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RESEARCH ARTICLE

When ERVs Go Solo: Making Sense of Polymorphic LTRs in Humans and Mice

By Donny Budinsky

Author's Note

This article continues my active research project on endogenous retroviruses (ERVs). In a previous post, I explained how polymorphic ERVs fit within a creation model. Here, we take the next step: what about the solo LTRs — the leftover fragments of ERVs that sometimes show function, yet aren't fixed in all humans?

The Puzzle of Solo LTRs

ERVs remain one of the most celebrated arguments for common ancestry. Critics often emphasize not just the fixed ERVs (present in all humans), but also the unfixed or "polymorphic" ones — those found in some individuals but not others. Within this discussion, solo LTRs (long terminal repeats) raise particularly interesting questions.

Here's what we know:

- In humans: most ERVs are fixed. Only a handful are polymorphic.

- In mice: the picture looks very different — hundreds of polymorphic ERVs are segregating across populations, some even contributing to immune system function.
- Solo LTRs: these are fragments left behind when recombination deletes most of an ERV. Many solo LTRs act as regulatory elements. Most functional ones studied are fixed, but intriguingly, a few unfixed solo LTRs in humans show population-specific effects on gene expression.

So the challenge is clear: if fixed ERVs are designed and functional, and unfixed ERVs are true viral insertions, how do we explain functional unfixed solo LTRs?

Two Creation-Based Explanations

1. Segregated Design Hypothesis

Some solo LTRs may have been created as regulatory sequences and were originally fixed in the human population. Over time — through post-Flood bottlenecks, recombination, or genetic drift — they became population-specific. Today they appear "unfixed," but in reality, they are remnants of original design.

2. Functional Co-option Hypothesis

Other solo LTRs may indeed be the result of viral recombination events after the Fall. Yet because their sequences resemble strong promoters or enhancers, the host genome can repurpose them for useful functions. Here, function does not imply evolutionary invention but reflects the built-in versatility of the genome to adapt and reuse available DNA.

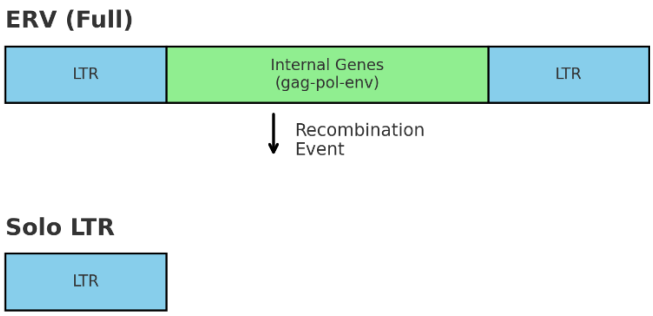

Figure 1: A full ERV consists of two LTRs flanking internal genes. When recombination removes the internal genes, only a "solo LTR" remains. These fragments can sometimes act as regulatory switches, which critics see as evidence of viral history — but within a creation model, they may reflect either segregated design or functional co-option.

Predictions of the Model

This framework makes clear, testable predictions:

- In humans: unfixed ERVs should rarely (if ever) be essential.
- In animals like mice: with rapid reproduction and large population sizes, more polymorphic ERVs are expected — some reaching high frequencies and being co-opted for functional roles.
- For viruses: tracing exogenous retroviruses back to their original hosts should show they were less harmful there, consistent with a design-based origin of retroelements.

Conclusion

Far from undermining the creation model, the case of solo LTRs actually strengthens it. By considering both **Segregated Design** and **Functional Co-option**, we can account for functional, population-specific solo LTRs without appealing to evolutionary storytelling. Instead, these findings highlight the foresight of a Creator who designed genomes with adaptability and resilience.

And this is just the beginning. In the next article, I'll dive deeper into the concept of **Segregated Design** — a powerful new way of understanding why some ERVs are fixed, some are unfixed, and how both fit into a creation model.

Additional Reading

Budinsky, D. (2025, September 7). *The future of ERV research: Predictions, models, and surprises*. Standing for Truth Ministries. **https://standingfortruthministries.com/the-future-of-erv-research-predictions-models-and-surprises/**

PDF Article

Budinsky, D. (2025). *Rethinking endogenous retroviruses*. Standing for Truth Ministries. https://standingfortruthministries.com/wp-content/uploads/2025/09/Rethinking-Endogenous-Retroviruses-by-Donny-Budinsky.pdf

Book (Black & White Edition)

Budinsky, D. (2022). *The endogenous retrovirus handbook: Dismantling the best evidence for common descent* (Black and white ed.). Amazon. https://www.amazon.com/dp/B0B14KHL8G

Book (Full Color Edition with Variant Cover)

Budinsky, D. (2022). *The endogenous retrovirus handbook: Dismantling the best evidence for common descent* (Full color ed., Variant cover). Amazon. https://www.amazon.com/dp/B0B1B1N8F6