

that of the HERV-S. Phylogenetic analysis from the HERV-S family indicated that the LTR elements were mainly divided into 2 groups through evolutionary divergence in the primate evolution. Further investigation of the HERV-S LTR elements in primates may cast light on the integration timing into the primate genome and understanding of human evolution.

A807 Identification and Phylogeny of the Human Endogenous Retrovirus HERV-W LTR Family in Human Brain cDNA Library and Xq21.3 Region

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Human endogenous retroviral long terminal repeats (LTRs) have been found to be coexpressed with sequences of genes 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. HERV-W family has been identified in the cerebrospinal fluids and brains of individuals with schizophrenia. Using cDNA library derived from human brain, we examined the HERV-W LTR elements and identified five new LTR elements. We also examined such elements using YAC clone panel from the Xq21.3 region linked to psychosis that was replicated on the Y chromosome after the separation of the chimpanzee and human lineages. Fourteen elements of the HERV-W LTR were identified in that region. Those LTR elements showed a high degree of sequence similarity (91.8–99.5%) with HERV-W LTR. A phylogenetic tree obtained by the neighbor-joining method revealed that new HERV-W LTR elements were closely related to the AX000960, AF072504, and AF072506 from GenBank

database. The data indicates that several copy numbers of the HERV-W LTR elements exist on Xq21.3 region and are also expressed in human brain. These LTR elements deserve further investigation as potential leads to neuropsychiatric diseases.

A808 Wheat evolution : Polyphyletic origin of the B genomes and differences of the B genomes between *Triticum turgidum* and *T. aestivum*

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Common bread wheat (*Triticum aestivum*, AABBDD, $2n=2x=42$) had evolved relatively recently. *Triticum monococcum* and *T. tauschii* (*Aegilops squarossa*) were to be the donors of A and D genomes in polyploid wheat by several lines of evidences. However, the B genomes in polyploid wheats had not been resolved for their genome donors. Either one or several diploid B genome plants should have donated their chromosomes to the polyploid wheats. The putative B genome donor plants are *T. searsii*, *T. speltoides*, *T. sharonensis*, *T. bicornis*, and *T. longissima*. We are not sure that there were a single or multiple events of hybridization between Einkorn A genome plant with Emmer B genome plants. Monophyletic or polyphyletic origins of the B genome chromosomes are not clear. As well, identity of the B genome chromosomes in *T. turgidum* (AABB) and *T. aestivum* (AABBDD) was not clear either. We have isolated a fungal microsatellite DNA which can hybridize in selective chromosomes in wheat species. With this DNA as a probe, we sought the B genome donors to polyploid wheats and the identity of the B genome chromosomes between *T. turgidum* and *T. aestivum*.