

Paleovirology expanded: Non-retroviral virus fragments found in animal genomes

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Understanding the evolution of life-threatening viruses like influenza, Ebola and dengue fever, could help us to minimize their impact. New research points the way to a fossil record of viruses that have insinuated themselves into the genomes of insects and other animals, providing clues about their evolutionary history.

The findings, published online on November 18 in the open-access journal [PLOS Genetics](#), could enable scientists to elucidate general principles in virus evolution from their genetic "fossils", which in turn could inform approaches for controlling disease.

Robert Gifford (Rockefeller University), and colleague Aris Katzourakis (Oxford University) used the rapidly advancing technology for [genetic screening](#) to analyze a database of insect, bird and mammal DNA for fragments of virus genomes, which they named endogenous viral elements (EVEs). The pair discovered representatives of ten families of viruses, including [hepatitis B](#), Ebola, rabies, and dengue and yellow fevers integrated into the genomes studied.

"In some cases, we've got the first evidence of an ancient origin for some of these virus groups", said Gifford. While scientists have been aware of genetic signatures for retroviruses in animal genomes since the 1970s, much remains to be learned about these newly-discovered EVEs from non-retroviral viruses, including exactly how these virus fragments find their way into nuclear DNA.

Most of the fragments documented by Gifford are no longer functional, appearing like what is commonly referred to as "junk DNA." However, the findings suggest that some of these virus fragments may have been co-opted by their hosts at some point in their [evolutionary history](#), perhaps as a defense against related infections. In particular, Gifford says that finding EVEs in insect genomes promises to reveal a new dimension in paleovirology, allowing scientists to probe the relationship and evolution of the virus, its vector and its host, potentially providing insight into the complex ecological relationships that underpin insect-borne diseases.

More information: Katzourakis A, Gifford RJ (2010) Endogenous Viral Elements in Animal Genomes. PLoS Genet 6(11): e1001191. [doi:10.1371/journal.pgen.1001191](https://doi.org/10.1371/journal.pgen.1001191)

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