UAMS Research Team Finds COVID-19 Has Mutation Limits

LITTLE ROCK — A University of Arkansas for Medical Sciences (UAMS) research team has found that while the coronavirus can create dangerous variants like delta and omicron, its ability to mutate has limits that should help drug and vaccine makers trying to thwart it.

Drawing from global databases with millions of sequenced SARS-CoV-2 genomes, the multinational team, led by David Ussery, Ph.D, has shown that the virus has a limited genetic range for new mutations. The team’s observations are published in FEMS Microbiology Reviews.

“The surprising finding is that the virus is pretty stable, and it is not changing that much,” said Ussery, professor and director of the Arkansas Center for Genomic Epidemiology & Medicine at UAMS. “It’s somewhat restricted. That’s good news for designing drugs that can fight it effectively.”

The virus’ structure makes it slower to mutate and gives it fewer mutation possibilities. Ussery contrasted it with HIV as an example of a virus that is much more adept at evading new drug therapies. A typical viral escape mechanism has to do with regulation of its production of epitopes, which are protein segments of different shapes that antibodies bind to as part of the immune defense.

“Instead of the frightening theoretical possibility of this virus producing millions of different epitopes that need to be therapeutically anticipated during vaccine development, we may now be able to predict a very limited subset of probable epitopes,” Ussery said.

The team analyzed coronavirus genomes in GenBank and Global Initiative on Sharing Avian Influenza Data (GISAID) databases. It used the high performance UAMS-based computer known as GRACE to perform much of the computational work. The infrastructure to help run this computer is supported in part by a grant from the National Science Foundation (NSF) in 2020, “Data Analytics That Are Robust and Trusted (DART).” This was an Arkansas state-wide grant ($24 million), funded by the Arkansas NSF EPSCoR program.
Ussery, who holds the Helen Adams & Arkansas Research Alliance (ARA) Endowed Chair in Biomedical Informatics, said the analysis was inspired by “Ebolavirus Comparative Genomics,” published in 2015 by an international team that included all four authors of the COVID-19 paper. The Ebola publication earned a FEMS Microbiology Reviews Editor’s Choice Award.

“I think our SARS-CoV-2 findings are breaking some new ground, helping people see the big picture with a systematic look at the virus’ genomics,” Ussery said. “We now have several million genomes and that allows us to tease out the variance within different lineages that are causing major outbreaks like delta and omicron.”

The research team was also able to identify numerous incomplete or erroneous sequences housed in the databases.

In addition to Ussery, the co-authors are:
- Trudy Wassenaar, Ph.D., (first author) director of Molecular Microbiology and Genomics Consultants, Zotzenheim, Germany
- Visanu Wanchai, Ph.D., currently a post-doctoral fellow, Department of Biomedical Informatics, UAMS College of Medicine
- Gregory Buzard, Ph.D., microbiologist (retired from Centers for Disease Control and Prevention)

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