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Human Endogenous Retrovirus HERV-W LTR Family in Placenta cDNA Library

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Abstract

Human endogenous retroviral long terminal repeats (LTRs) have been found to be coexpressed with sequences of genes closely located nearby. It has been suggested that the LTR elements have contributed to the structural change or genetic variation of human genome connected to various diseases and evolution. Using cDNA library derived from placenta tissue, we performed PCR amplification and identified five new HERV-W LTR elements. Those LTR elements showed a high degree of sequence similarity (98~99%) with HERV-W LTR (AF072500). A phylogenetic tree obtained by the neighbor-joining method revealed that HERV-W LTR elements could be mainly divided into two groups through evolutionary divergence. Five new HERV-W LTR elements (pla-1, 4, 5, 6, 7) belonged to the group I with AX000960, AF072504, and AF072506 from GenBank database. The data suggest that several copy numbers of the HERV-W LTR elements are transcribed in placenta and may contribute to an understanding of biological function such as human placental morphogenesis