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Is Big Data safe for knowledge management?

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Abstract

Coronavirus disease 2019 (COVID-19) may be a global ill health that causes many deaths worldwide. The clinical manifestation of COVID-19 widely varies from asymptomatic infection to severe pneumonia and systemic disease. It is thought that host genetic variability may affect the host's response to the viral infection and thus cause severity of the disease. The SARS-CoV-2 virus requires interaction with its receptor complex within the host cells before infection. The trans membrane protease serine 2 (TMPRSS2) has been identified together of the key molecules involved in SARS-CoV-2 virus receptor binding and cell invasion. Therefore, during this study, we investigated the correlation between a genetic variant within the human TMPRSS2 gene and COVID-19 severity and viral load.

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