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Novel RNA-binding Proteins Upregulated in Human Ovarian Tumors

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Using a model system of young, senescent and SV40-immortalized WI-38 fibroblasts, we identified two mRNAs upregulated in immortalized cells(imup-1, immortalization-upregulated protein 1, and imup-2). In-vitro translated proteins bound to poly(rG), but did not interact with single-stranded DNA or double-stranded DNA. However, the roles of IMUP-1 and IMUP-2 are not known in human ovarian epithelial tumors. imup-1 (4.0-fold) and imup-2 (2.4-fold) mRNA expression in ovarian epithelial tumors were significantly higher than in normal ovarian tissues ($p < 0.05$). The mRNAs of imup-1 and imup-2 in the ovarian cancer cell lines were about 4.9- and 2.9-fold compared to the normal ovarian cell line, respectively. The subcellular expression of these two proteins in immunohistochemical stains was detected mainly in the nucleus of tumor cells, whereas adjacent normal ovarian stromal cells were faintly or negatively stained with these proteins. However, the staining intensity of IMUP-1 and IMUP-2 in ovarian epithelial tumors were not different between histological types or grades.

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A Novel Bak-like Gene without a Conserved BH3 Domain Induces Apoptosis

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Apoptotic cell death is critical for the maintenance of tissue homeostasis in a healthy organism as well as for pathogenesis during diseased states including cancer, neurodegenerative disorders, autoimmune diseases, and viral infection. We have found a novel cDNA encoding a 101 amino acid protein possessing a Bak-like sequence in our full-length cDNA bank. Bak-like shared the conserved domains BH1 and BH2 with other proapoptotic proteins but lacks the BH3 domain. Bak-like is expressed in a wide variety of tissues. Using probes with or without homology to Bak, we performed southern blots in order to find out whether Bak and Bak-like are splicing variants. Confocal microscopy of HeLa revealed that EGFP-Bak-like was found diffusely throughout the cytosol. However, upon induction of apoptosis, EGFP-Bak-like redistributed in to a punctuate pattern colocalizing with mitochondria. Like Bak, Bak-like gene product primarily enhanced apoptotic cell death following an appropriate stimulus.

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Molecular Cloning and Expression of P450 Aromatase Gene

in Ovary of Wrasse, *Halichoeres tenuispinis*

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P450 aromatase(P450arom), encoded *CYP19* gene, is a member of the cytochrome P450 superfamily, which catalyzes the formation of aromatic C18 estrogens from C19 androgens. P450arom is expressed in a wide variety of tissues in human. According to the previous studies, there are two types of P450arom in teleost fish, termed CYP 19a, CYP 19b, respectively. Estrogen is an important hormone responsible for developmental, physiological and behavioral responses in vertebrates. Especially in teleosts, estrogen is essential for induction of the precursor of yolk protein in the liver and oocyte development. In this study, we isolated a full-length P450arom cDNA from an ovary library and characterized the tissue-specific expression of *Cyp 19a* by RT-PCR. The size of the cDNA is 2.1kb which encodes a protein of 519 amino acids. *Cyp 19a* is expressed in various tissues in male and female wrasse. The sequence of *CYP 19a* shares 71-77% sequence identity with ovary aromatase of other fish species. Also, we isolated partial P450arom cDNA fragment from brain. This result indicates a possibility that there are two types of P450 aromatase in wrasse.

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Comparative Analysis of Endogenous Retrovirus HC2 Family in Humans and Monkeys: Expression, Evolution, and Phylogeny

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We investigated the HC2-like elements in various tissues from Japanese monkeys (*Macaca fuscata*), squirrel monkeys (*Saimiri sciureus*), and humans. Its pol fragment was shown tissue-specific expression pattern in various tissues of squirrel monkeys and humans by RT-PCR analysis. Those of HC2-like elements showed a high degree of sequence similarity (73.7-99.0%) to the HC2 family in human retrieved from NCBI database. No frameshift and termination codon by deletion/insertion or point mutation in two clones (SM-HC27-1 and SM-HC27-4, JM-HC21-5 and JM-HC25-2) in squirrel monkeys lung and Japanese monkeys seminal vesicle and cerebellum, whereas, in case of the human, twenty-three clones from eleven different human tissues showed pure peptide sequences. Those phenomena indicated negative selective pressure is acting on those clones according to the ratio of synonymous (Ks) and non-synonymous substitution (Ka) was < 1 . Phylogenetic analysis suggested that the HC2 family derived from monkey and human tissue mRNA with those of human genome indicated close relationships during primate evolution. Comparative analysis between humans and monkeys by human endogenous retrovirus HC2 is great use for exploring human disease related to causing by mobile genetic elements.