



Possibilities for the Entrance of SARS-Cov-2 as an Archaeal Virus into the Ecosystem

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Dear Editor-in-Chief

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is a positive-sense single-strand RNA virus (+ssRNA) belongs to the genus Betacoronavirus, sub-family Coronavirinae, family Coronaviridae, and order Nidovirales (1, 2). This highly contagious virus, as the causative agent of coronavirus disease 2019 (COVID-19), has confronted the human beings with an unexpected phenomenon. The SARS-CoV-2 genome is very prone to mutations, some of which have strengthened its infectiousness (3). On the other side, notable stability of this virus in different circumstances (following over 15 months experience worldwide) has led to a global emergency situation. There are many ambiguities in the SARS-CoV-2 advent origin. Regarding the clearing the Earth of primitive creatures due to the ice age, meteor shower, and especially microbial pandemics, we anticipate that the SARS-CoV-2 may indirectly be associated with the defined phylogeny for Archaeal viruses, acting toward the clearing this planet of creatures (similar to what happened in the beginning of life).

The Archaeal viruses are mainly isolated from two types of habitats: extreme geothermal and hypersaline environments. Albeit, it has recently been found that they are able to inhabit disparate ones (4, 5). The majority of isolated Archaeal viruses

have DNA genome (4, 6). However, in the year 2012, some positive-sense RNA viruses were identified in high-temperature acidic hot springs in Yellowstone for the first time using metagenomics analysis, which were able to infect hyperthermophilic Archaea (6). Based on the homology of RNA-dependent RNA polymerases (RdRps) and capsid proteins, these researchers declared that they may be the ancestors of viruses infecting Eukarya (6). The Archaeal viruses have survived since the beginning of life and probably caused infections in diverse conditions (7).

On this basis, we assumed that the SARS-CoV-2 might be an Archaeal virus, preserved for a long time and accidentally entered the human ecosystem. First of all, given that the Archaeal viruses are halophile, and also due to the primary transmission manner of the SARS-CoV-2 infection (from cave bats to the human in Wuhan, China) and appropriate halogen conditions of the caves, we predicted that there may be the Archaeal viruses-infected cadavers of primitive creatures or Archaea in the depth of the caves (without UV irradiation) and protected these viruses for a long time. In the next step, infection of the cave bats and consequently human have occurred.

According to the evidence, there is a tendency for hunting and eating of these animals in the East



Asian countries, especially in China. There is also this possibility that visiting researchers or tourists have accidentally contacted with the infected bats, followed by the virus spread. Our second assumption was based on the Earth climate changes, resulting in ice melting. It is feasible that the SARS-CoV-2 (as a probable Archaeal virus) has remained in inactive form among the polar ice, and the human infection happened following the global warming, ice melting, and integration of the contaminated water with the seawater. Particularly that the seafood consumption (mostly in raw or half-cooked forms) is rampant between the East Asian people. What should be noted and can intensify the accuracy of our assumptions to some extent is the resemblance between the human immunodeficiency virus-1 (HIV-1) and the both considered viral groups (the Archaeal viruses and SARS-CoV-2). Open reading frame 157 (ORF157) of acidianus filamentous virus 1 (AFV1) possesses a distant structural homology with the α/β two-layer sandwich fold, identified in the HIV-1 integrase enzyme (5). On the other hand, several similarities have been observed between the HIV-1 and SARS-CoVs, especially the SARS-CoV-2. For instance, shielding the receptor binding sites by glycans has been observed in the S protein of SARS-CoV-1, -2, and Env protein of HIV-1 (8). Moreover, several analogous motifs have been reported in S2 subunit of SARS-CoVs and glycoprotein 41 (gp41) of HIV-1 (9, 10). Other similarities of the HIV-1 and SARS-CoV-2 are: having animal reservoirs, provocation of high levels production of pro-inflammatory cytokines, modification of enteric microbiota, and neutrophil extracellular traps (NETs) or NETosis (1).

Considering the above-mentioned content, we predicted that the SARS-CoV-2 may be a new Archaeal virus and carrying out the extensive evaluations using the bioinformatics, metagenomics, and experimental methods can elevate our knowledge in this field. Particularly, the clustered regularly interspaced short palindromic repeats (CRISPR) system, found in ~90% of sequenced Archaeal genomes (6), can be used to link the SARS-CoV-2 genome sequence to presumptive Archaeal hosts.

Conflict of interest

The authors declare that there is no conflict of interest.

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