

Study reveals how ancient viruses became genomic 'superspreaders'

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Scientists have uncovered clues as to how our genomes became riddled with viruses. The study, supported by the Wellcome Trust, reveals important information about the so-called 'dark matter' of our genome.

For years scientists have been struggling with the enigma that more than 90 percent of every mammal's [genome](#) has no known function. A part of this 'dark matter' of genetic material is known to harbour pieces of DNA from ancient viruses that infected our ancestors going back as far as the age of the dinosaurs.

Researchers at Oxford University, the Aaron Diamond AIDS Research Center in New York and the Rega Institute in Belgium wanted to know how these ancient viruses got into their hosts' genomes in such abundance.

The team searched the genomes of 38 mammals covering a large range of species: from mouse, rat and bat to human, elephant and dolphin. Genetic material from all of the residing viruses was collected and then compared using mathematical models.

The findings revealed that one particular group of viruses had lost the ability to infect new cells. Their genetic material is still able to amplify itself but the whole lifecycle of the [virus](#) is passed within a single cell. This change, they found, was followed by a dramatic proliferation of the virus' [genetic material](#) within the genomes.

A comparison with all of the other viruses in the genomes revealed this to be a universal phenomenon, and that loss of cell infectivity is associated with a roughly 30-fold increase in the abundance of the virus.

The pattern resembles that which we see during epidemic outbreaks, whereby a small proportion of infected people are often responsible for most of the spread of an infectious agent to the rest of the population. They are described as 'superspreaders'.

According to the lead author, Dr Gkikas Magiorkinis from Oxford University's Zoology Department: "We know that much of the 'dark matter' in our genome plays by its own rules, in the same way as an epidemic in an infectious disease, but operating over millions of years."

Robert Belshaw from the same department, who led the study, goes on to explain: "We suspect that these viruses are forced to make a choice: either to keep their 'viral' essence and spread between animals and species, or to commit to one genome and then spread massively within it. This is the story of the epidemic within every animal's genome, a story which has been going on for 100 million years and which continues today."

The findings are published today in the journal [Proceedings of the National Academy of Sciences](#).

More information: G. Magiorkinis et al. Env-less endogenous retroviruses are genomic superspreaders. *Proceedings of the National Academy of Sciences*, 2012. [Epub ahead of print]

Provided by Wellcome Trust

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