affected by 3-aminobenzamide(3AB). The percentages of apoptotic cells treated with UV and incubated with 3AB were lower than without 3AB in HeLa S_3 cells. The level of 116 kDa poly(ADP-ribose) polymerase(PARP) in cells treated with UV and then incubated with 3AB for 6 hours was higher than that without 3AB. Apoptosis induced in the cells were not affected by cycloheximide(CHX) and 2'3'-dideoxythymidine 5'-triphosphate (ddTTP). The 3AB and CHX inhibited expression of PARP during early stage of adaptive response, whereas ddTTP did not inhibit.

F111 Isolation and Characterization of UV-Inducible Genes from Schizosaccharomyces pombe

Nyon Ho Choi and In Soon Choi*
Department of Life Sciences, Silla University

The present study intends to characterize the DNA damage-inducible responses in eukaryotic cells. The fission yeast, *S. pombe*, which displays efficient DNA repair systems, was used in this study as a model system for higher eukaryotes. To study UV-inducible responses in *S. pombe*, five UV-inducible cDNA clones were isolated from *S. pombe* by using subtration hybridization method. To investigate the expression of isolated genes, the cellular levels of the transcripts of these genes were determined by Northern blot analysis after UV-irradiation. The transcripts of isolated gene (UVI30) increased rapidly and reached maximum accumulation after UV-irradiation. Compared to the message levels of control, the levels of maximal increase were approximately 5 fold to UV-irradiation. In order to investigation whether the increase of UVI30 trascripts was a specific results of UV-irradiation, UVI30 transcript levels were examined after treating the cells to Methylmethane sulfonate (MMS). The transcripts of UVI30 were not induced by treatment of 0.25% MMS. These results implied that the effects of damaging agents are complex and different regulatory pathways exist for the induction of these genes. To characterize the structure of UVI30 gene, nucleotide sequences were analyzed. The nucleotide sequence of 1,340 nucleotide excluding poly(A) tail contains one open reading frame, which encodes a protein of 270 amino acids. The predicted amino acid sequences of UVI30 do not exhibit any significant similarity to other known sequences in the database.

F112 Glucose-Dependent rrg1+ Expression Is Regulated at Posttranscriptional Level by Control of mRNA Stability Mediated by Downstream Region of Poly(A) Site in Schizosaccharomyces pombe

Min Ji Kim and Sang Dai Park*
School of Biological Sciences, Seoul National University

rrg1$^+$ (rapid response to glucose) was previously reported to show rapid glucose-inducible expression at transcript level in *Schizosaccharomyces pombe*. Here, we investigated its transcript level in various glucose conditions. In addition, the glucose-dependent expression of *rrg1*$^+$ was revealed to result from changes of mRNA half-life and its rapid regulation of mRNA stability required new protein synthesis. Serial and internal deletions within 3'-flanking region of *rrg1*$^+$ revealed that a 210-nt region downstream of distal poly(A) site was critical for the glucose-regulated expression and 3' end formation of mRNA. Taken together, this is the first report on glucose-inducible expression regulated posttranscriptionally by control of mRNA stability in *S. pombe*.

F113 Characterization of

Chromodomain Proteins, Hrp1 and Hrp3, which are Required for Heterochromatin Silencing in Schizosaccharomyces pombe

Eung Jae Yoo and Sang Dai Park*
School of Biological Sciences, Seoul National University, Seoul, 151-742, Korea

Hrp1 and Hrp3 are members of the CHD protein family of *Schizosaccharomyces pombe*. CHD proteins are thought to be required for modification of the chromatin structure in transcription, but the exact roles are not known. In this study, the effects of Hrp1 and Hrp3 on heterochromatin silencing were examined using the *S. pombe* strains containing marker gene in the highly transcriptional repressed regions such as centromere, telomere, mating type locus, and rDNA. Hrp1 was found to be involved in the transcriptional repression in the heterochromatin region such as centromere, mating type locus and rDNA repeats. ChIP assay showed that Hrp1 interacted to mating type locus directly. An *S. pombe* homologue of *hrp1*$^+$, named *hrp3*$^+$, was identified and found to be a non-essential gene. Silencing effect was also examined using the strains that contained marker gene in heterochromatin regions. *hrp3* deletion mutant alleviated the repression of silencing regions such as centromere, mating type locus, telomere and rDNA repeats. These results showed that Hrp1 and Hrp3, CHD1 proteins, are related with heterochromatin silencing and play a role as chromatin remodeling factors in vivo.

F114 Characterization of Chromodomain Proteins, Hrp1 and Hrp3, which are Required for Heterochromatin Silencing in Schizosaccharomyces pombe

Eung Jae Yoo and Sang Dai Park*
School of Biological Sciences, Seoul National University, Seoul, 151-742, Korea

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F115 Cloning, Expression and Characterization of NIP2, A Novel Nek2 Interacting Protein

Yeon Tae Jeong*, Jae Cheal Yoo and Kunsoo Rhee
School of Biological Sciences, Seoul National University, Seoul 151-742, Korea

Nek2 is a mammalian ser/thr kinase that is closely related to *Aspergillus* NIMA. The structural homology between Nek2 and nimA suggests that, like NIMA, Nek2 is involved in the cell cycle regulation. From yeast two hybrid screening Nek2 as a bait, we cloned a novel gene named as NIP2 (Nek2-Interacting-Protein 2). Northern blot hybridization analysis using human tissue