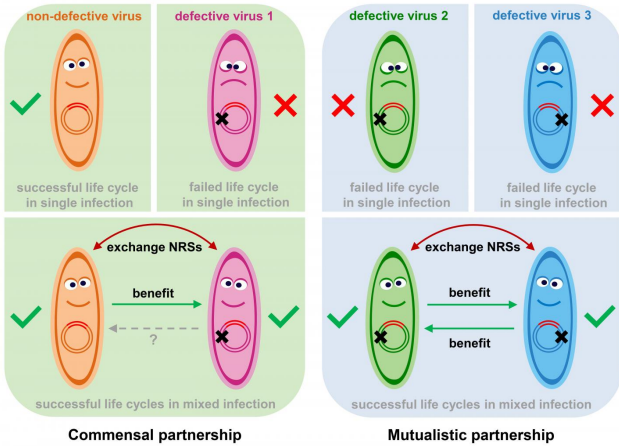


Genetic 'fossils' reveal long-term viral partnerships in grass

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pararetroviruses (PRVs), which don't integrate into host DNA as part of their normal life cycle, but may incidentally leave viral "fossil" in host genomes while retaining the ability to complete their life cycle."

The researchers sequenced and analyzed PRV fossils integrated into modern grass genomes and identified several different PRV species, three of which were found to be defective. These defective species lacked DNA that codes for proteins needed by PRVs to co-opt host cellular machinery and make new copies of the virus, completing the viral life cycle.

To complete the life cycles, defective pararetrovirus species have evolved to form partnerships which are maintained by frequent exchanges of their noncoding regulatory sequences (NRSs). Credit: Sunlu Chen & Yuji Kishima

Defective viruses incorporated into grass genomes may adapt to form partnerships with other genome-incorporated viruses in order to complete their life cycle, according to a new *PLOS Pathogens* study. The findings suggest that partner viruses evolve in concert, enabling them to maintain their relationship over time.

The genomes of animals, plants, and fungi contain stretches of DNA that originated in viruses, integrated into ancient host genomes after infection, and were passed down to host offspring. These viral "fossils" provide an opportunity to study interactions between viruses within host cells on an evolutionary scale.

To better understand viral interactions, Sunlu Chen and colleagues at Hokkaido University, Japan, focused on viral fossils passed down from ancient grasses in the Poaceae grass family. Specifically, they were interested in fossils of viruses known as

To investigate how defective PRVs might still be able to complete their life cycle, the scientists analyzed genetic relationships between the fossil PRV sequences. They found that one defective PRV species may have evolved to form a commensal relationship with a non-defective species, allowing it to use the non-defective protein machinery to complete its life cycle.

Evidence suggests that the other two defective PRVs may have developed a mutualistic partnership, with each species providing complementary protein machinery lacked by the other species.

The research team found that the two species in each partnership have frequently exchanged DNA stretches called noncoding regulatory sequences (NRSs) with each other over time. This concerted evolution has resulted in the partnered species sharing highly similar NRSs, and it appears to have enabled development and maintenance of the partnerships over time.

"Virus fossils in grass genomes revealed that defective pararetrovirus species were prosperous due to compensations of functional deficiencies by partnerships with intact viruses, or with complementary defective viruses."

More information: Chen S, Zheng H, Kishima Y (2017) Genomic fossils reveal adaptation of non-autonomous pararetroviruses driven by concerted evolution of noncoding regulatory sequences. PLoS Pathog 13(6): e1006413. [DOI: 10.1371/journal.ppat.1006413](https://doi.org/10.1371/journal.ppat.1006413)

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