G105

CP2b Synergizes the Transcriptional Activity of CP2c by Heteromerization with the DNA-bound CP2c in a Cell Context-dependent Manner

Ho Chul Kang[P], Ji Hyung Chae[1], June Ho Shin[1], Chul Geun Kim[C]

Department of Life Science, Hanyang University, Seoul 133-791

As a member of ubiquitous transcription factor family, how CP2 critically exerts its effect on the expression of a variety of tissue-specific genes? As an effort to address this question, we previously identified three mouse CP2 family genes, CP2a, CP2b, and CP2c, and demonstrated that they are distinguished in their intrinsic DNA binding and transcription activities. Here, as a better understanding on tissue-specific expression of the -globinCP2 target genes, we tested how CP2b affects the CP2c activity on the promoter by transfection assays of a reporter construct in two different cell lines, kidney 293T cells and erythroleukemic K562 cells in which endogenous globin genes are expressing. Whereas both transcriptional and DNA binding abilities of CP2c were suppressed by CP2b in 293T cells, CP2c activity was rather augmented by CP2b in K562 cells. Moreover, this CP2b effect on CP2c in K562 cells was reduced by either co-expression of the CP2c dominant-negative or the N-terminal deletion-mutant of CP2b. We confirmed by electrophoretic mobility shift assays that CP2b exerts its effect by heteromerization with the DNA-bound CP2c in K562 cells. Overall data suggests that CP2b activity is regulated by a novel CP2b modification and/or interaction with other partner proteins in a cell context-dependent manner and, consequently, the activated CP2b synergizes the transcriptional activity of CP2c by heteromerization with the DNA-bound CP2c.

G106

Understanding the Key Events Occurring during the Reprogramming of Erythroleukemia Cells: Large-Scale Gene Expression Profiling during Murine Erythroleukemia Cell Differentiation Using cDNA Microarray

Ju Hyun Kim[1], Young Jin Lee[P], Bo Mee Chung[1], Chul Geun Kim[C]

Department of Life Science, Hanyang University, Seoul 133-791

MEL cells are transformed erythroid precursors that are blocked at about the proerythroblast stage of differentiation. Treatment of cells with agents, like HMBA, causes them to reinitiate erythroid terminal differentiation culminating in accumulation of erythrocyte-specific markers, cell-cycle arrest, and loss of tumorigenicity. MEL cells also provide an opportunity to study the changes occurring during reprogramming of tumor cells into their normal differentiation program. Although a great deal has been learned about the factors controlling gene expression during differentiation of MEL cells, much less is known about the mechanisms that determine the commitment of differentiation and maintain fully mature cells in the state of permanent cell cycle withdrawal. As an effort to uncover the cellular and molecular mechanisms of erythropoietic differentiation, we have compared gene expression profiles between uncommitted and differentiating MEL cells using cDNA microarray and identified a set of genes that preferentially expressed in uncommitted or differentiating cells. During HMBA-induced differentiation, changesin signal transduction-, transcription-, cell metabolism- and extracellular matrix-related genes were dominated over preferentially expressed genes and some of them were correlated with the published data. This kind of study may provide fundamental clues for the understanding of erythropoiesis as well as for leukemia therapy.

G107

Expression of Bcl-2, Caspase-2 and Extracellular Signal-regulated Kinase 2 in Relation to Apoptosis Induced by Ultraviolet Radiation in HeLa S_3 Cells

Jeong Hyun Chang[P], Hyun Jin Park[1], Kyung Il Um[C]

Department of Biology, Dong-A University, Busan 604-714

The present study has been performed to elucidate the expression of Bcl-2, Caspase-2 and Extracellular signal-regulated kinase 2 (ERK2) in relation to apoptosis induced by Ultraviolet radiation (UV) in HeLa S3 cells. Three assays were employed in this study : Morphological assessments of apoptotic cells, analysis of DNA fragmentation pattern and expression of Bcl-2, Caspase-2 or ERK2 by western blot analysis. The number of apoptotic cells or DNA ladder pattern in this cell line irradiated with UV was increased continuously at 3 hour. Bcl-2 and Caspase-2 proteins inhibited apoptosis, whereas ERK2 protein indirectly affected to apoptosis in the cells. These results suggest that apoptosis may proceed through mechanism according to DNA damaging agents and the location of proteins in the cell.

G108

Optimization of RNA Purification Condition from a Soft Coral *Alcyonium gracillimum* Kuekenthal

JJong Sung Ahn[P], Jongrak Lee[1], Sa Heung Kim[1], Seungshic Yum[C]

[PC1]Department of Biological Sciences Sungkuynkwan University, Suwon 440-746; [2]In the Sea Korea Co., Ltd., Science Technology Park, Sungkyunkwan Univeristy, 440-746

As environmental destruction is accelerated by increment of human activities, the biodiversity in marine ecosystem has been widely damaged. Many efforts have attempted to conserve biodiversity. One of them is to conserve or to maintain biodiversity through managing and restoring the major marine benthic organisms of coastal ecosystems such as kelps, seagrasses and corals. Coral reefs, composed with hard corals, in tropical waters are believed to be the most diverse and species-rich ecosystem on earth. In subtropical region, on the other hand, soft corals are more abundant than hard ones and form a bed or a unique community. Recently the soft coral, *Alcyonium gracillimum* EST sequencing project has been promoted to construct extensive expressed gene profiling. The project would give new ideas how to manage and restore the species for conservation or recovery of biodiversity using molecular techniques. The initial stage of our project found that currently developed RNA extraction methods could not be applicable to adult colonies of this species due to large amount of mucus acting against the bacterial infection. As a preliminary result, the RNA purification for this species was strongly effective using appropriate combinatior. of lithium chloride, EDTA and SDS.