Virol Curr Res
Volume 5:3, 2021

Virology: Current Research

Short communication

Open Access

SARS CoV-2 Viral Mutations

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Introduction

The concern rose even more last week when Anthony Fauci, MD, head of the National Institute of Allergy and Infectious Diseases (NIAID), broached the idea during an online chat. A mutation that speeds up COVID-19's spread might explain why the virus known as SARS-CoV-2 has so rapidly moved through North America and Europe, where the G614 mutated version is predominant [1]. The original version of the virus, D614, was most widely seen in China and other parts of Asia.

Genetic variants of SARS-CoV-2 have been emerging and circulating around the world throughout the COVID-19 pandemic. Viral mutations and variants in the United States are routinely monitored through sequence-based surveillance, laboratory studies, and epidemiological investigations.

A US government interagency group developed a Variant Classification scheme that defines three classes of SARS-CoV-2 variants. Laboratory studies suggest specific monoclonal antibody treatments may be less effective for treating cases of COVID-19 caused by variants with the L452R or E484K substitution in the spike protein [2].

A variant has one or more mutations that differentiate it from other variants in circulation. As expected, multiple variants of SARS-CoV-2 have been documented in the United States and globally throughout this pandemic. To inform local outbreak investigations and understand national trends, scientists compare genetic differences between viruses to identify variants and how they are related to each other.

Variant classifications

SARS-CoV-2 Interagency Group (SIG) to improve coordination among the Centers for Disease Control and Prevention (CDC), National Institutes of Health (NIH), Food and Drug Administration (FDA), Biomedical Advanced Research and Development Authority (BARDA), and Department of Defense (DoD) [3]. This interagency group is focused on the rapid characterization of emerging variants and actively monitors their potential impact on critical SARS-CoV-2 countermeasures, including vaccines, therapeutics, and diagnostics.

A variant with specific genetic markers that have been associated with changes to receptor binding, reduced neutralization by antibodies generated against previous infection or vaccination, reduced efficacy of treatments, potential diagnostic impact, or predicted increase in transmissibility or disease severity [4].

Conclusion

Specific genetic markers that are predicted to affect transmission, diagnostics, therapeutics, or immune escape. Evidence that it is the cause of an increased proportion of cases or unique outbreak clusters. Limited prevalence or expansion in the US or in other countries

A variant of interest might require one or more appropriate public health actions, including enhanced sequence surveillance, enhanced laboratory characterization, or epidemiological investigations to assess how easily the virus spreads to others, the severity of disease, the efficacy of therapeutics and whether currently authorized vaccines offer protection.

References

1. Sarah E, John, Tomar Sakshi, Stauffer Shaun, and Mesecar Andrew, et al. “Targeting Zoonotic Viruses: Structure-based Inhibition of the 3C-like Protease from Bat Coronavirus HKU4-The Likely Reservoir Host to The Human Coronavirus that Causes Middle East Respiratory Syndrome (MERS).” *Bioorg Med Chem* 23(2015):6036-6048.
2. Grinter, Sam, and Zou Xiaoqin. “Challenges, Applications, and Recent Advances of Protein-Ligand Docking in Structure-Based Drug Design.” *Molecules* 19(2014):10150-10176.
3. Rainer, Storn, and Price Kenneth. “Differential Evolution–A Simple and Efficient Heuristic for Global Optimization over Continuous Spaces.” *J Global Optimization* 11(1997):341-359.
4. Omar, Jone, Olivares Maitane, Alonso Ibone, and Vallejo Asier, et al. “Quantitative Analysis of Bioactive Compounds from Aromatic Plants by Means of Dynamic Headspace Extraction and Multiple Headspace Extraction-Gas Chromatography-Mass Spectrometry.” *J Food Sci* 81(2016):C867-C873.

How to cite this article: Shaghaghi, Neda. “SARS CoV-2 Viral Mutations” *Virol Curr Res* 5 (2021): 129.

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Received: May 03, 2021; **Accepted:** May 20, 2021; **Published:** May 28, 2021