in biological systems. The cellular sources responsible for the generation of damage-causing reactive oxygen species (ROS) are widespread. Xanthine dehydrogenase (XDH) / oxidase (XOD) catalyzes the oxidation of xanthine to uric acid. The rosy (*ry*) gene encodes XDH/XOD in *Drosophila melanogaster*. XDH codes for uric acid which is a ROS scavenger. XOD however is an enzyme system implicated in ROS production. In this study, we investigated the roles of XDH in the fly\'s immune defense response to infection and in the aging process. We first compared ROS generation and nitric oxide (NO) level in the whole body and the gut of XDH mutant with those of wild type. Our results suggested that XDH has a protective effect with respect to both ROS and NO levels, particularly in the gut. We also examined the effect of a XDH deletion mutant on the relative sensitivity of the organism against bacterial infection, on the immune inducibility of antimicrobial peptides and on the effect of aging in the defensive response to infection. Our results strongly suggest that XDH plays an important role in the innate immune response and that the age-associated deterioration of the innate immune response might be, at least in part, associated with the loss of XDH activity in the aging process. Xanthine dehydrogenase (XDH) / oxidase (XOD) catalyzes the oxidation of xanthine to uric acid. XDH codes for uric acid which is a ROS scavenger. XOD however is an enzyme system implicated in ROS production. In this study, we investigated the roles of XDH in the fly\'s immune defense response to infection and in the aging process. We first compared ROS generation and nitric oxide (NO) level in the whole body and the gut of XDH mutant with those of wild type. Our results suggested that XDH has a protective effect with respect to both ROS and NO levels, particularly in the gut. We also examined the effect of a XDH deletion mutant on the relative sensitivity of the organism against bacterial infection, on the immune inducibility of antimicrobial peptides and on the effect of aging in the defensive response to infection. Our results strongly suggest that XDH plays an important role in the innate immune response and that the age-associated deterioration of the innate immune response might be, at least in part, associated with the loss of XDH activity in the aging process.

F802 Karyotype Analysis and Physical Mapping of the 5S and the 45S Ribosomal DNAs in Cucumis sativus L.

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Abstract A karyotype analysis was performed on the mitotic chromosomes of *Cucumis sativus* L. (2n=2x=14) by means of Feulgen staining and Giemsa C-banding. Chromosome pairs were chracterized on the basis of length and arm ratio value. C-banding analysis showed that all chromosomes were stained centromeric, telomeric and intercalary resions, except chromosome 2 with a heavy staining in the long arm region. Multi-color fluorescence *in situ* hybridization (FISH) using 45S and 5S rDNA probes was also carried out for identifying the cucumber chromosomes. The signals for 45S rDNA were detected in the pericentrimeric regions of chromosome 1, 2 and 4, while the signal for 5S rDNA in the short arm of chromosome 5. FISH gave us additional information for karyotyping, because the similar band pattern as C-banding was observed when chromosomes were counter-stained with 4',6-diamidino-2-phenyoindole (DAPI). *key words*: karyotype, ribosomal DNA, Multi-color FISH, *Cucumis sativus* L.

F803 Cytogenetic studies in Rumex

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There are 11 species in the genus *Rumex* in Korea. The shape of leaves are very similar but seed type and chromosome numbers are differents. Analysis of genus *Rumex* in Korea have been carried out using chromosomal, RAPD and FISH techniques. There are two dioecious plants, *Rumex acetosa* and *R. acetocella*. The chromosome number of *R. acetosa* was 2n=14 in the female and 2n=15 in the male individuals and *R. acetocella* was 2n=42 and 43. The somatic chromosome numbers of *R. crispus* and *R. japonicus* were 2n=60 and that of *R. niponicus* were 2n=50, *R. obtusifolius* was 2n=40. The chromosomal locations of 45s rDNA genes using FISH technique were determined in *R. crispus*. One pair of 45s rDNA signals was detected with avidin-FITC conjugate. Key words : *Rumex*, FISH, RAPD

F804 Functional roles of a Novel Zinc Finger Protein, FAX-ZFP in Xenopus laevis

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A subfamily of the many C2H2 type zinc finger protein (ZFP) in *Xenopus laevis* contains a highly conserved N-terminal nonfinger portion designated finger-associated box (FAX). Neither the biological roles for most of the FAX-containing ZFP (FAX-ZFP) have been yet to be discovered. We isolated a gene encoding a member of *Xenopus* FAX-ZFP family protein that interacts with the *Xenopus* TATA-binding protein (xTBP) by employing yeast two-hybrid system. A chimeric construct encoding a fusion FAX protein with Gal4 DNA binding domain repressed the transcriptional activity of a heterologous promoter containing the Gal4-binding sequence in both A6 cells (*Xenopus* kidney) and NIH3T3 cells (mouse). xTBP was also shown to make a direct contact with the FAX-ZFP protein in vitro pull down assay. These data support that the FAX-ZFP family transcription factors may interact TBP in order to negatively regulate the expression of target gene(s). In order to elucidate eleven bp consensus sequence, GCGA(A/G)GGGGTG, was selected to bind strongly with FAX-ZFP.

F805 Analysis of Anther-specific and -preferentially Expressed Genes from Lily

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We have randomly selected 2,000 cDNA clones from an anther cDNA library of oriental lily. Using differential screening, 150 anther-specific clones and 400 anther-preferentially expressed clones were isolated. The selected clones were partially sequenced at the putative 5'-end of insert cDNAs. Among 150 anther-specific expressed sequence tags (ESTs), 139 cDNA clones were nonredundant. Twenty-two clones had sequence homologies with functionally defined genes at peptide level and only five clones encoded known anther/pollen-specific proteins. One hundred twenty-eight clones showed little or no similarity with previously reported genes. Using slot blot hybridization, expression patterns of the 150 ESTs were examined during anther development. Most of the genes (123 ESTs) were strongly expressed