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URINARY BIOMARKERS FOR BLADDER TRANSITIONAL CELL CARCINOMA

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Bladder cancer ranks 9th in world cancer incidence and has a high complex nature. The most prevalent form of bladder cancer is transitional cell carcinoma (TCC). The non-invasive diagnosis of bladder cancer is principally based on the urinary cytology. This test has a high specificity but a low sensitivity and an intrinsically subjectivity that depends on the pathologist expertise.

Today's efforts to diagnose early stages of bladder cancer and to predict the progression of the disease are based on the discovery of urinary biomarkers. Proteomic technologies are providing the tools needed to discover and identify disease-associated biomarkers. In this context, the objective of the present work is to use proteomic approaches for the identification of novel molecular markers in urine samples.

Urine samples from 10 bladder cancer patients and 10 control subjects were used to perform a differential expression analysis. We have designed a simple protocol to separate the cellular and soluble components from urine and analyze them separately. Protein extracts from urine cells were obtained and analyzed using 2D-DIGE technology. Peptide profiles from the soluble component were determined by MALDI TOF mass spectrometry.

Several differential protein spots were detected ($p<0.05$ after FDR correction) by 2D-DIGE experiments from which only 5 different proteins were identified. One of these proteins showed over a ten-fold increase in tumor samples and it being evaluated as a biomarker by immunohistochemistry. Peptide profiles are also capable to differentiate between the two groups of samples.