

Potential Biomarkers in the Diagnosis of Acute Kidney Injury

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Editorial

Acute Kidney Injury (AKI) occurs when the gradual reduction of the filtering capacity of the kidneys leading to failure of the kidney. The rise in the blood potassium levels leads to paralysis in the extreme causes of AKI. It causes approximately 47,000 deaths a year and is alluded to as a silent killer since most patients do not recognize they have it till the condition is well advanced. Diagnosis of acute kidney injury includes the urine output measurements and serum creatinine levels that serve as the benchmark.

The metabolic changes in AKI are identical for pediatric and neonatal patients contrary to previous theories, so the differences in metabolite profiles could facilitate the development of a novel method for early identification of AKI patients.

Nicotinamide Adenine dinucleotide (NAD), a molecule involved in metabolism also serves as a key to the aging process when working with the gene called PGC1 alpha provides protection for the kidneys. They hypothesized that mitochondria might also be serving as an essential and early target for the various risk factors leading to kidney injury as the kidney is a highly metabolic organ that utilizes mitochondrial metabolism to generate adenosine triphosphate (ATP) that enables it to filter blood and remove toxins from the body.

Studies say that doctors should check for protein in the urine before determining the blood pressure target for patients with kidney disease. If the patient has protein in the urine, the reduced blood pressure target has the ability to slow down the progression of AKI.

Nakagawa T, et al. in their review discussed the role of fructose in several types of cancers and proposed that blocking

fructose metabolism could be an additional therapy while discussing the novel approaches to alleviate the cancer growth [1].

Trachtman H, et al. in their Short-communication on Environmental chemicals and kidney diseases stated the importance of comprehensive and realistic developments in the analytic methods to evaluate the impact of mixtures of chemical exposures serially over time in adults that will enable more effective exposure reductions approaches for the recognition of the exposure to environmental chemicals and hazards like air and water pollution as they are beyond the control of individuals [2].

Mylsamy S, et al. in their analysis using bioinformatics tool identified the key genes and the associated pathways to understand the mechanism behind the tumor progression and its diagnosis. 196 up regulated genes and 279 down regulated genes out of 475 differentially expressed genes were obtained from the four data sets analysis. The dysregulated expression of CCNB2, NUSAP1 and ADAM22 play a vital role in G2/M transitions and promotes the mitotic cell division. They can be used as a marker and also therapeutic target.

References

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