Z606 **Novel Splicing Variant of Amphiphysin II, Amphiphysin IIb-1 regulates the Function of p73b through Protein-Protein Interaction**

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p73 is a nuclear protein that shows similar structure and function to p53. Especially, C-terminal region of p73 displays regulatory function through interaction with a positive or negative regulator. Here, we identified new p73β binding protein by using yeast two-hybrid technique, and designated amphiphysin IIb-1. Amphiphysin IIb-1 is one of amphiphysin II splicing variants, and has a shorter protein product than amphiphysin IIb which is previously reported by Ramjaun et al. We confirmed that amphiphysin IIb-1 bound to full-length p73β in vitro and in vivo. This association was mediated through SH3 domain of amphiphysin IIb-1 and C-terminal region of p73β. Although amphiphysin IIb-1 was localized in cytoplasm, overexpression of amphiphysin IIb-1 significantly inhibited the transcriptional activity of p73β as dose dependent manner. Moreover, cell death function of p73β was also inhibited by amphiphysin IIb-1. Therefore, these results show that amphiphysin IIb-1 can regulate the function of p73β by direct binding, suggesting a new insight of the regulation mechanism of p73β.

Z607 **Molecular Cloning and Phylogenetic Analysis of New Human Endogenous Retrovirus HERV-W Family in Cancer Cells**

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Human endogenous retroviral family(HERV-W) has recently been described that is related to multiple sclerosis-associated retrovirus(MSRV) sequences. Using the PCR approach with human genomic DNA derived from cancer cell lines(HepG2, Jurkat, MCF-7, UO-31), five env fragments of HERV-W family were newly identified and analyzed. They showed a high degree of nucleotide sequence similarity(94-99%) with that of the HERV-W. Translation of the env fragments showed no frameshift and termination codon by deletion/insertion or point mutation in clones HepG2-1 and JUR-3. The ratio of synonymous to non-synonymous substitutions indicated that negative selective pressure is acting on HepG2-1 and JUR-3 sequences. These env gene sequences could be associated with an active provirus in human cancer cells(HepG2 and Jurkat). The HepG2-1 and JUR-3 showed sister relationship with the HERV-W and W-7-1 derived from human chromosome 7. Phylogenetic analysis from the HERV-W family indicated close relationship of the env gene sequences across human chromosomes.