

Editorial

Functionalities of recombinant virus

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A recombinant virus can develop naturally or be created using recombinant DNA technology to recombine bits of DNA. In most viruses, recombination is a common process that results in variety. It brings variants together that emerge separately within the same molecule, giving virus' new ways to adapt to novel surroundings, hosts and resist selective constraints. As a result, doctors, epidemiologists, molecular biologists, and evolutionary biologists are all interested in studying viral recombination. Viruses can have a wide range of genomic architectures. Although the majority of viruses have RNA genomes, several also have DNA genomes, and others may have both DNA and RNA genomes at different stages of their life cycle. When it comes to genome architecture, they can be single-stranded (or) double-stranded. Certain virus families have both single-stranded and double-stranded genomes. Viruses can modify their genetic makeup through a variety of processes, including point mutation and recombination. RNA viruses, on average, have smaller genomes than DNA viruses, owing to their greater mutation rates. When at least two viral genomes infect the same host cell and exchange genetic segments, recombination occurs. The structure of the cross over site distinguishes different types of viral recombination.

In viruses, recombination is a common occurrence that can have a significant impact on their evolution. Indeed, recombination has been linked to viral host range expansion, the formation of novel viruses, changes in transmission vector specificities, increases in virulence and pathogenicity, changes in tissue tropisms, evasion of host defence, and the evolution of antiviral resistance.

Herpes viruses and bacteriophages share a mechanistic model in which recombination and DNA replication are linked, implying an ancestral mechanism. In addition, all Herpes viruses share a common replicative complex with highly conserved replication and recombination proteins. Many of

these proteins can actually be swapped between various Herpesviruses. Recombination is also important in the repair of DNA damage in DNA viruses, especially during latency. However, contrary to previous findings, analysis of complete genomes of many Herpesviruses has revealed that the repair-initiating DNA sequences differ between and Herpesviruses, implying possible differences in recombination mechanisms between these two subfamilies.

The various groups of RNA viruses have highly diverse recombination rates. In general, SSRNA viruses have the lowest recombination rates, whereas SSRNA viruses have a lot of recombination. This overall pattern, however, has a few noteworthy deviations. Recombination is rare in flaviviruses, which are members of the SSRNA virus family, with rates 10 times greater than previously thought in natural populations.

In RNA viruses, recombinant genomes can be generated by two separate processes. Recombination practically occurs in all RNA viruses, whereas re-assortment occurs primarily in segmented RNA viruses. The latter is responsible for the development of a hybrid RNA sequence after intermolecular exchange of genetic information between two nucleotide sequences. HIV-1 is the most well-known paradigm for this situation. Recombination's extent and dispersion are hotly debated topics. The study of linkage disequilibrium can reveal a lot about how viral populations evolve. Phylogenetic and population genetic investigations, as mentioned in this review, may help us learn more about the interactions of recombination, migration, and natural selection. Understanding and interpreting data from genetic studies of viruses requires a thorough understanding of the principles of recombination in population genetics. Virus research is becoming more defined by vast amounts of genomic data, despite the fact that viral populations frequently develop through recombination. As a result, using population genetics models and advanced statistical analysis to account for recombination is expected to become a cornerstone in understanding viral genetic variation.

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