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Methanol dehydrogenase (MDH) was purified from a marine methylotroph *Methylophaga* sp. strain YC using amonium sulfate fractionation, anion-exchange chromatography, and gel permeation chromatography in order. The relative molecular mass of the native enzyme was found to be 145 kDa. The purified MDH was composed of two subunits having 64 kDa and 12 kDa in size, as judged by SDS-PAGE. These results suggest that the MDH from *Methylophaga* sp. strain YC is composed of two subunits with an $_{22}$ conformation as in other MDHs. Interestingly, the purified enzyme could maintain its activity even in high alkali and the optimum activity could be observed at 60?, not at 30?. The estimated Km values were 0.93 mM for methanol and 2.16 mM for ethanol, respectively when they were used as substrates. The enzymatic activity of the purified MDH was strongly inhibited by Fe^{2+} ion, not by EDTA.

F601 Genetic Variation of Apolipoprotein AI-CIII Gene Cluster in Korean Essential Hypertensiveas

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Essential Hypertension is a multifactorial disease associated with lipid metabolism. The apolipoprotein AI and CIII (apo AI and CIII) are known to play an important role in the metabolism of plasma lipoproteins and lipids. The apo AI-CIII gene cluster is located in chromosome 11q23 and more than 20 different RFLPs have been described in this gene cluster. To search for a useful genetic marker on the essential hypertension in Korean population, we investigated the distribution of alleles of Msp I polymorphism located in the APO AI gene and a Sst I polymorphism located in the APO CIII gene in 163 Korean individuals. The allele or genotype frequency Sst I RFLP at the APO CIII gene was no significantly different between the two groups- normotensive and hypertensive. However, the Msp I RFLP of the apo AI gene was significantly($P<0.05$) associated with essential hypertension in Korean population. The distribution of the genotypes of all RFLPs was in Hardy-Weinberg equlibrium in this population. Therefore, this result suggest that this polymorphism of the apo AI gene may be useful as a genetic marker on the essential hypertension in Korean population.

F801 Role of Xanthine Dehydrogenase and Aging on the Innate Immune Response of Drosophila

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It has been proposed that uric acid is an important scavenger of deleterious oxygen species and peroxynitrite in biological systems. The cellular sources responsible for the generation of damage-causing reactive oxygen species (ROS) are widespread. It has been proposed that uric acid is an important scavenger of deleterious oxygen species and peroxynitrite

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