

COVID-19: Scenarios of Lethal Advanced Version of its Class

Vanya Bawa*

ABSTRACT

The viral disease named COVID-19 caused by family coronavirus is one of the biggest outbreaks reported on December 31, 2019, when China reported to the World Health Organisation (WHO) of a cluster of cases of pneumonia and lungs related ailments due to some unknown causative agent in Wuhan City in Hubei Province. The panic grew more when the disease spread recorded in Provinces of China, and now the problem has engulfed all the developed and developing nations of the world. The WHO has now declared it a major pandemic. Origin of virus and its evolutionary history can solve the mystery of this international pandemic outbreak. In the present review, various scenarios are discussed in reference to its origin and its rate of reproducibility in the mammals.

Keywords: ACEII, COVID, Disease, Pandemic.

Asian Pac. J. Health Sci., (2020); DOI: 10.21276/apjhs.2020.7.2.9

INTRODUCTION

The outbreak of COVID-19 (Coronavirus Disease 2019) has brought the world to a stalemate, exposing our vulnerability to these invisible enemies and has invariably affected the whole world's economy, in a way that for the first time, price of an oil barrel dropped below US \$0 recently. Posing a great threat to human lives, the disease has now engulfed most of the developed nations, with USA being the most badly hit country both in terms of positive cases and deaths. Unfortunately, India hasn't been untouched by this lethal disease and is taking all possible health measures amidst a 40-day long national lockdown to avoid the benchmarks of mortality established by other countries like Italy, Spain, China, France, UK, and USA. According to reports, aged people and those with a weaker immune system are more prone to this disease and do certainly qualify as easy prey to COVID-19. To date, a range of quick tools and techniques have been discovered and implemented for rapid detection of viral disease by numerous established labs. Still, the way to find an effective cure for this deadly disease looks uncertain in the near future. The genome size of this coronavirus and complexity of its origin has added difficulty in designing its accurate drug. The recently published news and articles claimed that it was genetically engineered by a well-established laboratory, but the variability in genetic makeup and relevance to its evolution points to the evidence of it being a modified version of coronavirus family with high affinity towards mammalian cells. Few scenarios related to its origin, transmission and binding to immune system probabilities have been discussed subsequently.

The structure and conformational pattern of coronavirus-2 exhibits its complexity and raises concerns of researchers towards its zoonotic nature. To extract facts, available online platforms were accessed using various keywords viz. SARS, coronavirus, COVID-19, etc. and numerous reviews related to the spreading of disease and its historical trends were collected. The data collected suggests its adaptability against humans.^[1,2] Also, the evolutionary pattern of its origin displays a variety of facts about the novelty of this virus. Moreover, most of the research carried out pertains to case studies of different COVID-19 patients in affected countries.

Falling in the criteria of life-threatening viral diseases and gaining much importance due to its higher rate of transferability has made it a great matter of concern for humankind. Today, every researcher is aware of the fact that coronavirus-2 has evolved as a better version

Chandigarh University, Gharuan, Punjab, India

Corresponding Author: Vanya Bawa, Chandigarh University, Gharuan, Punjab, India, Email: vanya.e8573@cumail.in

How to cite this article: Bawa V. COVID-19: Scenarios of Lethal Advanced Version of its Class. *Asian Pac. J. Health Sci.*, 2020; 7(2):36-37

Source of support: Nil

Conflict of interest: None

Received: 02/05/2020 **Revised:** 20/05/2020 **Accepted:** 26/05/2020

of its family with a higher transferability rate among humans. The statement can be justified as the susceptibility of human exposure to disease depends upon the basic transferability and incubation period of disease-causing agents, which is a virus possessing RNA as genetic material. In concurrence of that the central concept of disease epidemiology ponders around the reproduction number of COVID-19, which indicates the risk of an infectious agent with regards to its spread. Various mathematically derived estimates were used to find out the basic reproduction number, which falls within the range produced by the statistical and stochastic estimates denoted as R_0 (R-naught). Here, R_0 is an indication of the transmissibility of a virus, representing the average number of new infections generated by an infectious person, who can be asymptomatic (if showing symptoms) or silent spreader (if not showing symptoms but serving as a carrier and spreader of a virus) in a totally native population. For $R_0 > 1$, the number infected is likely to increase, and for $R_0 < 1$, the transmission is likely to die out.^[3] As per reports, the range of R_0 value for severe acute respiratory syndrome (SARS) was between 2 and 5, which is similar to the range of the mean R_0 for COVID-19. As the region of exposure was same for both the viral diseases, having similar R_0 values, despite the heightened public awareness with impactful, impressive and strong interventional control measures, COVID-19 has already been more widespread than SARS till date and has taken over one lakh lives so far, indicating it may be more transmissible and dangerous.^[4] Based on these considerations, R_0 for COVID-19 is expected to be more than 2–3. The justification of the statement lies with the study revealed by doctors, as a patient with no symptoms became the carrier and spreader of disease to its family in China. The reports claimed that a familial cluster in Anyang, China tested COVID-19 positive after interacting with one of their family members, an asymptomatic carrier who came back from Wuhan. These facts and sequence of events further exacerbate the fact that

the coronavirus 2 was transmitted by that particular asymptomatic carrier to its family.^[5]

As far as the theories are concerned, various scenarios can be concluded by following the online published researches. Many studies showed collinearity of COVID-19 to the other outbreaks, such as Middle East Respiratory Syndrome (MERS), believed to be developed from camels and SARS (Severe Acute Respiratory Syndrome), which claimed to be sharing the genome origin from cat-like civets.^[6] Whereas, the genomic data of the coronavirus 2 responsible for COVID-19 confirms that the characteristic feature of its spike-like protein structure consists of some unique adaptations for disease cause. One of these adaptations provides special ability to this coronavirus to bind onto a specific protein on human cells called *angiotensin-converting enzyme (ACE-2)*.^[7] The same can be cited as the first scenario of coronavirus-2. The scientists and researchers claimed that coronavirus is evolved and mutated to bind to diverse systems of organisms believed to be originated from bats or pangolins. The spike proteins of COVID-19 mutated to bind to molecules, similar in the structure of the human ACE2 protein, lead to the distribution of infection in human cells. A related coronavirus that causes SARS in humans also seeks out ACE2, supporting their common binding pattern to the ACE2.

But on the other hand, existing computer models predicted that the new coronavirus would not bind to ACE2 like the SARS virus and has a better binding pattern than any other virus of its family. This is due to the pattern of natural selection on ACE2 enzyme that enables the virus to take advantage of a previously unidentified alternate binding site present, thereby infecting the human body dangerously. Conclusion, as suggested by the researchers, was that the above mentioned could be strong evidence that this virus is not a result of purposeful lab manipulation. To further establish this fact, the bioinformatic prediction tool suggests that evidence for an alternate binding site with the present conformation of spike protein can never be chosen by any bioengineer.

The second scenario is that the coronavirus 2 transmitted from animals to humans before it became capable of causing human disease. Its pattern of infection and similarity to other viral species shows that it has resulted from gradual evolutionary changes over decades by natural means of genetic engineering or mutation and thus, gained the ability to spread from human-to-human and cause serious, often life-threatening situations.

In the third scenario, its transmission from human to animal was reported in New York, wherein felines showed COVID-19 like symptoms after getting the infection from their human caretakers, showing that it has the reverse of zoonotic mode as well. This case suggests that the adaptability of this virus is not limited to humans only, and other animal species may also be a threat in time to come. Its fast reproduction and efficiency towards the diverse fauna on earth highlight that this matter is of deep concern as no firm medication has been reported so far.

In such difficult times research is and should always be incessant and in the right direction. The importance of next-generation

sequencing using integrated approaches is the only tool to accelerate disease detection protocols and drug designing. Certain researchers claim that using CRISPR technology is more useful in detection and cure. Cas13 based tools for transcript tiling and permutation screening in mammalian cells have also been claimed to be useful for the detection of COVID-19. The study reported that there is an identification of information for more than 24,000 RNA-targeting guides, and the use of an optimized Cas13 screening system to target non-coding RNAs will be useful like the technology generated in the USA.^[8] This can greatly expand the CRISPR toolbox for forwarding genetic and transcriptomics screens.

Whereas, recent progress in research has also claimed that the nutritional status of each infected patient is a matter of concern and should be evaluated before the administration of general treatments. In addition, convalescent plasma which has now opened the doors as a therapy for this COVID -19 can be given to patients post deliberate tests.^[3]

The keynote should be underlined for the layman as addressed by Dr. Tedros Adhanom Ghebreyesus, the director general of the WHO "Pandemic is not a word to use lightly or carelessly", hence, until the efforts are under process, there is an urge to repel this disease which can be achieved by observing good hygiene and sanitation, practicing frequent social distancing, cooperating with law makers and most importantly encouraging and supporting the efforts of dedicated health-care professionals and researchers who are working endlessly and tirelessly against the pandemic for well-being of humankind.

REFERENCES

1. Chen N, Zhou M, Dong X, Qu J, Gong F, Han Y, Qiu Y, Wang J, Liu Y, Wei Y, Yu T. Epidemiological and clinical characteristics of 99 cases of 2019 novel coronavirus pneumonia in Wuhan, China: a descriptive study. *The Lancet*. 2020 Feb 15;395(10223):507-513.
2. Ng MY, Lee EY, Yang J, Yang F, Li X, Wang H, Lui MM, Lo CS, Leung B, Khong PL, Hui CK. Imaging profile of the COVID-19 infection: radiologic findings and literature review. *Radiology: Cardiothoracic Imaging*. 2020 Feb 13;2(1):e200034.
3. Chen L, Xiong J, Bao L, Shi Y. Convalescent plasma as a potential therapy for COVID-19. *The Lancet Infectious Diseases*. 2020 Apr 1;20(4):398-400.
4. Liu Y, Gayle AA, Wilder-Smith A, Rocklöv J. The reproductive number of COVID-19 is higher compared to SARS coronavirus. *Journal of travel medicine*. 2020 Mar 13.
5. Bai Y, Yao L, Wei T, Tian F, Jin DY, Chen L, Wang M. Presumed asymptomatic carrier transmission of COVID-19. *Jama*. 2020 Apr 14;323(14):1406-1407.
6. Banerjee A, Baid K, Mossman K. Molecular Pathogenesis of Middle East Respiratory Syndrome (MERS) Coronavirus. *Current Clinical Microbiology Reports*. 2019 Sep 15;6(3):139-47.
7. Wu F, Zhao S, Yu B, Chen YM, Wang W, Song ZG, Hu Y, Tao ZW, Tian JH, Pei YY, Yuan ML. A new coronavirus associated with human respiratory disease in China. *Nature*. 2020 Mar;579(7798):265-269.
8. COX, DBT, PYZOCHA, N. and Zhang, F., Novel cas13b orthologues crispr enzymes and systems. *Cell Reports*. 2019;26(13):3741-3751