Aldehyde and active form of free oxygen produced in alcohol metabolism in liver are the cause of liver cell damage. The main system of alcohol metabolism is composed of alcohol dehydrogenase(ADH), aldehyde dehydrogenase(ALDH) and cytochrome P4502E1. Alcohol dehydrogenase is reversible in alcohol metabolism. To block the backward reaction and enhance alcohol oxidation, acetaldehyde trapping agents were assayed. The assay was carried out by measuring decreasing NADH at 340nm, using acetaldcehyde and NADH as substrate and coenzyme respectively. Semicarbazide, cysteine, L-alginine, taurine as aldehyde trappping agents were tested.

[PC2-4] [2003-10-10 09:00 - 13:00 / Grand Ballroom Pre-function]

Characteristics of Chitosanase from Aspergillus fumigatus KB-1

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Two chitosanses produced by Aspergillus fumigatus KB-1 were purified by ion exchange and size exclusion chromatographies. Molecular weights of chitosanses were 111.23 KDa (chitosanase Ⅰ) and 23.38 KDa (chitosanase Ⅱ). The N-terminal amino acid sequence of chitosanase Ⅱ was determined: YNLPNNLKQIYDKHKGKXSXVLAK(?)GFTN. The optimum pH of the chitosanase Ⅰ and Ⅱ were 6.5 and 5.5 respectively. The optimum temperatures were 60℃ and 70℃. Two chitosanases were most stable at 10℃. The stability of chitosanase Ⅰ was declined along with increase of pH, but chitosanase Ⅱ stability was less variable to pH. Chitosanase Ⅰ was strongly inhibited by Bi^{2+}, Cu^{2+}, Fe^{2+} and Hg^{2+}. Chitosanase Ⅱ was also inhibited by Cu^{2+}. Hydrolysis products of two chitosanases were analyzed by HPLC and GPC. Chitosanase Ⅰ was exo-splitting type which hydrolyzed substrate to glucosamine. Chitosanase Ⅱ showed endo-splitting mode which produced dimer, trimer and tetramer of glucosamine.

[PC2-5] [2003-10-10 09:00 - 13:00 / Grand Ballroom Pre-function]

Distribution of Pathogenic Genes and Molecular Typing of Yersinia pseudotuberculosis isolated from Spring Water in Seoul

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In order to investigate the pathogenic genes and genetic relationships of Y. pseudotuberculosis, we isolated 9 strains of Y. pseudotuberculosis from about 380 spring water sites in Seoul and carried out antibiotic susceptibility test, biological test and molecular typing. All isolated strains were distributed throughout the northeast area in Seoul (Mt. Bookhan, Mt. Soorak, Mt. Boolam and etc...).Antibiotic susceptibility test revealed that all the strains were susceptible to chloramphenicol, gentamicin, neomycin and amoxicillin/clavulanic acid, but were resistant to novobiocin and vancomycin.For the identification of pathogenic Y. pseudotuberculosis, the strains were analyzed for chromosomal virulence gene(inv) and plasmid-borne genes(yadA and lcrF) by PCR., All the strains were positive for the inv, but only five strains were positive for the yadA and lcrF.Finally, RAPD-PCR and PCR-Ribotyping were carried out and the strains were grouped with 90% similarity. RAPD-PCR revealed 4 clusters of the strains and PCR-Ribotyping revealed 2 clusters. The results of these tests confirmed the view that RAPD-PCR had stronger discriminating power than PCR-Ribotyping.

[PC2-6] [2003-10-10 09:00 - 13:00 / Grand Ballroom Pre-function]

Antiallergic Activity of Ginsenoside R_{h2}

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Ginseng (the root of Panax ginseng C.A M_{EYER}, family Araliaceae) is frequently used as a crude substance in Asian countries as a traditional medicine. The major components of ginseng are ginsenosides, which have been reported to

show various biological activities including antiinflammatory activity and antitumor effect. In addition, Sugiyama et al. reported that ginsenoside Rg3 suppresses histamine release from mast cells due to stimulation with compound 48/80 in vitro. However, the antiallergic effects of ginsenoside Rh2, which is metabolized by human intestinal bacteria to ginsenoside Rg3, have not been studied. We therefore isolated ginsenoside Rg3 from red ginseng, transformed it to ginsenoside Rh2 by human intestinal bacteria, isolated ginsenoside Rh2 and measured antiallergic activities. In result, ginsenoside Rh2 had the most potent inhibitory activity on β-hexosaminidase release from RBL-2H3 cells and in the passive cutaneous anaphylaxis reaction. This compound also showed membrane stabilizing action upon differential scanning calorimetry and inhibitied nitric oxide and prostaglandin E_2 in lipopolysaccharide-stimulated RAW cells. However, this ginsenoside Rh2 did not inhibit the activation of hyaluronidase and scavenge active oxygen.

[PC2-7] [2003-10-10 09:00 - 13:00 / Grand Ballroom Pre-function]

Validation and optimization of the in vitro LAL test for detection of endotoxin in hepatitis B vaccines

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Endotoxin has been detected by the Limulus amoebocyte lysate (LAL) test. However, aluminum hydroxide used as an adjuvant and adsorbent for the recombinant protein antigen is known to increase efficacy of lipopolysaccharide vaccine in vivo thus interfering endotoxin test. The aim of this study is to determine effect of aluminum hydroxide on the LAL test using the hepatitis B vaccine as a model and to optimize the LAL test condition not to be interfered by aluminum hydroxide. When currently used 3 methods (gel clotting, chromogenic kinetic and turbidometric kinetic methods) were compared to detect endotoxin, gel clotting method was the most appropriate method not to be interfered by aluminum hydroxide although the sensitivity was much higher in the kinetic methods. To remove the interference by aluminum hydroxide, filtration and dilution method was tested. The results revealed that endotoxin was bound to 0.2 um filter and only small amount was retrieved in the filtrate. But endotoxin could be detected by gel clotting method after serial dilution of the samples thus dilution method could provide more reliability in less time for endotoxin detection. * This work was supported by the Korea Food and Drug Administration Grant (KFDA-03092-LIF-015-2).

[PC2-8] [2003-10-10 09:00 - 13:00 / Grand Ballroom Pre-function]

Role of Spc105p in the maintenance of genome stability

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Microtubule-organizing center (MOTC) plays pivotal roles in cell division process. Integrity of the spindle pole body (SPB) in Saccharomyces cerevisiae is required for migration and separation of sister chromatids in mitotic phase. Role of an essential SPB component, Spc105, is poorly understood. Here we show that throughout all stage of cell division cycle, GFP-tagged Spc105p localizes at SPB and its protein stability is fluctuated with mitosis-specific modifications. To gain new insights into the function of Spc105, we generated and characterized novel temperature sensitive spc105 mutants. The spc105-5 mutant exhibited chromosome missegregation and hypersensitivity to a microtubule-depolymerizing agent benomyl. Consistent with this the ts mutant has a fragmented or polyploid chromosomal structure at the nonpermissive temperature.To understand more about the SPC105 function, we tried to find out SPC105-interacting proteins using two-hybrid analysis. With LexA-DNA binding domain fusion as a bait, we isolated several candidates including a component of SUMO modification system. The putative binding protein NfiI strongly interacted with a truncated version of Spc105 homologous to myosin heavy chain. Thus, it appears to be that Spc105p complex including its binding partner harmonizes the proper segregation of sister chromatids with structural integrity of SPB.

[PC2-9] [2003-10-10 09:00 - 13:00 / Grand Ballroom Pre-function]