J Biotechnol Biomater 2012, 2:6
http://dx.doi.org/10.4172/2155-952X.S1.020

OMICS Group Conferences
Accelerating Scientific Discovery

3rd World Congress on
Biotechnology

September 13-15, 2012 Hyderabad International Convention Centre, Hyderabad, India

Serum based prospective biomarkers for early detection of hepatocellular carcinoma (HCC): A proteomic approach

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The completion of human genome project resulted in opening of new vistas for understanding the gene expression. A number of specialized fields of studies, the 'omics' have been initiated. The proteomics is one of these branches that deals with the analysis of protein profile of a cell or tissue under different physiological condition. All the metabolic activities of cell are regulated directly or indirectly by proteins. The analysis of proteins, therefore, gives better insight into the metabolic status of cell than studying its genomics. This approach is now being used for discovering novel biomarker(s) that can be used to diagnose, predict the susceptibility and monitor progression of diseases. Direct analysis of serum or other biological fluids is one of the most convenient strategies for the search of protein biomarkers. Hepatocellular carcinoma (HCC) is an international problem. It is the third most prevalent cancer and the fifth leading cause of cancer deaths worldwide (WHO-2008). The current standard diagnosis of HCC is based on the detection of serum α-fetoprotein (AFP) level. However, AFP has relatively low sensitivity (64.8% - 78%) and low specificity (50% - 93%). More reliable and accurate biomarkers are urgently needed to overcome the shortcoming of the current tools for HCC diagnosis. We report the development of an animal model for study of HCC by modifying the Solt –Farber protocol. The protein profiles of serum have been analysed by 1D SDS PAGE and 2D electrophoresis. Few specific changes in proteins profiles have been detected that bear correlation with disease progression. Marker enzymes have also been monitored to decipher the disease condition. Histopathology of liver tissue was performed to confirm liver damage. Differentially expressed proteins and the novel proteins that are expressed during tumor progression have been characterized by MALDI-TOF and LC-MS/MS techniques. The expressions of genes for the proteins of interest are in progress in our laboratory. Further, patient sera from clinically confirmed cases have been used to validate these markers. Our results suggest that some of these proteins have showing potential for the development of biomarker(s) for early detection of HCC.

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Identification of Lactobacillus Bacteria involved in municipal solid waste leachate biodegradation

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Bio-digestion comprises a series of processes in which microorganisms break down biodegradable materials. The digestion process begins with hydrolysis in which bacteria transform complex polymers into monomers. In the second stage, acidogenic bacteria transform the products of hydrolysis into volatile fatty acids. Many authors have suggested that during anaerobic digestion, long chain fatty acids are converted to propionic acids, butyric acids and acetic acids. Then propionic and butyric acid are converted to acetic acid. We observed that lactic is also produced in good quantity during anaerobic digestion. For identification of Lactobacillus Bacteria (LAB), we first enriched the leachate in MRS media, which is specific for LAB. Two reactors were set up, one containing acidified and filtered leachate (to remove humic acid portion) with MRS and second one with crude leachate with MRS. Then the reactors were first run aerobically. Genomic DNA was extracted from the reactor samples and subjected for PCR using lactobacillus specific primer. No PCR product was obtained. Then the reactor was subjected to anaerobic conditions. After running the reactor for more than 21 days, in anaeorobic condition genomic DNA was extracted and subjected to PCR using lactobacillus specific primers. PCR products were cloned and sent for sequencing. Result shows that both homo lactic acid and hetero lactic acid producing bacteria may be present in the MSW leachate.

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