We investigated what the high expression of Nramp2 influence pH dependent lead uptake in Astrocytes. The treatment of Deferoxamine increases mRNA level of Nramp2 in astrocytes. It was time- and concentration-dependent, and saturable. Lead uptake in astrocytes increased time-, pH-, and concentartion-dependently, and was saturable. At pH 7.5 it was the highest level. It was proportional to the amount of Nramp2 expression in pH 5.5, but not proportional to it at pH 6.5 and 7.5. We may suggest that Nramp2 in astrocytes functions at a low pH.

[PA1-68] [10/18/2001 (Thr) 14:00 - 17:00 / Hall D]

Study of diabetic animal model

Kim YoungLim[O] Chung SungHyun

경희대학교 약학대학 약물학교실

To compare the characteristics of diabetic animal models, several mice strains aged 6 week, KKAy, NZO, C57BL/6J obese(ob/ob) mice with long-lasting genetic diabesity and C57BL/6J mice with high-fat diet induced diabesity were studied for 20 weeks. We determined plasma glucose, body weight biweekly and serum insulin, creatinine, urine albumin, plasma HbA1c, total cholesterol, triglyceride levels at 10, 20 week. We also examined PPAR gamma, GLUT4, TGF beta 1, fibronectin protein expressions by immunoblotting and glucokinase, glucose-6-phosphatase enzyme activities. Ob/ob mice exhibited marked obesity, hyperglycemia, hyperinsulinemia and glucokinase activities were decreased, glucose-6-phosphatase activities increased at 20 week when compared to those of 10 week. High-fat diet induced diabetic mice showed remarkable weight gain rate and KKAy mice showed increased triglyceride, total cholesterol, HbA1c levels at 20 week. At 20 week, renal TGF beta 1 and fibronectin protein expressions increased, skeletal muscluar GLUT4 decreased in all strains, whereas adipose PPAR gamma decreased in only high-fat diet induced diabetic mice when compared to those of 10 week.

[PA1-69] [10/18/2001 (Thr) 14:00 - 17:00 / Hall D]

Increase in the Expression of Fibrinogen B β Chain, B Cell Translocation Gene1 and Thyroid Hormone Responsive Protein Genes in the Liver of Rats with Protein-Calorie Malnutrition by DD-PCR

Lee AeKyung[O], Kang KeonWook, Kim YoonGyoon, Cho MinKyung, Lee MyungGull, Kim SangGeon

College of Pharmacy, Seoul National University, Seoul 151-742, Korea ([O] Predoctoral Candidate of Duksung Women's University)

Protein-calorie malnutrition (PCM), as one of global health problems, arises during protein and/or energy deficit due to disease and nutritional inadequacy. Previously, we showed that PCM elicited oxidative stress with activation of the phase II detoxifying gene expression, which was reversed by cysteine supplementation. As part of the attempts to identify the cellular adaptive responses and the associated gene expression during PCM, the current study was initiated to analyze the genes differentially expressed in the rat during PCM. Among 1,916 bands amplified, 85 putative differentially amplified bands were enhanced by PCM in the liver, while the expression of 64 bands was suppressed. Northern and/or reverse transcription-polymerase chain reaction (RT-PCR) analyses revealed that PCM increased the expression of fibrinogen B β chain, B cell translocation gene1 (BTG1) and thyroid hormone responsive protein (THRP) mRNAs. The increase in the hepatic fibrinogen B β chain mRNA was not prevented by cysteine supplementation. Cysteine was also active in reversing the increase in BTG1 mRNA during PCM. Northern blot analysis revealed that THRP, highly expressed in the brain in a tissue-specific manner, was induced by PCM and that cysteine supplementation abolished the THRP induction. Conversely, the level of hepatic albumin mRNA was markedly decreased by PCM, which was partially restored by cysteine supplementation. Differential display RT-PCR analysis allowed us to identify the genes that are responsive to oxidative stress during PCM and to characterize the differential role of