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## Molecular Cloning and Phylogenetic Analysis of the Human Endogenous Retrovirus HERV-K LTR Elements in Various Cancer Cells

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### Abstract

Long terminal repeats (LTR) of the human endogenous retroviruses K family (HERV-K) have been found to be coexpressed of genes closely located nearby. It has been suggested that the HERV-K LTR elements have contributed to structural change in the genome and to genetic variation connected to various diseases. We examined the HERV-K LTR elements in human cancer cells. Using genomic DNA from the various cancer cells, we performed PCR amplification and identified forty-nine HERV-K LTR elements. Those LTR elements showed a high degree of sequence similarity with human-specific HERV-K LTR elements. A phylogenetic tree obtained by the neighbor-joining method revealed that twelve HERV-K LTR elements were closely related to human-specific HERV-K LTR elements. Such elements proliferated recently were detectable in human cancer cells, suggesting that they could be implicate a pathogenic role although this phenomenon may directly not lead to human cancers. Further studies on the biological function and expression of HERV-K LTR elements in these cancer cells are indicated.