COVID-19 mutation variant mechanism

Pardis Tabaee Damavandi

Queen Mary University of London

Author Note

Copyright notice © 2020 by Pardis Tabaee Damavandi. All rights reserved. No part of this publication may be reproduced, distributed, or transmitted in any form or by any means, including photocopying, recording, or other electronic or mechanical methods, without the prior written permission of the publisher, except in the case of brief quotations embodied in critical reviews and certain other non-commercial uses permitted by copyright law.

Abstract

The UK government has recently announced how the Covid19 virus has mutated, causing a surge in the cases in Essex, and other parts of England, however, this mutation had already been observed later in the Summer 2020 in a population of Minks and in Denmark. A “prescient” analysis of the mutation is explored in this short paper.

Keywords: Covid19 variant.

COVID-19 mutation variant mechanism

In the current pandemic scenario several news have impacted the world, from the arrival of numerous types of vaccines, worldwide, to the administration of the same which still persists as the main effective strategy in an attempt to at least weaken the virus and strengthen the immune response by our human body. It is also true that management of the viral variations needs to be considered and remains particularly important in non-vaccinated patients.

The mutations at the level of the Coronavirus 2019 spike protein

The covid19 spike protein has adopted a few mutations, of note are the deletion of a valine amino acid, Val320, which is not found in the mutant strain reported in November 2020, compared to the March 2020 strain, as well as an insertion of a previously absent Threonine (Thr329) between an Arginine and an Asparagine. These changes are effective in destabilizing the spike protein itself, which also becomes more hydrophilic.

Nevertheless, the primary variation affects two different amino acids, two main serines Ser673 and Ser691, among which it can be observed that the hydrophobic sequence YQTSQ has been lost (in the new strain). As a consequence the β sheets deriving from the original two serines are “softer”, shorter as well as partially less lipophilic, with the residual loops mainly visible. It is therefore possible to conclude that the stability of those sheets has been lost, due to the reduced hydrophobic interactions between the “remnants” of the two loops, formed, merely, by the two serine amino acids.

Parenthetically, serine is a target of Serine kinases (MAP kinases, etc) and it has been antecedently discussed as a potential target for treatment in Coronaviruses (Tabaee D., 2020).

Why has the Covid19 mutated

Most viruses vary as a response to several changes in the surrounding environment, typically when exposed to organic stimulations of different kinds (example during animal host to other animal or to other microbe host transmissions). Thus, reasons can include a simple adaptation to environmental stressors, but also a desire to increase survival and to continue the viral parasitic activity within a preferred host (notably the most populating one, thus the *homo sapiens sapiens*).

In this case, a destabilization in a protein structure usually connotes a response to our organism's stressors which are still mediated by our immune responses, such as pH variations that influence mucus thickness and secretion for example, temperature (fevers), fevers are harmful to the viral proteins as they denature them, thus inactivating them temporarily, or of osmotic pressure variations, where salt accumulation can again act as a denaturant. All these factors make life for the virus uneasy.

Another main motive why mutation is a prospect for the virus is for trophic objectives; the virus may need to have access to several compartments and not just the pulmonary compartment to satiate its necessity for ampler resources (energetic or enzymatic), in order to replicate more effectively and enhance symbiosis.

Potential symptoms.

The potential symptoms to this variation for patients affected by the new strain, could view a more persistent and higher fever, because the spike protein is more destabilized, making denaturation a little bit more difficult. On the upside, serine inhibition by the immune response should be easier due to more accessibility which is a "side-effect" to protein destabilization for the microorganism.

Potential management

Although paracetamol is partially immunosuppressive, it could be very helpful as an antipyretic for persistent high fever (at a dosage of 1000 mg *i.v.*), as prescribed normally for hyperthermia.

Conclusion

This analysis is preliminary due to errors within the deposited structure of the novel strain available on the *Protein Data Bank*, however, the analysis based on what is presently therein obtainable allowed this small study.

No conflict of interest to disclose.

References

Tabaee Damavandi, P. (2020). Map kinase dysregulation by coronaviruses. *OSF preprint server*,
10.31219/osf.io/da5r7