UAF researchers tracking mutations in the COVID-19 viral genome

FAIRBANKS, Alaska (KTVF) - Friday sees the conclusion of our three-part series on the University of Alaska Fairbanks' (UAF) work with COVID-19 genome sequencing. Dr. Devin Drown told us about specific mutations being tracked throughout the pandemic, and how COVID-19 differs from the flu in its ability to mutate.

By sequencing and comparing COVID-19 samples, scientists can look at and track the mutations that have occurred in the genome as it’s been spreading across the globe.

“There’s a particular mutation that many people have become fascinated by because it appears to be related to transmissibility. Genomes that have this mutation appear to be more common circulating throughout the globe right now than the genomes that don’t have this mutation,” said Drown.

This is the D614G mutation.

“There’s still a lot of work that needs to be done to really provide strong evidence that this mutation increases transmissibility; or, some people have suggested that it increases virulence, the harmfulness of the virus. We’re still working on that evidence,” said Drown.

By looking at the genome, Drown and the team can uncover whether a particular sample has this mutation or not.

“What we’re seeing here in Alaska, very early cases didn’t have this mutation back in March. But most of the cases we see now do have this mutation -- and that’s true not just in Alaska but across the United States and globally. So far we’ve sampled a number of cases. We’d love to be able to do this kind of work on the vast majority of cases to really get a great understanding of clusters of cases and how they might be connected across Alaska. We’re still building that kind of information, and unfortunately it’s getting harder to kind of keep up with the cases that are occurring in Alaska.
Unfortunately we’re seeing a sharp rise in cases, and we’re now thinking about using our efforts for more localized kinds of issues. So rather than trying to understand a survey of all the cases in Alaska, [we] use our kinds of methods and techniques to help with specific outbreaks in small locations,” said Drown.

Even as vaccines are developed, scientists will track mutations within the genomes of the virus and how they relate to the vaccines.

“We have to get a flu shot every year because the flu virus changes so rapidly. The novel coronavirus that were dealing with now, it doesn’t change as rapidly as flu. It has more proofreading mechanisms in it's genome, so it’s a lot more stable. Coronaviruses, they have more of this machinery, this kind of checking and error checking machinery than flu does for instance -- which is good for vaccines, is good for us. But as we apply pressure to it through vaccines, we may see kind of escapes. So we want to be on the lookout for any mutations that allow a virus to not be impacted by a vaccine. That will be something important in the long run to keep track of that information,” Drown concluded.

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