

Z 106 **Phylogenetic Analysis of Schizophrenia Associated Retroviruses (SZRVs) by Blast Search from the GenBank Database.**

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SZRV (schizophrenia associated retrovirus) element is similar to three known sequence of retroviral origin; MSRV (multiple sclerosis-retrovirus), HERV-W, and ERV-9. For identification of the SZRV families on human genome, we used sequence data derived from SZRV-1 (GenBank accession no. AF135487, 2309bp), SZRV-3 (GenBank accession no. AF188999, 3921bp) and SZRV-4 (GenBank accession no. AF189000, 1622bp). With the aid of the BLAST search, we found 24 large retroviral sequences (> 2,000bp) and 27 small sequences (< 500bp) from the GenBank database using SZRV-1 sequence, whereas no homologous sequences were identified using the SZRV-3, SZRV-4 sequence data. From the family of the SZRV-1 sequence, the large length of the retroviral sequences were dispersed into the human chromosome 1, 3, 4, 5, 6, 7, 12, 20, and X during primate evolution. A retroviral sequence (GenBank accession no. AF009668) among 24 sequences identified from the GeneBank database revealed as an identical sequences of the pol gene of MSRV (multiple sclerosis associated retrovirus). The small length sequences were associated with the pol region HERV-W, MSRV, ERV-9 in human and primate genomes. Phylogenetic analysis using the retroviral sequences from the GenBank database suggests the possibility that there could be another retroviral families related to SZRV except for the HERV-W, MSRV, and ERV-9 in human genome.

Z 107 **Phylogeny of Korean Cobitidae Inferred from Mitochondrial DNA cytochrome *b* Gene**

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Phylogenetic relationships among fifteen species of Korean Cobitidae were examined by comparing partial sequences of mitochondrial cytochrome *b* gene (965bp). Generally the results agree with previous morphological studies, but new interesting relationships were found. All phylogenetic trees we constructed suggest that *Orthrias* and *Lefua* early diverged in *Cobitidae*, and *Koreocobitis* branched secondarily. The present data also show that *Misgurnus* is monophyletic with strong statistical support, but *Cobitis* paraphyletic. The unexpected phylogenetic relations of *Iksookimia* and *Cobitis* species demonstrate natural intergeneric and interspecific hybridizations in the species of two genera. Sequence divergence values between *Orthrias* and *Lefua* correspond to interfamilial sequence divergences (21-24%) between *Cobitidae* and *Cyprinidae*. Another remarkable result is the sequence divergence (11-12%) between Chinese *Misgurnus aguillicaudatus* and Korean *M. aguillicaudatus* which collected from Yongdok, Somgin River and Mankyung River. This value is comparable to intergeneric sequence divergences (14-17%) in *Cobitidae*.