Medical Case Reports and Therapeutic Studies [CRTS]

Volume 2020 Issue 01

Editorial

New Coronavirus, Covid19, Neo Darwinian Evolution or Biological Manipulation in Lab?

Prof. Par Iradj Sobhani*

Professor in medicine, Dir. of the EC2M3 (Early detection of colonic cancer by using molecular and microbial markers) research Lab at the University of Paris Est Créteil-UPEC and head of the Department of Gastroenterology and Endoscopy

Received: March 27, 2020; **Accepted:** March 31, 2020; **Published:** April 03, 2020

Citation: Prof. Par Iradj Sobhani (2020) New Coronavirus, Covid19, Neo Darwinian Evolution or Biological manipulation in Lab? *Med Case Rep Ther Stud* 01(01): 1–3.

Coronavirus or COVID19, known to scientists as "SARS-CoV-2," is the seventh coronavirus inducing an infectious disease in humans. SARS-CoV in 2002, MERS-CoV in 2012, and now SARS-CoV-2 is known to cause a deadly disease affecting the human respiratory system. Viruses from the same family, including HKU1, NL63, OC43 and the 229E, although highly contagious, are associated with mild symptoms. The rapid contagiousness of the new COVID19, is associated with Acute Respiratory Distress Syndrome (ARDS) forced the Chinese authorities to impose a general draconian confinement to the population of Wuhan, the first area from which virus spread, which aimed to limit the rapid incidence of death due to ARDS. In addition, because of overflowing of ICU beds by a dramatic raise of infected individuals, they built a modern, well-equipped new hospital within ten days.

All observers also soon agreed that the economic consequences of this new health crisis were going to be more devastating than the medical issues caused by the virus. These events came only a few months before an economic cold war between the United States and China, which the thoughtless remarks of the American president amplified. Thus, the most egregious rumors alleged that SARS-Cov2 could possibly be a production of American laboratories bringing the world into the new era of biological warfare with the economic consequences to world markets. However, considering that the planetary ramifications of the industrial world and its economic fabric, the rumor made more informed observers skeptical, and should lead us all to see the rumor as "Fake News." Surprisingly, the incredibly high number of exchanges of these rumors through social networkers suggests that the scenario has won over more than one of us.

Rapidly spreading viruses, such as SARS-Cov, SARS-Cov2 and MERS viruses are RNA viruses possessing, a short single-stranded gene material. This is for encoding more than a dozen proteins, including those that have to facilitate attachment of the virus to host cells, the penetration of the virus into these cells, those ensuring the synthesis of RNA (RNA polymerase), and those intended to facilitate its exit from cells just few hours later after intra cellular viral replication. Contrasting with DNA polymerase (ensuring the synthesis of DNA in humans), RNA polymerase is not able to repair RNA replication errors, conferring a high rate of mutations into these viruses during the replication; this may average 1000 times more than with human DNA polymerase. All characteristics (rapid spreading, short multiplication time, high mutation rate) contribute to an extremely rapid viral evolution. For example, five years of viral evolution roughly corresponds to the lapse of time separating man from chimpanzee, his last common ancestor.

Recent Data from The Past Few Weeks Shed Light On This

Two teams of scientists involved in virus genetics have independently sequenced the SARS-Cov2 genome and compared it to that of SARS-Cov, MERS and several

other viruses of the same family isolated from bats. The first group [1] draws attention to a greater homology of the gene sequences between all the viruses of the COVID family they isolated in bats. More intriguing was the SARS-Cov2 virus appears to be structurally closer viruses in bats, which shares up to 92% homology with them than to the SARS or MERS virus presently known as the cause of two previous fatal respiratory epidemic diseases. The second tam [2] gives more structural details of the genome from COVID19 allowing us to better speculate on its origin. By structural gene analysis supported by biochemical verifications, they showed that genetic codes of COVID19 seem to be optimized for a better binding to the human ACE2 receptor, an enzyme involved in the regulation of blood pressure localized in pulmonary tissues. The SARS-CoV-2 spike protein has a functional polybasic cleavage site (furin) at the S1 - S2 border of the genome by the insertion of 12 nucleotides. These allow the protein acquiring oxygenated O-glycan residues around the binding site too. This constitutes a receptor binding domain (RBD) in the viral protein. Notably, this part of the viral protein raises from the most variable part of the corona virus genome.

Six residues of RBD are essential for the binding of the virus to its receptor, ACE2. While in SARS-CoV virus, these residues are Y442, L472, N479, D480, T487 and Y4911, the corresponding sites in COVID19 virus are L455, F486, Q493, S494, N501 and Y505, meaning five of these residues are genetically different between SARS-CoV-2 and SARS-CoV. Based on biochemical studies, COVID19 appears to have a high affinity RBD for ACE2 in humans, ferrets, cats, and other species that also have high structural homology to each other. Therefore, scientists believe that the RBD portion of theCOVID19's proteins has evolved to efficiently target ACE2 molecules located outside of human host cells.

The new virus's protein is so effective at binding to human cells that it could only result from a natural selection of a viral bat species and not resulting from a lab genetic engineering. Especially biology system analysts' outputs on the whole genome indicate that overall the RBD sequences of COVID19 are less close to those of SARS. Thus, according to the theory of plasticity, the natural selection of a new mutated virus by animal ACE2 (structurally close to human ACE2) amongst different viruses in bats should be acknowledged. This was exactly what we knew from SARS and MERS as new viral variants capable of optimizing the binding virus-receptor. This is solid evidence that COVID19 did not result from deliberate manipulation of man, but results from his lack of care of the environment. If someone had to design a new coronavirus as a pathogen, they would have to build it from already known virulent viruses (SARS and MERS), which are already potentially fatal and not from bat or pangolin viruses whose severity is not guaranteed. Intentional manipulation would have combined both the greatest structural gene homology and highest affinity due to binding sites.

Alert launch in 2017

Three years ago, researchers who studied the genetic structure of bat viruses [3–4] revealed that all pieces of a great pandemic human disease were gathered from a cave from a village in China. They observed during five years bats, isolated viruses and analyzed genes and proteins. On one hand, they showed respectively that natural selection of viruses by the host bats occurred continuously with accumulated rates of mutations in their RNA codes in accordance with the neo-Darwinian theory of biological plasticity. Structural gene mutations from generation to generation were aimed at adapting viruses to the animal. On the other hand, the gene mutation at the level of at least one of the proteins of the viral membrane, namely the binding site with the membrane protein close to the structure of the human Angiotensin Converting Enzyme (ACE2) appeared intriguing. The authors indicated that the proximity of the cave to the human habitation by less than one kilometer would facilitate the passage of viruses from bats to humans, and if necessary via other animals. This scenario should cause worry about an accidental and rapid transmission of virus to humans.

Conclusion

Although we have now evidence that new COVID19 virus is not a product of gene manipulation in Lab, we should be more worried about more catastrophic pandemics in the future due to the lack of attention of man to its environment.

References

1. Chan JF, Kok KH, Zhu Z, Chu H, To KK, et al. (2020) Genomic characterization of the 2019 novel human-pathogenic coronavirus isolated from a patient with atypical pneumonia after visiting Wuhan. *Emerg Microbes Infect* 9: 221–236. [View]
2. Andersen KG, Rambaut A, Ian Lipkin W, Holmes EC, Garry RF (2020) The proximal origin of SARS-CoV-2. Correspondence in Nature 17 March 2020. [View]
3. Mendenhall IH, Mendenhall IH, Wen DLH, Jayakumar J, Gunalan V, Wang L, et al (2019) Diversity and evolution of viral pathogen community in cave nectar Bats. *Viruses* 11: 250. [View]
4. Hu B, Zeng L-P, Yang X-L, Ge X-Y, Zhang W, Li B, et al. (2017) Discovery of a rich gene pool of bat SARS-related coronaviruses provides new insights into the origin of SARS coronavirus. *PLoS Pathog* 13: e1006698. [View]

***Corresponding author:** Prof. Par Iradj Sobhani, Dir. of the EC2M3 (Early detection of colonic cancer by using molecular and microbial markers) research Lab at the University of Paris Est Créteil-UPEC and head of the Department of Gastroenterology and Endoscopy;

Email: iradj.sobhani@aphp.fr