



# Role of Glycoprotein Hemagglutinin-Esterase in COVID-19 Pathophysiology?

Milad Zandi<sup>1,2</sup> · Emad Behboudi<sup>3</sup> · Saber Soltani<sup>1,2</sup>

Accepted: 19 June 2021 / Published online: 28 June 2021

© The Author(s), under exclusive licence to Springer Science+Business Media, LLC, part of Springer Nature 2021

One and a half year has passed since the outbreak of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) the causative agent of coronavirus disease 2019 (COVID-19) pandemic. Nowadays information on SARS-CoV-2 and its receptors are increasing. It's been showed that O-acetylated sialic acids (SAs) can interact with viral spike glycoprotein for the primary attachment of virus and its penetration into the host cells [1]. Most beta coronaviruses recognize 9-*O*-acetyl-SAs but it has changed to 4-*O*-acetyl-SA through the evolution of Coronaviruses [1]. Its viral ligand, the hemagglutinin esterase (HE) gene was transmitted to a beta coronavirus lineage A through horizontal gene adaption from a 9-*O*-acetyl-SA-specific HEF, as in influenza C [1, 2]. Adaption of HE occurs via cross-species transmission and HE evolution [1]. This fact demonstrates viral evolutionary compatibility to host glycans. Thus, studying emerging viruses like SARS-CoV-2 may result in better recognition of viral evolution process. For instance, as mentioned above,

HE gene transfer is discovered in the beta coronaviruses, which choose 9-di-*O*-Ac-SAs. A more interesting example of such events happens in the murine CoVs, with attachment to two various subtypes of the canonical 9-*O*-Ac-SA (type I) and unique 4-*O*-Ac-SA (type II) [3]. But noticeably it must be mentioned that same as SARS-CoV-2, SARS-CoV genome has no HE gene [4]. Incorrectly a recent published article in the journal of stem cell reviews and reports states that SARS-CoV-2 has HE and hemagglutinin protein [5], also the authors has illustrated viral hemagglutinin glycoprotein on viral envelope. This is in contrast to previous studies which experimentally showed that SARS-CoV-2 lacks HE gene and glycoprotein. According to data from different full genome sequencing studies using next generation sequencing (NGS) and phylogenic analysis of SARS-CoV-2 virus has no HE gene and consequently HE glycoprotein [4]. Therefore this virus lacks HE gene and cannot carry HE protein (Fig. 1).

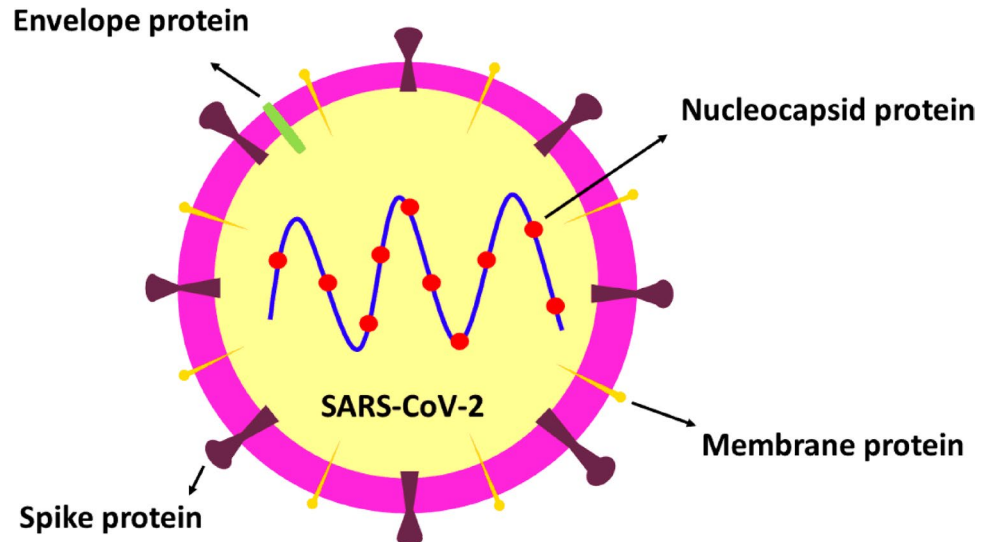
✉ Milad Zandi  
Miladzandi416@gmail.com

<sup>1</sup> Department of Virology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran

<sup>2</sup> Research Center for Clinical Virology, Tehran University of Medical Sciences, Tehran, Iran

<sup>3</sup> Department of Microbiology, Golestan University of Medical Sciences, Gorgan, Iran

**Fig. 1** Structural proteins of SARS-CoV-2



## References

1. Kim, C.-H. (2020). SARS-CoV-2 evolutionary adaptation toward host entry and recognition of receptor O-Acetyl sialylation in virus–host interaction. *International Journal of Molecular Sciences*, *21*(12), 4549.
2. Kienzle, T. E., Abraham, S., Hogue, B., & Brian, D. A. (1990). Structure and orientation of expressed bovine coronavirus hemagglutinin-esterase protein. *Journal of Virology*, *64*(4), 1834–1838.
3. Langereis, M. A., Van Vliet, A. L., Boot, W., & De Groot, R. J. (2010). Attachment of mouse hepatitis virus to O-acetylated sialic acid is mediated by hemagglutinin-esterase and not by the spike protein. *Journal of Virology*, *84*(17), 8970–8974.
4. Chan, J.F.-W., Kok, K.-H., Zhu, Z., Chu, H., To, K.K.-W., Yuan, S., et al. (2020). Genomic characterization of the 2019 novel human-pathogenic coronavirus isolated from a patient with atypical pneumonia after visiting Wuhan. *Emerging Microbes & Infections*, *9*(1), 221–36.
5. Bagheri, H. S., Karimpour, M., Heidarzadeh, M., Rajabi, H., Sokullu, E., & Rahbarghazi, R. (2021). Does the global outbreak of COVID-19 or other viral diseases threaten the stem cell reservoir inside the body? *Stem Cell Reviews and Reports*, *17*, 214–230.

**Publisher's Note** Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.