Indian Journal of Experimental Biology
Vol. 62, November 2024, pp. 884-894
DOI: 10.56042/ijeb.v62i11.5858

# Exploring urinary biomarkers for the diagnosis of diabetic and hypertensive chronic kidney disease: A promising pilot study

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*Received 27 September 2023; revised 28 February 2024*

In the current clinical setting, conventional serum biomarkers such as serum creatinine (Scr) and estimated glomerular filtration rate (eGFR) have several lapses in chronic kidney disease (CKD) diagnosis. Diagnosing CKD using non-invasive methods is crucial for implementing prompt therapeutic interventions and preventing disease progression. This study aims to identify the potential diagnostic urinary biomarkers and their correlation with existing renal markers, Scr, eGFR, and proteinuria in diabetic and hypertensive CKD. RNA was extracted from eighty-two urine samples of CKD patients and healthy controls (HC) and reverse transcribed for gene expression analysis using quantitative polymerase chain reactions. The expression of *NGAL*, *MMP9*, *ANXA3*, *OLFM4*, *PI3*, and *PRMT3* genes was analyzed relative to the reference gene, *B2M*. Fold changes (FC) in gene expression in diabetic nephropathy (DN), and hypertensive nephropathy (HT) were calculated against HC. $Log_2$ normalized FC was used to determine significance levels and correlation with existing serum markers. *NGAL*, *ANXA3*, and *OLFM4* exhibited the highest upregulations in DN with mean $Log_2$FC 1.42, 2.66, and 5.87, respectively. A two-fold increase in *NGAL* FC was observed in early DN than in late DN, suggesting its potential as an early urinary biomarker for DN. *PI3* and *MMP9* were upregulated in HT patients with higher FC values. *PRMT3* showed a significant negative correlation ($P<0.05$) in HT patients with Scr ($r=-0.738$) and proteinuria ($r=-0.906$). The gene panels including *ANXA3*, *OLFM4*, and *NGAL*, and *PI3*, *PRMT3*, and *MMP9*, could have potential diagnostic value in DN and HT, respectively.

**Keywords:** Gene expression analysis, Non-invasive diagnosis, RT-qPCR (Reverse transcription quantitative polymerase chain reaction), Serum biomarker