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,

and together lead to a better insight into the hybrid seed purity.

F202 Molecular cloning and charaterization of disease-resistant genes form apple

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Environmental stress is the major limiting factor in plant productivity. Naturally, plants have evolved a wide range of mechanisms to cope with such stresses, e.g. disease resistant gene (R-gene). Unfortunately, the crop and fruit plants developed by traditional breeding tend to have good food qualities but poor disease resistance, especially compared to wild type plants. Poor disease resistance can be partly originated by loss of certain R-genes. Once certain R-genes or other relevant genes are available, the use of gene transfer technology can provide the direct solution for this problem. As the approaches to provide the solution, R-genes from a wild type plant were isolated and characterized To obtain more R-genes, a cDNA library of Jung-Sun- Mae-Ju was constructed and utilized for the isolation of the R-genes. For the cloning of NBS domain DNA fragment, PCR clones from the genomic DNA of a wild type apple(root stock) were selected 5 clones in the 3 group out of 4 groups. From the screening of the cDNA library with probes of NBS DNA fragments, six new R-genes were isolated. The genes is supposed to generate 3~4.9 kb mRNAs and were expressed in the leaves of Yesan-Samyup, Hoengsung-Hwanyup and certain apple cultivars. These genes encode functional motif NBS-LRR family, TIR-NBS-LRR or truncated form of TIR-NBS that lacks the LRRs. The similarity of the nucleotide sequences with tobacco N gene and potato NL25 is extremely high. Next step can be the application of the isolated genes to improve the apple cultivars against biotic stress like fungal or viral pathogens by the gene manipulation of the isolated R-genes.

F203 Chromosomal assignment of the garlic BAC clones using FISH technique

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Two BAC libraries of Danyang garlic cultivar were constructed. First one has been constructed using the pIndigoBAC536 vector and HMW garlic DNA extracted from leaf protoplasts. Second BAC library was constructed using the pBAC1/SACB1 vector, which is designed to give zero background, and HMW garlic DNA extracted from leaf nuclei. Forty seven clones from first BAC library were characterized by Southern hybridization with garlic genomic DNA or HRY4, a repetitive sequence of garlic, as a probe. Several BAC inserts, contained low copy of repetitive sequence, were then labeled as probes for FISH analysis. GBC5e (100 kb), one of the BAC clones which does not interrupted by repetitive sequence, was detected on the chromosome 7 in garlic. And, GBC4d (110 kb) gave rise to two different hybridization signals on the prometaphase chromosome. However, the location of hybridization can not be assigned due to the difficulty of karyotyping in the FISH condition used.

F204 Genotyping of Field-Collected Soybean Mosaic Virus by RT-PCR and Restriction Fragment Length Polymorphism Analysis of the P1 Gene

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The genomic variability of soybean mosaic