

Predictors of SARS-CoV-2 infection: is there a comprehensive analysis?

Wen Tang

MM, School of Medicine, Nantong University, Nantong, China

Hong-Lin Chen

PhD, School of Public Health, Nantong University, Nantong, China

Correspondence:

Hong-Lin Chen

School of Public Health, Nantong University,

9#Seyuan Road, Nantong, Jiangsu, China, 226001

E-mail : honglinyjs@126.com

Dear Editor:

We have read with interest by the article Andrejko KL et al[1] on prediction of SARS-CoV-2 infection following high-risk exposure. The authors found that non-pharmaceutical interventions and vaccine were useful in reducing individual risk of infection. While we applaud the authors making people aware of wearing a sanitary face mask and vaccination, there are several unmentioned factors that the authors should have considered before establishing the relevance.

Epidemiologic studies have confirmed that, the SARS-CoV-2 infection rates and genotype distributions vary between different regions and countries, even varied in different regions of one country[2]. In the context of SARS-CoV-2 mutations since April 2020, the rapid spread of the D614G mutation is singular and has led us to aware that viruses with D614G have enhanced fitness[3]. As reported, P.1 and B.1.427/429 variants lead to increased transmissibility (2.2-fold and 1.2-fold increases, respectively) or to variants that evade prophylaxis[4, 5]. Unfortunately, the study by Andrejko KL et al does not consider this variable. To demonstrate the effectiveness of NPIs and vaccine, the authors would need to examine genotyping factors from these patients.

It was also surprising that the case group included in this study selected from individuals who had received a positive molecular SARS-CoV-2 test result, not new cases. Different from incidence cases, features of prevalence cases may have changed[6], especially behavioral change in life. This would imply that there might be a risk of Neyman bias arising from disease.

Furthermore, the authors considered that the diagnostic criteria were made based on the SARS-CoV-2 molecular test result. However, in fact, there may be false negatives associated with samples. As previously reported, true COVID-19 probably went undetected until several days into the disease course[7]. Inclusion criteria for this study should be stricter, and should be combined with clinical, imaging, and pathological manifestations[8].

Although we contend that the evidence from Andrejko KL et al's study is insufficient to conclude predictors of SARS-CoV-2 infection of patients, we applaud the emphasis the authors place on the need to use NPIs in populations with limited vaccine access or ineligible to be vaccinated, and in response to changing epidemiologic conditions.

Conflict of Interest: None

Reference

1. Andrejko KL, Pry J, Myers JF, et al. Predictors of SARS-CoV-2 infection following high-risk exposure. *Clin Infect Dis* **2021**.
2. Yi Zhang W-hZ. 2019 novel coronavirus variants: current status, trends and countermeasures. *Chinese Journal of Infectious Diseases* **2021**; 39(6): 321-4.
3. Korber B, Fischer WM, Gnanakaran S, et al. Tracking Changes in SARS-CoV-2 Spike: Evidence that D614G Increases Infectivity of the COVID-19 Virus. *Cell* **2020**; 182(4): 812-27.e19.
4. Faria NR, Mellan TA, Whittaker C, et al. Genomics and epidemiology of a novel SARS-CoV-2 lineage in Manaus, Brazil. *medRxiv* **2021**.
5. Deng X, Garcia-Knight MA, Khalid MM, et al. Transmission, infectivity, and antibody neutralization of an emerging SARS-CoV-2 variant in California carrying a L452R spike protein mutation. *medRxiv* **2021**.
6. Bagley SC, Altman RB. Computing disease incidence, prevalence and comorbidity from electronic medical records. *J Biomed Inform* **2016**; 63: 108-11.
7. Winichakoon P, Chaiwarith R, Liwsrisakun C, et al. Negative Nasopharyngeal and Oropharyngeal Swabs Do Not Rule Out COVID-19. *J Clin Microbiol* **2020**; 58(5).
8. Tan HZ. [An epidemiologic thinking on the diagnosis criteria of COVID-19]. *Zhonghua Liu Xing Bing Xue Za Zhi* **2020**; 41(7): 998-9.