

Proteomics and bladder cancer: Opportunities and challenges

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PAJO, December 2010, 3(4): 40-45

Abstract

Recent progress in life science technology and the availability of much information on genes obtained by genome analysis has enabled us to analyze the changes of proteins on a large scale. Sets of proteins are called proteomes, and proteomics is the scientific field of proteome analysis including differential, post translational modification and interaction analyses. Various proteomic approaches, particularly two-dimensional gel electrophoresis (2-DE), mass spectrometry and protein chip methods, are very useful for acquiring proteomes in cells, tissues and body fluid, for analyzing interactions between a protein and other biofactors including proteins. A proteomic analysis is also useful for determining biomarkers of diseases and key proteins involved in various stages of metabolism such as differentiation, cell cycle and apoptosis. The proteomic approach to revealing urologic diseases, including bladder tumor, has only recently been introduced. The proteomes of malignant and benign samples from bladder cancer have been compared using the 2-DE technique; the disease specific proteins have been identified, and their expressions have been assessed.

The aim of this review is to illustrate the proteomic technologies that have emerged for comprehensive and high-throughput protein analysis and to provide more detailed of their application in bladder cancer research and diagnosis