

OUR COVID-19 CONNECTION WITH PRIMITIVE CAVEMEN

Relevant for: Developmental Issues | Topic: Health & Sanitation and related issues

Hosting a virus: Understanding the host genome is paramount to studying both susceptibility and protection against the virus in a given population. | Photo Credit: [Gilnature](#)

Viruses can only survive and multiply in host cells. Therefore, studying SARS-CoV-2 virus will require studying the host. As the viral genome takes the help of host machinery, understanding the host genome is paramount to studying both susceptibility and protection against the virus in a given population. This is the main aim of multiple groups and international consortia of researchers like the Severe Covid-19 genome-wide association study Group, the COVID-19 Host Genetics Initiative, and the Genetics of Mortality in Critical Care (GenOMICC).

A series of published studies from these consortia shed light on the host genome's role in viral infection. These studies, published in *NEJM*, *Nature* and *MedRxiv* provide cues on how certain host genome regions confer an increased risk of developing the severe disease while others protect against the virus. Thus, studying the genomes of individuals in a group (for example, a particular genetic population group in India) can make us predict whether the individuals in that group are more or less likely to develop severe disease.

The recent papers pointed out that a region on host chromosome 3 acts as a significant genetic risk factor towards getting seriously ill and, at the same time, a group of genes on chromosomes 6, 12, 19, and 21 protect us against the virus. Enzymes coded by the OAS gene family on chromosome 12, a component of the interferon-induced antiviral system, are of particular importance as they can act as a drug target against the virus. An independent study from Canada in *Nature Medicine* corroborated this by showing that a protein from the same component in blood protects against getting severely ill among European ancestry people.

Interestingly, evolutionary biologists in Sweden and Germany showed that the regions of host genomes that increase the risk of getting severely ill and protect against the virus were inherited from Neanderthals. How can Neanderthal genes both increase the risk of getting the severe disease and at the same time protect against the virus?

Once, Neanderthals and modern humans came in contact with each other, and they interbred. As a result, genetic content between Neanderthals and humans got mixed in their offspring.

In their first paper, published in *Nature*, the researchers showed that modern-day humans share a stretch of 50,000 nucleotides (nucleotides are the basic building blocks of DNA) in chromosome 3 with Neanderthals. It is this stretch that increases their risk of getting severe COVID-19. They predicted that having a copy of this region of chromosome 3 nearly doubles the risk of getting severe COVID-19.

The same researchers published a second paper in *PNAS* showing that a part of host chromosome 12, previously shown to protect against the virus, also was inherited from Neanderthal genomes. While specific genes from Neanderthals are working against the virus and protecting us from getting a severe disease, others are associated with an increased risk of getting critically ill. This push and pull effect may be one of the intriguing facts about how the selection of genes happens during evolution.

These studies have special significance to India. About 50% of South Asians carry the region in chromosome 3 from Neanderthal genomes, the same region that make us more prone to getting severely sick with the virus. On the good Neanderthal gene front, nearly 30% of South Asians bear the chromosome 12 region that protects us from getting severely ill. As Indians are a diverse genetic group, the above risk was determined using samples used previously in an international consortium called the 1,000 genome project. The project is represented by Indian Gujaratis and Telugus, Pakistani Punjabis, and Bangladeshi Bengalis in the South Asian group. These recent studies only validate what the legendary evolutionary biologist Theodosius Dobzhansky wrote in his famous essay, "nothing in biology makes sense except in the light of evolution," and makes perfect sense when one thinks about the evolution of host genomes concerning SARS-CoV-2 infection.

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