

pylori-infected mice were sacrificed 4, 8, 16, 24, 36, 50 and 80 weeks after the bacterial infection. After 80 weeks of infection, almost all *H. pylori*-infected mice developed hyperplastic or atrophic gastritis, but did not show any evidence of adenoma, dysplasia or carcinoma. PCNA positive cells were the most abundant 50 weeks after the *H. pylori* infection, but their number decreased thereafter up to 80 weeks. Apoptotic cell death became evident 8 weeks after *H. pylori* infection, with 7–8 apoptotic cells/high power field, and increased thereafter. Production of normally observed neutral mucin was decreased gradually, with maximal reduction observed 50 weeks after *H. pylori* infection, which was accompanied by acid chracterization thereafter. The SS1 infected mouse seems to be a suitable animal model for *H. pylori*-related research, although *H. pylori* infection itself does not induce gastric cancer in a long-term normal wild-type mouse model, which could be explained by the balance between cell proliferation and apoptosis.

[PC1-24] [04/18/2002 (Thr) 14:00 - 17:00 / Hall E]

Effects of chitosan on renal dipeptidase in vivo

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Urinary dipeptidase (Udpase) which was detected in urine of various animals including rat, rabbit, pig and human is a released form of renal dipeptidase (RDPase, EC 3.4.13.19), a glycosylphosphatidylinositol (GPI) linked ectoenzyme of renal proximal tubules. Udpase activity was decreased in urine samples of acute and chronic renal failure patients. This study was undertaken to examine the effect of chitosan, a deacetylated derivative of chitin, on RDPase from rat kidney in vivo. Rats were fed with chitosan (0.1% in distilled water) for 3, 8 and 15 months and the urine samples were collected followed by ammonium sulfate precipitation (50~75% saturation). The activity of Udpase was measured with the modified fluorometric method of Ito et al (1984) and the protein was related with band intensity of SDS-electrophoresis. Approximately 4-folds increase of Udpase was observed in the chitosan fed rats for 3 months and such increase was less prominent in rats of 12 months or older. These results suggest that chitosan may elevate the renal function and speed up the recovery from renal failure, or even prevent the renal diseases.

[PC1-25] [04/18/2002 (Thr) 14:00 - 17:00 / Hall E]

Genetic structure responsible for catechol catabolism in *P.cepacia* G4

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The meta-cleavage pathway for catechol is one of the major routes for the microbial degradation of aromatic compounds. *Pseudomonas cepacia* G4 grows efficiently on toluene, cresol, or phenol via a plasmid-encoded catechol 2,3-dioxygenase and a subsequent meta-cleavage pathway. A recombinant plasmid pCNU 301 is a 23.0-kb BamHI restriction endonuclease-cleaved DNA fragment cloned from the chromosome of *Pseudomonas cepacia* G4. The pCNU 301 contains tomBCEGFD gene cluster which can encode six enzymes catabolizing catechol to acetyl CoA. In this study nucleotide sequences of tomBCEGFD gene encoding catechol-2,3-dioxygenase(C23O), 2-hydroxymuconic semialdehyde dehydrogenase (HMSD), 2-hydroxypenta 2,4-dienoate hydratase(HPDH), acetaldehyde dehydrogenase(ADH), 4-hydroxy-2-oxovalerate aldolase, and 4-oxalocrotonate decarboxylase were determined. The catechol 2,3-dioxygenase gene(tomB) was consisted of 945 bases. Amino acid sequence of the tomB gene product exhibited 82% identity with that of catechol 2,3-dioxygenase from *P. putida* UCC2. The 2-hydroxymuconic semialdehyde dehydrogenase gene(tomC) was consisted of 1458 bases. Amino acid sequence of the tomC gene product exhibited 78% identity with that of 2-hydroxymuconic semialdehyde dehydrogenase from *P. putida* CF600. The 2-hydroxypenta 2,4-dienoate hydratase gene(tomE) was consisted of 783 bases. Amino acid sequence of the tomE gene product exhibited 81% identity with those of 2-hydroxypenta 2,4-dienoate hydratase from *Pseudomonas* sp. LB400 and *P. pseudoalcaligenes* KF707. The acetaldehyde dehydrogenase gene(tomG) was consisted of 912 bases. Amino acid sequence of the tomG gene product exhibited 88% identity with those of acetaldehyde dehydrogenase from *Pseudomonas* sp. LB400 and *P. pseudoalcaligenes* KF707. The 4-hydroxy-2-oxovalerate aldolase gene(tomF) was consisted of 1047 bases. Amino acid sequence of the tomF gene product exhibited 87% identity with that of 4-hydroxy-2-oxovalerate aldolase from *Comamonas testosteroni* TA441. The 4-oxalocrotonate decarboxylase gene(tomD) was consisted of