P67

Application of Realtime RT-PCR Analysis for the Dissection of HERV-W Env Elements

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HERVs (Human endogenous retroviruses) and LTR (long terminal repeat) - like elements are dispersed over 8% of the whole human genome. There are at least 22 independent HERV families within the human genome, which originated from germ-cell infection by the exogenous retrovirus during primate evolution. Elucidation of expression pattern in HERV elements should provide information about fundamental cellular activities and the pathogenesis of multifactorial diseases such as cancer and autoimmune disease. HERV-W env gene is related to multiple sclerosis, and has potential roles for normal differentiation of human villous cytotrophoblast into syncytiotrophoblast. HERV-W env gene was expressed differentially in human tissues. Especially, it was highly expressed in human placenta. This phenomenon indicates HERV-W env gene have the different roles in each tissues. Here, we applied realtime RT-PCR for detection of its expression in various human tissues. We also analysed such amplification using cancer cells and monkey tissues, and discussed in relation to physiological function.

P68

Promoter Activity of LTR Element of the Human FPRL2 Gene

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The human genome is estimated to consist of approximately 8% human endogenous retroviruses (HERVs) and related sequences. FPRL2 (fomyl peptide receptor-like 2) gene has a solitary LTR (long terminal repeat). The LTR is located between first exon and promoter region of the FPRL2 gene. The FPRL2 gene containing LTR element was expressed in various human tissues except fetal brain and cerebellum. The LTR element was detected in hominoid, Old World monkeys, and New World monkeys except for common marmoset, whereas LINE (long interspersed repetitive element) and SINE (short interspersed repetitive element) elements were detected in prosimian (ring-tailed lemur) and common marmoset. We also examined promoter activity of the LTR element in FPRL2 gene, and discussed its biological role. Taken together, the insertion of retroelements into primate genome could have different biological roles during primate evolution.