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Nucleotide sequence analysis of long terminal repeats of leukemogenic and non-leukemogenic MCF MuLVs

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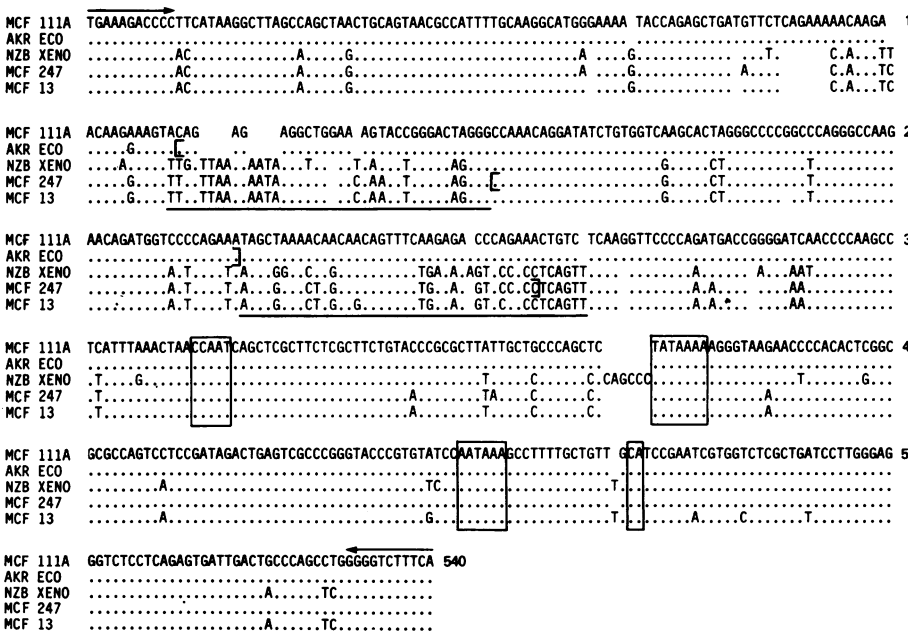
We sequenced the large terminal repeats (LTRs) present in infectious cloned DNA segments of leukemogenic, mink cell focus-forming MCF13 and non-leukemogenic, MCF111A murine leukemia viruses (MuLVs; 1). We compare these sequences with LTRs of AKR ecotropic (AKR ECO; 2), NZB xenotropic (NZB XENO; 3) and MCF247 (4) MuLV DNAs. MCF111A LTR is used as the "standard." Dots show identity; blank space, absence of bases; boxed nucleotides, regulatory signals; arrows, inverted repeats; underlines, regions of greatest nucleotide divergence; and brackets, enhancer region. Different nucleotides are shown. AKR ECO LTR was shortened by 99 bp by omission of the direct repeat. MCF111A LTR was identical except for one bp with AKR ECO LTR; MCF13 LTR had 94% base homology with NZB XENO LTR and 97% sequence homology with the LTR of leukemogenic MCF247 MuLV DNA.



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