

Scientists uncover history of ancient viruses as far back as 30 million years ago

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Researchers from Boston College, US, have revealed the global spread of an ancient group of retroviruses that affected about 28 of 50 modern mammals' ancestors some 15 to 30 million years ago.

Retroviruses are abundant in nature and include human immunodeficiency [viruses](#) (HIV-1 and -2) and human T-cell leukemia viruses. The scientists' findings on a specific group of these viruses called ERV-Fc, to be published in the journal *eLife*, show that they affected a wide range of hosts, including species as diverse as carnivores, rodents, and primates.

The distribution of ERV-Fc among these ancient mammals suggests the viruses spread to every continent except Antarctica and Australia, and that they jumped from one species to another more than 20 times.

The study also places the origins of ERV-Fc at least as far back as the beginning of the Oligocene epoch, a period of dramatic global change marked partly by climatic cooling that led to the Ice Ages. Vast expanses of grasslands emerged around this time, along with large mammals as the world's predominate fauna.

"Viruses have been with us for billions of years, and exist everywhere that life is found. They therefore have a significant impact on the ecology and evolution of all organisms, from bacteria to humans," says co-author Welkin Johnson, Professor of Biology at Boston College where his team carried out the research.

"Unfortunately, viruses do not leave fossils behind, meaning we know very little about how they originate and evolve. Over the course of millions of years, however, viral genetic sequences accumulate in the DNA genomes of living organisms, including humans, and can serve as molecular 'fossils' for exploring the natural history of viruses and their hosts."

Using such "fossil" remnants, the team sought to uncover the natural history of ERV-Fc. They were especially curious to know where and when these pathogens were found in the ancient world, which species they infected, and how they adapted to their mammalian hosts.

To do this, they first performed an exhaustive search of mammalian genome sequence databases for ERV-Fc loci and then compared the recovered sequences. For each genome with sufficient ERV-Fc sequence, they reconstructed the sequences of proteins representing the virus that colonized the ancestors of that particular species. These sequences were then used to infer the [natural history](#) and evolutionary relationships of ERV-Fc-related viruses.

The studies also allowed the team to pinpoint patterns of evolutionary change in the genes of these viruses, reflecting their adaptation to different kinds of mammalian hosts.

Perhaps most interestingly, the researchers found that these viruses often exchanged genes with each other and with other viruses, suggesting that genetic recombination played a significant role in their evolutionary success.

"Mammalian genomes contain hundreds of thousands of ancient viral fossils similar to ERV-Fc," says lead author William E. Diehl from the University of Massachusetts, who conducted the study while a post-doctoral researcher at Boston College.

"The challenge will now be to use ancient viral sequences for looking back in time, which may prove insightful for predicting the long-term consequences of newly emerging viral infections. For example, we could potentially assess the impact of HIV on human health 30 million years from now. The method will allow us to better understand when and why new viruses emerge and how long-term contact with them impacts the evolution of host organisms."

More information: William E Diehl et al. Tracking interspecies transmission and long-term evolution of an ancient retrovirus using the genomes of modern mammals, *eLife* (2016). [DOI: 10.7554/eLife.12704](https://doi.org/10.7554/eLife.12704)

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