

Scientists uncover ancient coronavirus epidemic in East Asia

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In a stunning breakthrough that has considerable implications for the current day, scientists have shown that a coronavirus epidemic ravaged East Asia 25,000 years ago. The study published in *Current Biology* in June was titled, “An ancient viral epidemic involving host coronavirus interacting genes more than 20,000 years ago in East Asia.”

The research team was led by Yassine Souilmi, of the University of Adelaide Australian Centre of Ancient DNA, along with scientists based in the United States. The study highlights that a coronavirus similar to the SARS-CoV-2 currently ravaging the world, with 191 million people infected and claiming over 4.1 million lives, afflicted humanity many millennia ago.

The researchers found strong suggestion that 42 coronavirus interacting proteins (CoV-VIPs) in East Asian populations interacted with an ancient coronavirus about 900 generations ago—that is, approximately 25,000 years ago. This pattern was unique in East Asian populations.

The scientists estimated the ancient epidemic lasted until 5,000 years ago. They determined the timeline by looking at the number of mutations in a gene. Mutations occur at a regular rate so they can be used to determine a timeframe.

The coronavirus is a messenger RNA virus that attacks the lungs. Its spherical structure is surrounded by numerous protein spikes that enable the virus to attach itself to human cells. Coronaviruses are unique in that they reproduce by invading a host cell and hijacking its genetic structure in order to make more virus. The virus infection is known to leave telltale signs in an organism’s genetic structure.

The scientists examined thousands of genomes in the 1000 Genomes Project database across 26 populations around the world for signs that a coronavirus had infected humans in the past. The 1000 Genomes Project,

established in 2008, is a comprehensive international database of human genetic variations. The study found evidence that a previously unknown ancient coronavirus infected people in China, Japan and Vietnam.

“There have always been viruses infecting human populations,” said David Enard of the University of Arizona Department of Ecology and Evolutionary Biology, a collaborating scientist in the study. “Viruses are really one of the main drivers of natural selection in human genomes.”

Scientists examined several hundred genes that are known to interact with coronavirus. They identified five groups of people who had 42 genes with mutations that suggested interaction with coronavirus. The modified genes may have given some sort of protection from the virus.

“So what happens over several generations is the gene variants that are beneficial will rise in frequency, and that leaves a very distinctive mark several generations later,” Souilmi told the Australian Broadcasting Corporation (ABC).

Scientists think it takes 500 to 1,000 years for these modifications to emerge as a shared trait in the genome.

Souilmi and his team examined virus interacting proteins (VIPs), proteins that are known to interact with viral proteins, viral RNA and/or viral DNA. They targeted 420 VIPs that are known to interact with coronaviruses (CoV-VIPS).

According to the study, “throughout the evolutionary history of our species, positive natural selection has frequently targeted proteins that physically interact with viruses...”

The VIPs are important, as they are the central mechanism the virus uses to attack the host cell.

“Our focus on VIPs is motivated by evidence indicating that these protein interactions are the central mechanism that viruses use to hijack the host cellular machinery. ...

Accordingly, VIPs are much more likely to have functional impacts on viruses than other proteins,” the study stated.

“We really can’t tell if this was a periodic thing that occurred every winter like the flu, or slightly different viruses that jumped from animals to humans every five to 10 years like what happened in the past 20 years with SARS, MERS, and SARS-CoV-2. ... The adaptation of several genes around the same time and at the same rate can only be explained by the exposure to coronaviruses back in time,” Souilmi said.

Some scientists have expressed differences over the estimation of the timing of the epidemic. Aida Andres, an evolutionary geneticist at University College London, who was not involved in the research, commented: “The timing is a complicated thing. ... Whether that happened a few thousand years before or after—I personally think it’s something that we cannot be as confident of.”

The research is part of the deepening understanding of the evolutionary history of coronavirus. Although the scientists are not able to identify the actual viruses and only found an indirect expression of the impact of the viruses on the human genetic structure, their research still indicates the existence of ancient viruses.

An important study titled, “A Case for the Ancient Origin of Coronaviruses,” published in the *Journal of Virology* in 2013, discusses the evolution of coronavirus. The virus exists in four basic groups termed alpha, beta, delta and gamma coronaviruses. The alpha and beta groups are known to infect mammals while the others infect birds.

The research team led by Joel O. Wertheim of the Department of Pathology at the University of California, San Diego, found evidence of “thousands or millions of years of evolution in the coronavirus phylogeny.”

Wertheim speculates that coronaviruses have been infecting birds and bats possibly since their evolutionary divergence in the carboniferous period over 300 million years ago.

The discovery that a coronavirus outbreak lasted for approximately 20,000 years has very important implications for the current pandemic. Modern science has enabled humanity to understand viruses and intervene to predict and control any pandemic, but this scientific knowledge has been ignored by the political elite as they impose a herd immunity program that has allowed the virus to proliferate almost unhindered. Scientific knowledge has been shunted aside as governments act to defend the profit interests of the major corporations.

“It should make us worry ... What is going on right now might be going on for generations and generations,” Enard told the *New York Times* .

One of the starkest aspects of the pandemic is the disproportionate impact on the poorest layers of society, who have been systematically exposed to the virus, while wealthy people can easily isolate themselves.

The study identifies that the “research on SARS-CoV-2 epidemiology has revealed [that] socioeconomic (e.g., access to health care, testing, and exposure at work), demographic, and personal health factors all play a major role in SARS-CoV-2 epidemiology.”

Although Souilmi and his team do not comment on the current controversy that the current pandemic was the result of a deliberate or accidental leaking of the virus that causes COVID-19 from the Wuhan Institute of Virology, their research indicates the ancient lineage of cross infections from bats to humans that have occurred on numerous occasions in the past and present the most likely origin of the current pandemic.

The Wuhan laboratory hoax was originally proposed by extreme right-wing supporters of the Trump administration and has been resurrected by President Joe Biden in order to divert from the government’s disastrous response to the coronavirus in the US and to promote Washington’s geostrategic aims against China.

An important aspect of the study is that it indicates the areas for future investigation in how to treat coronavirus infections, targeting the 42 genes that evolved in response to the ancient epidemic.

“It’s actually pointing us to molecular knobs to adjust the immune response to the virus,” Souilmi said.



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