

HeLa cell lysates bound to E6AP protein, there is one protein not yet identified. Heat shock cognate 71 kDa protein, CTCL tumor antigen se2-5, HLA-A24, Ku70-binding protein, amphiphysin isoform 2, GR AF-1 coactivator-1, eukaryotic translation initiation factor 4A, and BTB domain protein, were bound to E6AP. These results suggest that E6AP can have several functions by interacting with several proteins related to transcription/translation and cytoskeleton, and heat shock cognate protein in cervical carcinoma cells (This work was supported from the Molecular Medicine Program M1-0106-00-0078, MOST).

[PC1-28] [04/18/2002 (Thr) 14:00 - 17:00 / Hall E]

Study of Metastatic Potential of Gastric Cancer Cell Lines by Comprehensive Proteomic Analysis

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Several methods have been developed for the comprehensive analysis of gene expression in cancer cells. Usually these approaches in the postgenome era begin with either a portion of the cellular transcriptome using cDNA microarray or a portion of the cellular proteome using a 2-D gel and MALDI-TOF analysis. Each approaches has distinct conceptual and methodological advantages and disadvantages. Whilst many detailed biochemical studies have been performed about them there are few clinically relevant studies using genomic and proteomic methods. Gastric cancer is very popular in Korea and metastasis of it is a main obstacle for the treatment of it. Like as many other cancers human gastric carcinoma often metastasizes to lymph nodes, but the mechanisms responsible for lymph node metastasis are not clearly understood. To investigate them, the factors associated with metastasis were identified using proteomic method. We have studied the protein expression profiles of gastric cancer cell line, OCUM-2M LN, with a high rate of lymph node metastasis and its parental cell line, OCUM-2M, which exhibited a low rate of lymph node metastasis by two-dimensional (2D) gel electrophoresis and MALDI-TOF. Protein expression profiles of OCUM-2MLN and OCUM-2M cell lines were generated by two-dimensional electrophoresis (2-DE). Twenty proteins in these cell lines were identified as differentially expressed ones. Mass spectrometric analysis of these spots revealed the metastasis-stimulatory or inhibitory proteins. This finding may explain a marked acceleration in metastatic potential of OCUM-2LN and we will discuss our findings based on known discovery.

[PC1-29] [04/18/2002 (Thr) 14:00 - 17:00 / Hall E]

The Investigation of joint diseases in Equine with Biochemical Factors: Analysis of synovial fluid and serum

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A modification of a colorimetric assay was used to determine synovial fluid total and individual sulfated-glycosaminoglycan concentration of joint disease in equine. For the identification of enzymatic digestion products of the equine synovial fluid, strong anion exchange-high performance liquid chromatography (SAX-HPLC) was performed. By the action of chondroitin ABC lyase, Three unsaturated disaccharides 2-acetamide-2-deoxy-3-O-(β -D-glucopyranosyluronic acid)-D-galactose(Δ Di-COS), 2-acetamide-2-deoxy-3-O-(β -D-glucopyranosyluronic acid)-6-O-sulfo-D-galactose(Δ Di-C6S) and 2-acetamide-2-deoxy-3-O-(β -D-glucopyranosyluronic acid)-4-O-sulfo-D-galactose(Δ Di-C4S) were produced from the equine synovial fluid. The synovial fluid low concentration of sulfated-GAG in abnormal samples. Total sulfated-GAG concentrations (mean \pm SD) were decreased in horses with joint disease (0.17 mg/ml \pm 0.12 mg/ml), but synovial fluid total sulfated-GAG concentrations of normal (0.82 mg/ml \pm 0.24 mg/ml). The mean value of HA on diluted normal and joint diseases serum were found to be 77.00 \pm 66.14 μ g/ml and 168.50 \pm 147.50 μ g/ml by labeled B-HABP. there appears to be some correlation between joint inflammation and circulating HA levels as determined by experimental studies of animals.