Polymorphism of tmprss2 (rs12329760) and severity of COVID-19 in the Ukrainian population: Response

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To the Editor,

We have read with interest the correspondence of Amnuay Kleebayoon and Viroj Wiwanitkit regarding our publication "Polymorphism of tmprss2 (rs12329760) but not ace2 (rs4240157), tmprss11a (rs353163) and cd147 (rs8259) is associated with the severity of COVID-19 in the Ukrainian population (1)." In this paper, we indicated the presence of an association between the tmprss2 (rs12329760) polymorphism and the severity of COVID-19 in the Ukrainian population. The background for this research was initiated by the supposed interaction between host gene variability and SARS-CoV-2 infection (2). After that we received the research results on the association of at1r (rs5186) polymorphism with COVID-19 severity (3). Recently, there are a lot of publications in this field and many gene polymorphisms associated with COVID-19 severity are described. We completely agree with correspondents that "a number of genetic variations … are associated with the severity of COVID-19". Unfortunately, there is not enough data supporting the idea that the current clinical manifestation of COVID-19 is connected to a previous asymptomatic COVID-19 (4, 5). Moreover, reactivation of SARS-Cov-2 after recovery from COVID-19 or reinfection with a genetically distinct mutant virus is under investigation. The deep, extensive, rapid, and real-time whole-genome sequencing studies, as well as an enhanced vaccination drive, and rigorous adherence to COVID-19 appropriate behavior, would be critical in limiting the severity of transmission and reinfection (6). Thus, humanity is still far from the final understanding of COVID.

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