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## Phylogenetic Analysis of New HERV-H Family in Hominoid Primates

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Human endogenous retroviruses (HERVs) contain at least 1% of the human genome and are dispersed over the whole human genome. They have been inserted into the germ cells of primates and have remained an essential part of the primate genome during evolution. HERV-H, a family of endogenous retroviral elements that has undergone successive expansion in the human genome, includes sequences that are expressed in placenta and T cells. We amplified *env* fragments of HERV-H by polymerase chain reaction (PCR) using genomic DNA of humans and primates (chimpanzee, bonobo, gorilla, and orangutan). Eighteen HERV-H *env* sequences from hominoid primates were identified and analyzed with other HERV-H family in the GenBank database. They have a high degree of sequence similarity (76.2 - 99.8%) with 13 different HERV-H families. Phylogenetic analysis indicated close relationships of *env* gene sequences across species among the hominoids. The data suggests that the HERV-H family has evolved independently during primate evolution.