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Endogenous retrovirus sequences and their usefulness to the host

Mammalian genomes contain an estimated 1–5% of retrovirus-related sequences, a figure that reaches 10–30% if all retrotranscribed sequences are included. Considering the millions of years in which virus and host have coexisted, it seems likely that the efficient integration and spread of these sequences in a host genome offers some benefits to the host, as well as to the virus. Recent reviews by Garfinkel and Best in this journal have shed some light on the value of retrosequences in the host genome. Apart from the virus, these sequences in a host genome offers some benefits to the host, as well as to the virus.

In summary, some types of retroviruses and their host species have developed a symbiotic coexistence, with the virus finding shelter in the host genome, and the host using the viral sequences for defence against new infections.

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Response from Stoye, Le Tissier and Best

We are in perfect agreement with Dr van der Kuyl concerning the potential ability of intact endogenous proviruses to restrict novel infection. Although both of our examples involve deletions of viral long terminal repeats (LTRs) and the use of cellular promoters for transcription, we did not state that such events were required and did not intend to imply that they might be. Indeed, the Fv1 open reading frame is transcribed at very low levels: in fact, lower than one might expect from a retroviral LTR. The immunosuppressive properties of a peptide derived from the transmembrane region of an exogenous retrovirus were first described over ten years ago, and this potential property of endogenous proviruses has been invoked on many occasions. However, we are not aware of any experimental data showing a physiological role played by this region of an endogenous retrovirus. Experiments to address this issue in an incisive fashion, once and for all, would be very welcome.

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References


Letters

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