

Could a newly discovered viral genome change what we thought we knew about virus evolution?

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A study published in BioMed Central's *Biology Direct* journal reports the existence of a previously undetected group of viruses and, more importantly, a new type of viral genome that could have huge implications for theories of viral emergence and evolution.

Viruses are the most abundant [organisms](#) on earth, yet little is known about their [evolutionary history](#) since they have exceptionally high rates of genetic mutation which are difficult to track. Viral metagenomics, however, is becoming an increasingly useful tool with which to glimpse [virus evolution](#), as it makes available vast amounts of new [sequence data](#) for analysis.

Kenneth M Stedman's team from Portland State University in Oregon, USA, used a metagenomics approach to investigate [virus](#) diversity in Boiling Springs Lake in Lassen Volcanic National Park, USA, an acidic, high temperature lake (ranging from 52-95°C, with a pH of ~2.5) that sustains a purely microbial ecosystem.

Astonishingly, they found a unique [viral genome](#) that has never before been reported - a circular, single-stranded DNA virus encoding a major capsid protein seen previously only in RNA viruses. This unusual genome provides proof that integration of an RNA virus into a DNA virus may have occurred between two unrelated virus groups at some point in evolution - something that has not been observed before.

Moreover, this suggests that entirely new virus types may emerge via recombination of functional and structural modules between vastly different viruses, using mechanisms that are as-yet unknown.

The team observed that the Boiling Springs Lake RNA-DNA hybrid virus (BSL RDHV) genome is circular, but its size is roughly double that of typical circoviruses, with the ORFs arranged in an uncommon orientation. They compared the BSL RDHV genome to other metagenomic DNA sequences from the Global Ocean Survey, and found strong evidence to conclude that previously undetected BSL RDHV-like viruses could be widespread in the marine environment and are likely to be found in other environments as well.

No mechanism has been proposed to account for the inferred instances of interviral RNA-DNA recombination, but the team speculate that a DNA circovirus-like progenitor may have acquired a capsid protein gene from a ssRNA virus via reverse transcription and recombination.

Lead author Kenneth M Stedman said, "As more viral metagenomic data are generated and analyzed, additional evidence of recombination between RNA and DNA virus groups will likely be discovered. The discovery that novel virus groups can emerge via recombination between highly disparate virus types will have broad implications for the early evolution of viruses and extends the modular theory of virus evolution to encompass a much broader range of possibilities than previously thought."

More information: A novel virus genome discovered in an extreme environment suggests recombination between unrelated groups of RNA and DNA viruses, Geoffrey S Diemer and Kenneth M Stedman, *Biology Direct* (in press)

Provided by BioMed Central

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