

G729

**Expression of Common Bean (*Phaseolus vulgaris* L.) Non-specific Lipid Transfer Protein Gene in Transgenic *Arabidopsis***Jun-Ho Cho<sup>P</sup>, Hoyeun Kim<sup>1</sup>, Sang-Gu Kim<sup>C</sup>*School of Biological Sciences, Seoul National University, Seoul 151-742*

We have previously isolated a genomic clone, *PvLTP* encoding root-specific nsLTP (non-specific Lipid Transfer Protein) from bean (*Phaseolus vulgaris* L.). To investigate the regulation mechanism of *PvLTP* expression, transgenic *Arabidopsis* containing *PvLTP* promoter-reporter gene fusion was generated (pLTP::GUS plant) and the transgenic *Arabidopsis* was treated with several signals. First, single-copy transgenic lines were screened and GUS expression of transgenic plants selected was analyzed further. GUS staining of pLTP::GUS plant showed that tissues dividing vigorously were highly stained in shoot. GUS expression was developmentally regulated in root of pLTP::GUS plant. Therefore, it was presumed that some of *cis*-elements which regulate *PvLTP* expression are located in 3 kb of *PvLTP* promoter region and they promote expression of *PvLTP* in transgenic *Arabidopsis*. By PLACE program for signal scan search, we found various *cis*-elements located in *PvLTP* promoter region and most of them related to light regulation and hormonal response. When pLTP::GUS plants were treated with dark and ABA, it showed 2.4-fold and 2.8-fold induced expression, respectively. Considering that no other *LTP* gene responsive to dark or expressed exclusively in root was reported, one of the signals which determined *PvLTP* expression would be dark condition. These results suggested a possibility that adaptation to environmental stress and defense could be a role of *PvLTP* protein.

G730

**Mutation and Expression of Retrotransposon LINE-1 in Human Cancer Cells and Fibroblasts**Sang-Hyun Han<sup>P</sup>, Ju-Hyung Oh<sup>1</sup>, You-Sung Oh<sup>1</sup>, Jae-Hwan Kim<sup>1</sup>, Ji-Hoon Song<sup>1</sup>, Dae-Ju Oh<sup>1</sup>, Yong-Hwan Jung<sup>2</sup>, Moon-You Oh<sup>C</sup>*<sup>P</sup>Ci Department of Life Science, Cheju National University, Jeju 690-756; <sup>2</sup>National Jeju Agricultural Experiment Station, Rural Development Administration, Jeju 690-150*

Functional L1 elements are autonomous non-LTR retrotransposons that can insert into humangenes and cause diseases. Especially, activation of L1 accelerated the genomic instability in tumorigenesis by retrotransposition activity or aberrant transposition. We analyzed the expression of L1 *p40* gene in cellular mRNA transcripts in various human cancer cell lines and normal fibroblasts. L1 *p40* is encoded by the first ORF and is found in a large cytoplasmic ribonucleoprotein complex, the p40 RNP-complex, in association with L1 RNA(s) in human teratocarcinoma cell lines. L1 transcripts were observed in cellular mRNAs of all cancer cell lines tested. Sequencing result shows that L1 transcribed from various loci of human chromosomes, and that active loci were dependent on cell lines. Various mutations, such as nucleotide substitutions, insertion and deletion were also found. Although, as described in previous reports, most L1 detected in this study are non-functional because of mutations, but several sequences may have active capacity as a L1 *p40*. Consequently, the locations of active L1 found on the chromosomes suggested a certain associations between activation of L1 and human diseases.

G731

**Expression of Human Endogenous Retrovirus K Genes in Human Cancer Cells and Fibroblasts Treated with Carcinogens**Sang-Hyun Han<sup>P</sup>, Ju-Hyung Oh<sup>1</sup>, You-Sung Oh<sup>1</sup>, Jae-Hwan Kim<sup>1</sup>, Ji-Hoon Song<sup>1</sup>, Dae-Ju Oh<sup>1</sup>, Yong-Hwan Jung<sup>2</sup>, Moon-You Oh<sup>C</sup>*<sup>P</sup>Ci Department of Life Science, Cheju National University, Jeju 690-756; <sup>2</sup>National Jeju Agricultural Experiment Station, Rural Development Administration, Jeju 690-150*

Human genome contains some members of HERV-K, known as functionally active retroelements, and coded for the characteristic retroviral protein Gag, Pol, Env and flanking two promoter-like long terminal repeats (LTRs). In this study, we have investigated the expression of HERV-K genes in various human cancer cells and examined the effects on their expression after treatment with various chemical carcinogens. We detected the transcripts of HERV-K genes (K10 LTR, T47D LTR, K10 *env*, and C4 *env*) in all cell lines tested, showing cell type specificity as the relative amount observed were different. Especially, each transcription level showed different in fibroblasts derived from distinct developmental stages as well as in leukemia cells. In addition, the expression patterns of HERV-K genes and regulatory proteins were changed by the treatment of chemical carcinogens. This study could not get the evidences for direct associations between the expression of HERV genes and human cancers, however, we suggest that the alteration of activity level of the retroelements will contribute to transform the nature of the cell, because the carcinogens affected the expression of HERV-K.

G732

**Genetic Characterization of Ancient Cattle DNA Excavated from Archaeological Sites, Jeju, Korea**Jae-Hwan Kim<sup>1</sup>, Sang-Hyun Han<sup>1</sup>, Ju-Hyung Oh<sup>1</sup>, You-Sung Oh<sup>1</sup>, Ji-Hoon Song<sup>1</sup>, Yong-Hwan Jung<sup>2</sup>, Moon-You Oh<sup>C</sup>*<sup>P</sup>Ci Department of Life Science, Cheju National University, Jeju 690-756; <sup>2</sup>National Jeju Agricultural Experiment Station, Rural Development Administration, Jeju 690-150*

We studied on the ancient animal remains excavated from the archaeological sites in Jeju, Korea. We analyzed the ancient remains with molecular genetic technique for identifying the species and verifying the relationship with the various extant animals. Ancient DNA was extracted with the remains from two archaeological sites, Gonae (humerus, A.D. 700 - 800) and Kwakji (radius and tooth, A.D. 800 - 900), respectively. We determined the complete nucleotide sequences of mitochondrial DNA displacement loop (D-loop) region using PCR amplification and DNA sequencing. The results showed that these remains were the bones and tooth of the cattle, *Bos taurus*. In the neighbor-joining and maximum likelihood trees, four ancient cattle remains were formed a monophyletic group with Jeju native blacks. However, the variation of nucleotide sequences and the previous reports on some archaeological sites suggest that a few wild cattle may have existed in Jeju Island, Korea before the introduction of cattle around A.D. 200. Our results will be contributed to further studies on the origin of Jeju native cattle and the existence of local wild cattle.