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A Brief Note on the Role of Endogenous Retroviruses in Animals

Alec Wade*

Department of Veterinary Science, Addis Ababa University, Bishoftu, Ethiopia

Editorial Note

Endogenous Retroviruses (ERVs) are viral sequences in the genome that are similar to retroviruses and can be produced from them. They're found mainly in the genomes of jawed vertebrates, and they make 5-8% of the human genome. ERVs are a form of vertically inherited proviral sequence and a subclass of a gene termed a transposon, which can be packaged and transported within the genome to play a key role in gene expression and regulation. ERVs, on the other hand, lack most transposon capabilities, are rarely infectious, and are usually faulty genomic legacy of retroviral replication.

They are known as germline provirus retroelements because they incorporate and opposite into the host cell's nuclear genome. Retroviruses are thought to have evolved from a form of transposon known as a retrotransposon, also known as a Class I element; these genes can mutate and become exogenous or pathogenic instead of transferring to another region in the genome. This suggests that while not all ERVs are the consequence of retrovirus insertion, some of them may have been the source of genetic information in the retroviruses they resembled.

A retrovirus's replication cycle begins with the insertion ("integration") of a DNA copy of the viral genome into the host cell's nuclear genome. The majority of retroviruses infect somatic cells, but they can also infect germline cells (cells that create eggs and sperm). Retroviral integration can happen in a germline cell that develops into a viable organism on rare instances. This organism will carry the inserted retroviral genome as an important part of its own genome, creating a "endogenous" retrovirus that can be acquired as a novel allele by its children. For millions of years, many ERVs have remained in their hosts' genes.

However, during host DNA replication, the most of these have acquired inactivating mutations and are no longer capable of producing the virus. Recombinational deletion in which recombination between identical sequences surrounding newly integrated retroviruses results in deletion of the internal, protein-coding sections of the viral genome, can also partially remove ERVs from the genome.

The retrovirus genome is divided into 3 genes that are essential for the invasion, replication, escape, and spreading of its viral genome. GAG (structural proteins for the viral core), pol, and env are the three genes involved. Polyproteins are used to encode these viral proteins. The retrovirus relies greatly on the host cell's machinery to complete its life cycle. Protease breaks it down the peptide bonds of viral polyproteins, allowing the individual proteins to function. Before entering the nucleus, reverse transcriptase combines viral DNA from viral RNA in the cytoplasm of the host cell. Integrase is a protein that helps viral DNA integrates into the host genome. Endogenous retroviruses have the ability to influence genomes. The majority of research in this area has concentrated on the genomes of humans and higher primates, but mice and sheep have also been extensively researched. Long terminal repeat (LTR) sequences surrounding ERV genomes commonly operate as alternate promoters and enhancers, resulting in tissue-specific variants that contribute to the transcriptome. However, retroviral proteins have been repurposed to perform different initiatives in the host, particularly in reproduction and development.

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***Address for Correspondence:** Dr. Alec Wade, Department of Veterinary Science, Addis Ababa University, Bishoftu, Ethiopia; Tel: 9657493661; E-mail: wadealec77@gmail.com*

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