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Press Release

Virulence factor of many deadly viruses including novel coronavirus causing COVID-19 decoded by JMI Professor

Virulence factor of many deadly viruses including novel coronavirus causing COVID-19 has been decoded in an important research conducted jointly by Dr. Mohammad Irfan Qureshi of Department of Biotechnology, Jamia Millia Islamia (JMI) and Dr. Mohammad Asim from Department of Clinical and Experimental Medicine, University of Surrey, UK. This novel information has been added and generated through computational biology.

The preprint of the research article has been uploaded by highly reputed Elsevier Publishers on the portal of the Biology Research Network (SSRN) with ID 3605888.

Explaining about the new findings Dr. M. Irfan Qureshi said that they were bioinformatically analyzing the new mutations in the novel coronavirus-2 spike which is detrimental to initiate virus-host interaction, an event that subsequently leads to the infection.

Surface-to-surface compatibility of virus and human is decisive for deciding if an infection will take place. A comparative evaluation of spike glycoproteins with other deadly viruses, we noticed occurrence of 4 amino acid residues viz. Serine-Proline-Arginine-Arginine (SPRR) in their surface proteins. Strikingly, the same residues seem to be a hallmark for higher degree of contagiousness in many viruses, Dr. Qureshi adds.

In other words, virus strains which have SPRR residues in their surface proteins seem to be highly contagious. In general, viral substrates are processed for activation by a human enzyme called Furin which is a proprotein convertase. Whether SPRRs are directly targeted by furin to facilitate virus-host fusion or there is another mechanism exclusively reserved for SPRR-based virus activation, would be revealed by further researches.

If it is not furin, further studies will open doors for identification of novel mechanism, or redefine furin-cleavage mechanism, says Dr. Qureshi.

It is worth mention that this tetra peptide SPRR stretch has been adopted by many viruses with the passage of time, perhaps due to natural mutations.

Shockingly, Hepatitis-B virus has 3 stretches of SPRR in capsid proteins, all very near to furin-cleavage sites but not fully complying to the fixed rules. Different isolates of Hepatitis- B show that lysine is prone to be replaced by argenine. These tetrapeptide stretches are also present in important proteins of hepatitis C, HIV-1 subtype c, denguvirus 1, chikungunyavirus, Zaire ebolavirus, zikavirus and dependovirus, etc. Amazingly, Porcine epidemic diarrhea virus (PEDV), Avian infectious bronchitis virus, Roussetus bat coronavirus HKU9/KY06/HKU12-600 also harbor SPRR residues in their glycoprotein spike.

“It seems, first instance of emergence of SPRR in any betacoronavirus SARS-CoV is in a sample collected from Kenya fruit bat coronavirus (KY06/2006) and not Wuhan, China; at least at that time. It is shocking to learn about a possibility of COVID-19-like disease outbreak that could have taken place way back around 2006”, suspect authors.

“We have also demonstrated possible mechanisms of higher pathogenicity caused by SARS-CoV-2 virus in human cell. Biggest threat in the cell could be posed by limitation of furin due to which many important proteins required in cellular defence and metabolism are remained un-cleaved hence non-activated, thus weakening host immunity”, said Dr. Qureshi.

The study has also provided RNA-interference based inhibition of important human genes. One of the other highlights of this novel study is prediction of top 50 possible hosts that could be susceptible to infection by novel coronavirus-2. “We are sure that this finding is going significantly contribute in controlling and treatment of COVID-19 disease through targeting of SPRR residues. We dedicate this research to all the people who in one or other way suffered due to present COVID-19 crisis and offer it as a gift of Eid to India as well as world, added Dr. M. Irfan Qureshi.

JMI Vice Chancellor Professor Najma Akhtar congratulated Dr. M. Irfan Qureshi for this important research and promised all possible support in getting more insights of the disease. I am committed for promotion of world class research at Jamia, said Prof. Akhtar.

COVID-19 disease is caused by Severe Acute Respiratory Coronavirus-2 (SARS-CoV-2) which has so far infected more than 5.3 million people and caused 340 thousand deaths worldwide.

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Pictures of Dr. M. Irfan Qureshi



