group is involved in the homologous recombination pathway. Among the group, the Rad51 and Rad52 are regarded as key components for this pathway. The proteins are known to interact each other. However, the nature of this interaction and their role on recombinational repair are not fully understood. Here we investigated the role of interaction between Rhp51 and Rad22, a Rad51 and Rad52 homologues of *S. pombe*, respectively. Direct association of the two proteins was manifested both in vivo and in vitro, using the co-immunoprecipitation, GST-pull down and two-hybrid assays. Each protein also associates homotypically as well as heterotypically. In addition, the domains in each protein that mediate the both types of interactions were determined by two-hybrid analysis. To characterize the role of Rhp51/Rad22 interaction on recombinational repair, we isolated binding mutants of each Rhp51 and Rad22. Interestingly, we found that Rhp51/Rad22 interaction is crucial for the DNA repair ability of Rhp51, but Rhp51 self-interaction is not. These results suggest that direct binding of Rhp51 to Rad22 may be necessary for the proper DNA repair by Rhp51.

F119 Atf1 and Pcr1, Stress -Responsive Transcription Factors, Are Required for Heterochromatin Silencing from *Schizosaccharomyces pombe*

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Atf1 and Pcr1 contain bZIP DNA binding motive and belong to CREB/ATF family. They are required for expression of a variety of genes in sexual development and stresses and also for activation of M26 meiotic recombination hot spot. Here, we report that a null mutation of the *atf1*$^+$ reduces significantly silencing of *mat3-M* locus but conversely increase the transcriptional repression at centromere and telomeres. Likewise, *pcr1* reduces moderately silencing of *mat3-M* locus, implying that the silencing may require heterodimer formation between Atf1 and Pcr1. Deletion of atf1 and pcr1 increases the transition rates between repressed and derepressed states as revealed by colony color assay. This suggests that they are involved in establishment of silencing rather than in its maintenance. Chromatin immunoprecipitation (ChIP) assay revealed that both Atf1 and Pcr1 are associated in vivo with a flanking region of *mat3-M* containing their potential binding site. Thus, we suggest that Atf1 and Pcr1 involve in maximal silencing at mat locus by direct binding with their binding site and subsequently recruiting other silencing factors for formation of stable heterochromatin structure

F120 The Effect of PD 098059, Inhibitor of ERK2, in HeLa S3 Cells

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In the present study, we examined the effect of PD 098059, inhibitor of ERK(extracellular signal-regulated kinases) 2, in HeLa S_3 cells. The role of ERK2 considered to be important mediators of proliferative and apoptotic signals in serum-induced HeLa S_3 cell. Four assays were employed in this study : gel electrophoresis of isolated DNA, apoptotic cells, cell viability and western blot analysis. Apoptosis was detected by demonstration of DNA ladder pattern in agarose gel electrophoresis. Nuclear condensation and fragmentation, which are part of the early events of apoptosis, were evaluated by fluorescence microscopy. The cells were labeled with acridine orange/ethidium bromide. Viable cells were assessed by trypan blue dye exclusion method. Expression of ERK2 were

determined by western blot analysis. The 50M of PD098059 did not affect DNA fragmentation and cell death, whereas inhibited the level of ERK2.

F121 세포 사멸을 유도하는 신규유전자 Bak-like

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Bak, a member of the Bcl-2 protein family, accelerates apoptosis by an unknown mechanism. We have found a novel cDNA encoding a 101 amino acid protein with sequence homology to Bak in our full-length cDNA bank. Bak-like shares the conserved domains BH 1 and 2 with other proapoptotic proteins but lacks the BH 3 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 if Bak and Bak-like are splicing variants. Confocal microscopy of HeLa revealed that GFP-Bak-like was found diffusely throughout the cytosol. However, upon induction of apoptosis, GFP-Bak-like redistributed in to a punctuate pattern colocalizing with mitochondria. Like Bak, the Bak-like gene product primarity enhances apoptotic cell death following an appropriate stimulus

F122 Characterization of New CHD1 Family Genes of DNA Damage in Yeast

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The SNF2/SW ATPase/helicase family comprises proteins from a variety of species with in vivo functions, such as transcriptional regulation, maintenance of chromosome stability during mitosis, and various types of DNA repair. Here, we reported the characterization of *hrp2+* gene which was isolated by PCR amplification using the conserved domain of SNF2 motifs. Sequence analysis of PCR product showed striking evolutionary conservation among the SNF2 family of proteins. Two transcripts of 6.7 and 3.4 kb were detected by Northern blot analysis. Furthermore, the intensities of these two bands were increased by ultraviolet (UV) irradiation. These results indicate that the *hrp2+* is a novel member of the SNF2 family of proteins and is one of the UV-inducible genes in *S. pombe*. To determine the level of transcripts of *hrp2+* gene during cellular growth, Northern blot analysis were performed. This result indicates that the level of *hrp2+* transcript reached its maximum before the cells entered the exponential growth phase. This suggests that *hrp2+* gene is expressed mainly at the early stage of cell growth.

F201 Determination of Seed Purity in Radish (Raphanus sativus L.) using RAPD and Isozyme

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Radish (*Raphanus sativus* L.) is an important crop plant. The use of random amplified polymorphic DNA (RAPD) marker and allozymes for evaluating seed purity in a commercial F_1-hybrid radish cultivar is demonstrated. The 13 primers result in 57 variable RAPD loci scored for all 128 individuals across varieties. RAPD analysis of hybrid seeds from the male harvest revealed 17 of the 128 (13.6%) seeds tested were sibs. Three hundred sixty seeds from the male and female harvest were subsequently screened for seed purity using 27 isozyme loci. Only *Est-1* locus revealed that 15 (8.3%) seeds from the female harvest and 26 (14.4%) seeds from the male harvest were sibs. Both the allozyme and RAPD methods may supplement each other,