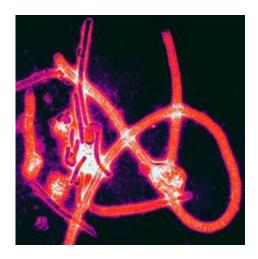


## All viruses 'can be DNA stowaways'

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Relatives of Ebola are among the 'fossil viruses' researchers have identified. Image: Thomas W Geisbert

(PhysOrg.com) -- 'Fossil viruses' preserved inside the DNA of mammals and insects suggest that all viruses, including relatives of HIV and Ebola, could potentially be 'stowaways' transmitted from generation to generation for millions of years, according to new research.

A team from Oxford University and the Aaron Diamond AIDS Research Center built on earlier work at Oxford that discovered the fossilised remains of an ancient HIV-like virus in the genomes of animals including sloths, lemurs and rabbits.

The team's new research, reported in this week's *PLoS Genetics*, shows that many more different types of viruses are endogenous – capable of



being transmitted from generation to generation – with 'fossil viruses' turning up in the genomes of creatures as different as mosquitoes, wallabies, and humans.

'Many of these viruses, such as the ancestors of <u>Ebola</u>, are far more ancient and spread across many more animal groups than anyone ever suspected,' said Dr Aris Katzourakis of Oxford University's Department of Zoology, an author of the report. 'We've demonstrated that viruses have been integrating within animal genomes for at least 100 million years.'

'We've also shown that, in some cases, viral genes have been domesticated by their hosts, and put to use by the hosts for their own purposes, demonstrating that captured viral sequences may have played a larger than expected role in animal evolution.'

Understanding the historical conflict between viruses and animal immune systems could lead to new approaches to combating existing viruses such as <u>HIV</u> and Ebola. It could also help scientists to decide which viruses that cross species are likely to cause dangerous pandemics in the future.

'These viruses represent the tip of the iceberg of endogenous viral diversity,' said Dr Katzourakis. 'We have discovered a large and diverse set of virus sequences preserved in animal genomes, which together include representatives of all known viral groups. This demonstrates a potential for endogenisation for any virus, and illustrates that viral fossil records may be uncovered for many elusive viral groups.'

## Provided by Oxford University

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