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Identification and Phylogenetic Analysis of HERV-W pol Fragments in Patients with Schizophrenia

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Schizophrenia is a serious brain disease of uncertain etiology. The nucleotide sequences identified in the CSFs of the individuals with schizophrenia or schizoaffective disorder were related to those of the human endogenous retroviral(HERV)-W family of endogenous retroviruses. Using the PCR approach with genomic DNA derived from individuals with schizophrenia, 14 pol fragments of the HERV-W family were newly identified and performed phylogenetic analysis. They showed a high degree of nucleotide sequence similarity(86.7%~92.4%) with that of the HERV-W. Translation of the pol fragments showed frameshift or termination codon by deletion/insertion or point mutation in all clones. Phylogenetic analysis of the HERV-W family indicates that HERV-W pol fragments could be divided into three groups through evolutionary divergence. Some HERV-W pol fragments (SWP22-1-1, SWP22-1-5, SWP22-2-1, SWP22-2-3, SWP22-3-1) belonging to the group A from genomic DNA of schizophrenia patients were closely related to the sequences of clones (HWP3-1, HWP3-2, HWP3-3) derived from human chromosome 3 and two fragments (SWP22-3-3, SWP22-3-5) were closely related to the sequence of clone RP11-847H18 from human chromosome 12, while the sequences of SWP22-1-3 and SWP22-2-2 belonging to the group B were closely related to the sequences of clone RP11-130I17 from chromosome 3 and clone B853K11 from chromosome 21. These HERV-K pol fragments deserve further investigation as potential leads in the treatment of schizophrenia.