Mini-symposium

Bioinformatics Approaches to Identify Biomarkers of Acute Kidney Injury

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Kidney disease is a major issue of public health with significantly increased prevalence and high mortality rates. Kim-1 (kidney injury molecule-1) is highly expressed in renal damage of various etiologies and has been well recognized as diagnostic and therapeutic markers of acute kidney injury. To elucidate the transcriptional regulation of Kim-1, we performed bioinformatics analyses of expression profiles obtained from I/R injury animal models. Chk1 and STAT3 showed temporal and regional coincidence of mRNA expression with that of Kim-1. Further molecular validation suggests that Chk1 and STAT3 as critical upstream regulator of Kim1 expression. Using the same expression profiles, we also identified fibrinogens whose RNA expression patterns are similar to those of Kim-1 (kidney injury molecule 1). The urinary excretion of fibrinogens was able to distinguish human patients with acute or chronic kidney injury from healthy volunteers and Fgβ-derived Bβ15-42 peptide showed renal protective effects after I/R injury. Functional analyses showed that genes associated with the molecular functions of cell cycle, immunity, inflammation, and apoptosis are globally activated during the renal regeneration after I/R injury but the genes encoding various transporters and metabolic enzymes were down-regulated. In addition, these expression signatures largely overlap with those of early kidney development. Taken together, our findings highlight the need of bioinformatics approach to reveal novel biomarkers associated with acute kidney injury and also to advance our understanding of molecular pathophysiology.