F101 Detection of *p53* Gene Mutations from Cervical Cancer Patients in Korea

Hye Suk Hwang*, Jung Hee Hwang, Nam Keun Kim[1], Hyun Sup Kim and Ki Wha Chung
Dept. of Biological Science and Jinseng Research Center, Kongju National University, [1]College of Medicine, Pochon CHA University

Mutations in the tumor suppressor gene *p53* are a common finding in nearly all types of human cancers. DNA damage through radiation or genotoxic agents, inducing *p53* overexpression, arrests the cell cycle in G1, leading to either DNA repair or induction of apoptosis. In the present study, we investigated three *p53* restriction fragment lenght polymorphisms (RFLP) on subjects with Korean populations of normal and cervical cancer patients (*Bst*UI RFLP in exon 4, *Msp*I RFLP in intron 6 and *Taq*I RFLP in exon 6). The mutation rates in *Bst*UI and *Msp*I RFLPs were estimated to 0.418 and 0.033, respectively. The *Taq*I sites was, however, monomorphic in Korea. It was revealed that the studied three RFLPs have no relevance to the risk of cervical cancer development.

F102 Isolation and Characterization of a Novel Mouse Gene HBMG010

June Ho Shin*, Mi Ae Park, Ji Hyung Chae, Hee-Suk Kweon, and Chul Geun Kim
Department of life science, College of Natural Sciences, Hanyang University

HBMG010 was identified as one of novel cDNAs from mouse embryonic stem (ES) cells during the modified screening approach in combination with expressed sequence tags. Northern blot, RT-PCR and reverse Northern slot blotting analyses revealed that about 1.6 kb HBMG010 mRNA is strongly expressed in most adult tissue types including testis, spleen, heart, liver, and brain, and in the sixth day of differentiating embryoid bodies (EBs) *in vitro*. It consists of 1561 nucleotides and contains an open reading frame encoding 420 amino acids. Deduced amino acid sequences of HBMG010 show very basic theoretical pI (9.67) and a high score of hydrophilicity with two coiled-coil structure regions and several nuclear localization signals. In order to get some insights on the functional role of HBMG010, we performed yeast two hybrid assay using a full length HBMG010 clone as a bait and human brain cDNA library as a target protein. Most of the positive clones encode novel genes, while two clones are highly homologous to the known genes: one clone encodes CDK-activating kinase assembly factor p36/MAT, whereas the other clone encodes tumor necrosis factor type 1 receptor associated protein (TRAP1) or HSP75, which is known to chaperone Rb refolding during mitosis or heat shock stress. Immunohistochemical analyses demonstrate that HBMG010 protein exists mainly in cytoplasm as clusters complexed with microtubles and variable amounts are in nuclei and mitochondria as cell cycle progresses. Furthermore, when reduced the level of HBMG010 gene expression in ES cells, several genes were up- or down-regulated comparing to the control ES cells. The overall data suggest that HBMG010, as a homologue of HAP46 (also known as RAP46 and BAG1) that interacts with HSP70 family, nuclear hormone receptors, and/or antiapoptotic protein BCL2, appears to cooperate in affecting the chaperoning activity of HSP90 family (HSP75) and other factors regulating cell cycle, and thus exerts its role in cell cycle progression and cell survival.