Expression pattern analysis of transcribed HERV sequences is complicated by ex vivo recombination.

BACKGROUND: The human genome comprises numerous human endogenous retroviruses (HERVs) that formed millions of years ago in ancestral species. A number of loci of the HERV-K(HML-2) family are evolutionarily much younger. A recent study suggested an infectious HERV-K(HML-2) variant in humans and other primates. Isolating such a variant from human individuals would be a significant finding for human biology.

RESULTS: When investigating expression patterns of specific HML-2 proviruses we encountered HERV-K(HML-2) cDNA sequences without proviral homologues in the human genome, named HERV-KX, that could very well support recently suggested infectious HML-2 variants. However, detailed sequence analysis, using the software RECCO, suggested that HERV-KX sequences were produced by recombination, possibly arising ex vivo, between transcripts from different HML-2 proviral loci.

CONCLUSION: As RT-PCR probably will be instrumental for isolating an infectious HERV-K(HML-2) variant, generation of "new" HERV-K(HML-2) sequences by ex vivo recombination seems inevitable. Further complicated by an unknown amount of allelic sequence variation in HERV-K(HML-2) proviruses, newly identified HERV-K(HML-2) variants should be interpreted very cautiously.