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Abstract
Proteome analysis with protein separation by two-dimensional polyacrylamide gel electrophoresis (2-D PAGE) and mass spectrometric measurement is utilized for comprehensive identification of proteins in various biological samples. The aim of the present study was to analyze the whole pattern of urine proteins present in urine samples of healthy persons in comparison to that present in the urine samples of patients with bladder cancer, and to find out the different proteins as potential biomarkers. Urine samples collected from 10 bladder transition cell carcinoma (BTCC) patients and 10 healthy volunteers. In this study, two-dimensional (2-D) gel electrophoresis was used to identify the differentially expressed proteins in BTCC patients and healthy individuals. Urine samples were dialyzed to remove any interfering molecules and concentration by lyophilization. With no fractionation, the proteome maps acquired in this study likely represents the total urine proteins. The proteome maps of urines collected from individual healthy and BTCC patients were compared in pairs. Protein spots were visualized using silver staining. Several spots, which have differential expression that present in urine samples of BTCC patients and healthy persons. The differentially expressed protein spots were scored when the difference is greater than 1.5-fold in magnitude. Of the deregulated spots that were consistently found in our studies, six were down-regulated and five were up- regulated in BTCC patients as compared with normal.These de-regulated proteins was identified using liquid chromatography electro-spray ionization tandem mass spectrometry (LC/MS/MS). Application of this methodology provides a coherent analysis of the urine proteome and contributes to the generation of the urine protein map in health and disease. The down-regulated spots in BTCC were identified as human haptoglobin precursor，human haptoglobin precursor，unknow，heparan sulfate proteoglycan perlecan，inter-alpha-trypsin inhibitor heavy chain H4 precursor，AMBP protein precursor. The up-regulated spots were identified as而peroxiredoxin 2，heparan sulfate proteoglycan perlecan，protease serine 1 fragment，heparan sulfate proteoglycan perlecan ，AMBP protein precursor respectively.
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