

Coming Out of Nowhere: The Paradox of the Birth of Omicron

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The explosive rise of Omicron variant is a strong warning sign. Some scientists believe that we can never solve the mysteries regarding the origin of COVID-19. Given this consideration, there are still very important unanswered questions about when, where and how the COVID-19 pandemic started [1]. A report published recently in Nature [2] states that “Omicron is so different from earlier variants, such as Alpha and Delta, that evolutionary virologists estimate its closest-known genetic ancestor probably dates back to more than a year ago, sometime after mid-2020 ([3]). It just came out of nowhere”. It has been estimated that over the same time period, Omicron can infect 3-6 times as many people as Delta [4].

Scientists believe that SARS-CoV-2 will continue to spread in the human population. Oberemok et al. stated that “Taking into consideration the natural genetic mechanisms of mutations and recombination, it is impossible to imagine how to deprive a virus of the opportunity to generate new strains and time to time threaten our world with new pandemics” [5]. Our prediction shows that this problem can be much more life-threatening. The unjustified mass administration of non-robust vaccines and some ineffective anti COVID-19 treatments exert a significant selective pressure on SARS-CoV-2 [6]. So, selective pressure paves the road for mutations and accelerates the process of viral evolution [7]. Kupferschmidt in a report published in Science has recently addressed the risk of the selective pressure caused by the advent of vaccines or new therapies [8]. Key factors such as the host immune response, the total number of viral replications, and the rate of viral mutations determine the human-to-human transmission of the novel corona virus [9].

Regarding the paradox of the birth of Omicron the Nature [2] report also notes that “Scientists are investigating three theories:

- Although researchers have sequenced millions of SARS-CoV-2 genomes, they might simply have missed a series of mutations that eventually led to Omicron.

- The variant might have evolved mutations in one person, as part of a long-term infection.

- It could have emerged unseen in other animal hosts, such as mice or rats” [2].

We strongly believe that the second theory is strongly supported by the evidence. Given this consideration, although virus evolution can be triggered by receiving selective-pressure-exerting factors such as antivirals or immune-based therapies including convalescent plasma or monoclonal antibodies, prolonged infections in immunosuppressed patients (patients with organ transplants, HIV or cancer patients) can be the cause of viral evolution.

We have previously reported that besides the key factors of vaccine inequity and lack of Neanderthal genes that affect human susceptibility to

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COVID-19, as millions of people live with HIV in Africa, long COVID paves the road for the emergence of new SARS-CoV-2 variants [10]. Given this consideration, any failure to efficiently treat patients with HIV gives rise to the emergence of more new variants after Omicron. Thus, we strongly suggested using selective-pressure-free treatments (e.g. low dose radiotherapy [11-14]) for COVID-19 pneumonia in sub-Saharan Africa. Moreover, effective vaccination of people with HIV in this region along with using high-efficiency face masks (with at least antibacterial, water repellent and water absorbing layers) would be of paramount importance.

It is also possible for chunks of coronavirus genomes to shuffle and recombine wholesale, adds Kristian Andersen, an infectious-disease researcher at Scripps Research in La Jolla, California. And viruses can evolve faster when there is selection pressure, he says, because mutations are more likely to stick around if they give the virus an increased ability to propagate under certain environmental conditions.

Authors' Contribution

SAR. Mortazavi prepared the draft of the manuscript. N. Jooyan helped supervise the project and edited the manuscript. BF. Baha'addini Baigy Zarandi and N. Jooyan provided additional medical scientific edition. M. Faraz edited the manuscript and SMJ. Mortazavi presented the main conceptual ideas, supervised and edited the manuscript. All authors discussed the results and contributed to the final manuscript.

Conflict of Interest

None

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