ISSN: 2474-3658

Mustafa and Makhawi. J Infect Dis Epidemiol 2023, 9:313
DOI: 10.23937/2474-3658/1510313
Volume 9 | Issue 12
Open Access

Journal of
Infectious Diseases and Epidemiology

COMMENTARY

Eg.5 Variant Approaching the Status of "Variant of Concern": A Future Perspective

Mujahed I. Mustafa* *and Abdelrafie M. Makhawi*

Department of Biotechnology, College of Applied and Industrial Sciences, University of Bahri, Khartoum, Sudan

***Corresponding author:** *Mujahed I. Mustafa, Department of Biotechnology, College of Applied and Industrial Sciences, University of Bahri, Khartoum, Sudan*

Abstract

The EG.5 subvariant of SARS-CoV-2 has emerged as the predominant COVID-19 variant in the United States, raising concerns among virologists due to its high transmissibility and ability to evade immunity. This variant is approaching the status of a Variant of Concern, which is defined as a variant that exhibits a noticeable increase in spread, virulence, and demonstrable impacts on diagnosis, treatment, and vaccines. Despite its potential significance, the EG.5 has not yet been officially designated as a Variant of Concern by authoritative bodies such as the World Health Organization or national public health agencies. Consequently, ongoing research is being conducted to determine the effectiveness of vaccines against this variant. The emergence of Variant of Concerns has prompted scientists to establish robust systems for detecting and tracking variants, collecting data on their impact on immunity and global public health. However, this early detection and analysis group faces challenges in identifying newly emergent variants for evaluation due to difficulties in disentangling epidemiological factors from evolutionary effects and working with limited and potentially biased data sets.

Keywords

EG.5 variant, Eris, Variant of concern

Introduction

A new subvariant called EG.5 "Eris" has recently emerged, being a descendant of a group of coronavirus strains labeled XBB [1]. These strains are all derived from omicron variant, which originated in late 2021 [2]. EG.5 was initially documented on February 17, 2023, and categorized as a “variant under observation on July 19, 2023 [3].

As of June 27, 2023, the World Health Organization (WHO) has received reports of 767,518,723 confirmed cases of COVID-19, with 6,947,192 deaths. It is important to acknowledge that the actual number of COVID-19 cases is likely much higher than the confirmed cases due to limited testing [4]. The World Health Organization (WHO) reported that the prevalence of EG.5 increased significantly from June to July, more than doubling from almost 8% to over 17% of global cases. As of August 8, 2023, EG.5 has been detected in over 51 countries worldwide, as stated by the WHO [1]. Based on this assessment of risk, EG.5 classified as a variant of interest (VOI) [4]. According to the WHO, there has been an 80% increase in globally reported COVID-19 cases in the past month compared to the previous month [4].

Symptoms of Eris are similar to those of other COVID-19 variants, including fever, cough, and fatigue. It is important to note that vaccines are still effective against Eris and other COVID-19 variants, and getting vaccinated is the best way to protect yourself and others from the virus [1].

EG.5 carry mutations that alter the pathogenicity of the virus, an extra F456L amino acid mutation in the spike protein compared to its parent XBB.1.9.2 subvariant and XBB.1.5. Among the EG.5 lineage, the variant EG.5.1 has an additional spike mutation Q52H and accounts for 88% of the available sequences for EG.5 and its descendant lineages [1]. The F456L amino acid change in the spike protein of EG.5 is significant for several reasons. Firstly, this mutation is unique to EG.5 and is not present in other COVID-19 variants [1].

Additionally, the F456L mutation is located in the

Citation: Mustafa MI, Makhawi AM (2023) Eg.5 Variant Approaching the Status of "Variant of Concern": A Future Perspective. J Infect Dis Epidemiol 9:313. doi.org/10.23937/2474-3658/1510313

Accepted: December 18, 2023: **Published:** December 20, 2023

receptor-binding domain (RBD) of the spike protein, which is the part of the virus that binds to human cells. This suggests that the mutation may increase the binding affinity of the virus to human cells, potentially making it more transmissible. Moreover, this mutation may also impact the effectiveness of certain monoclonal antibody treatments that target the spike protein. It has been identified as a key spike mutation in EG.5.1, a sub-lineage of EG.5 [1].

The EG.5 variant has become dominant in the United States [4]. Maybe this is due to the replication rate, it refers to how quickly a virus can reproduce within a host's body. Variants with faster replication rates can reach higher viral loads sooner, leading to increased transmissibility [5]. For instance, the B.1.1.7 variant has been found to replicate more efficiently than the original strain, resulting in a higher number of viral particles being produced within a shorter timeframe [6]. The EG.5 variant is highly transmissible [1], meaning it can spread easily from person to person. This is likely due to genetic changes that have made the virus more efficient at infecting cells. Future studies on EG.5 should focus on assessing its transmissibility including the R0 (basic reproduction number) and secondary attack rates compared to other variants. Epidemiological investigations should determine if EG.5 exhibits clustering and super-spreading events which are indicative of increased transmissibility.

In this future perspective, we shed light on the hypothetical scenario where the EG.5 variant approaches the status of a variant of concern, considering the current knowledge and possible implications. Before delving into the possible implications of EG.5 as a variant of concern, it is essential to understand what defines this status. Typically, a variant of concern is designated when it demonstrates increased transmissibility, leads to more severe disease outcomes, reduces the effectiveness of diagnostics, therapeutics, or vaccines, or shows other properties of substantial public health impact [7].

In this hypothetical scenario, the EG.5 variant emerges as a descendant of the SARS-CoV-2 virus and exhibits distinct genetic mutations. These mutations could affect various aspects of the virus's behavior, including its binding to human cells, replication rates, and evasion of the immune system.

If EG.5 were to approach the status of a variant of concern, it might possess mutations that enhance its ability to spread rapidly among human populations. This increased transmissibility could lead to more outbreaks, a higher number of cases, and potentially a more challenging containment of the virus.

The impact of EG.5 on clinical severity disease progression and mortality rates remains a critical concern. Prospective studies must be conducted to elucidate if EG.5 is associated with increased disease severity such as a higher rate of hospitalization ICU admissions and fatality rates. Comparisons with existing variants will be vital in understanding the true clinical impact [1].

Another crucial aspect is the potential for EG.5 to evade the immune response elicited by prior infections or vaccination. Extensive laboratory investigations and clinical studies should evaluate the neutralizing capacity of existing therapies and vaccine-induced immunity against EG.5 [8]. Longitudinal surveillance will be crucial in monitoring breakthrough infections and vaccine effectiveness in populations where EG.5 emerges.

To effectively address the hypothetical scenario where EG.5 approaches the status of a variant of concern, the following measures would be important:

Active surveillance and genomic monitoring: Enhanced surveillance systems and continuous genomic monitoring would be essential to detect the emergence of EG.5 or any other potential variants. Early identification would enable rapid response and targeted measures to control its spread [8].

Development of adaptive vaccines and therapeutics: Prompt development of adaptive vaccines and therapeutics tailored to EG.5's specific genetic mutations would be necessary to maintain the effectiveness of existing interventions. Scientists and pharmaceutical companies would need to collaborate to expedite the development and regulatory approval processes [9].

Public health communication and collaboration: As the EG.5 subvariant has the potential to spread globally, international collaboration and information sharing will be crucial in monitoring its spread and impact. This will involve coordination between health agencies, researchers, and policymakers to implement appropriate measures to mitigate its transmission [10].

While our perspective on the EG.5 variant approaching the status of a variant of concern is speculative, it highlights the importance of proactive measures in monitoring, understanding, and responding to emerging variants. By staying vigilant, investing in research, and maintaining effective surveillance systems, we can enhance our ability to address potential challenges posed by new variants and safeguard public health.

Source of Funding

This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

Conflict of Interest

The authors declare that they have no competing interests.

Authors' Contributions

MIM: wrote initial and final draft, conceptualization, collected and organize data. AM: wrote initial and final draft, conceptualization. AMM: wrote initial and final draft, supervision, conceptualization. All authors have critically reviewed and approved the final draft and are are responsible for the content and similarity index of the manuscript.

Ethical Approval

There is no ethical issue.

Acknowledgements

The authors acknowledge the Deanship of Scientific Research at University of Bahri for the supportive cooperation.

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