date banks of probes associated with known forms of coronaviruses. During outbreaks, they can use that information to track the evolution of viruses and spread of infections in animal and even human populations.