

## **ENVIRONMENTALLY INFLUENCED GENE EXPRESSION IN PATIENTS WITH CHRONIC KIDNEY DISEASE LIVING IN THE DRY ZONE OF SRI LANKA**

**S. Sayanthoran<sup>1</sup>, D.N. Magana-Arachchi<sup>1\*</sup>, S.D.S.S. Sooriyapathirana<sup>2</sup>,  
T. Abeysekera<sup>3</sup> and L. Gunarathne<sup>3</sup>**

<sup>1</sup>*Cell Biology, Institute of Fundamental Studies, Kandy, Sri Lanka*

<sup>2</sup>*Department of Molecular Biology and Biotechnology, Faculty of Science, University of Peradeniya, Sri Lanka*

<sup>3</sup>*District Hospital, Girandurukotte, Sri Lanka*

*\*dmaganaarachchi@gmail.com*

Chronic kidney disease of unknown aetiology (CKDu) is a major contributor to chronic kidney disease (CKD), highly prevalent in the dry zone of Sri Lanka. Most current hypotheses for its aetiology are related to the environment. As environmental stimuli greatly influence gene expression, the aim of this study was to analyze the expression patterns of genes associated with drug/xenobiotic metabolism (cytochrome P450 2D6-CYP2D6), oxidative stress (glucose-6-phosphate dehydrogenase-G6PD), kidney tissue damage (fibronectin - FN1), and diabetes/cardiovascular diseases (insulin like growth factor binding proteins 1 and 3 - IGFBP1, IGFBP3) in CKDu and CKD patients and compare with healthy individuals.

Ten CKDu patients and four CKD patients were selected from the Renal Clinic of the District Hospital Girandurukotte, a CKDu endemic area in the Uva Province of Sri Lanka. Three apparently healthy individuals served as controls. All were between 30 and 60 years of age, with a male to female ratio of 2:1. Reverse transcriptase quantitative PCR (RT-qPCR) using gene specific primers and dual-labelled hydrolysis probes, was done on RNA extracted from whole blood. The average threshold cycle ( $C_T$ ) of healthy individuals was considered as a baseline to calculate fold changes in the patients, using  $2^{-\Delta C_T}$ . Fold changes were correlated with disease aetiology, stage of disease, alcohol intake and smoking history.

On preliminary analysis, CYP2D6, G6PD and IGFBP3 showed decreased expression in CKDu patients compared to healthy individuals ( $p < 0.05$ ). CYP2D6 expression was further reduced in CKD patients compared to CKDu patients ( $p > 0.1$ ). IGFBP1 showed positive correlation ( $p < 0.1$ ), whereas IGFBP3 showed negative correlation ( $p < 0.1$ ) with the stage of disease. G6PD showed positive correlation ( $p > 0.1$ ) with alcohol intake, and negative correlation ( $p > 0.1$ ) with the stage of the disease. Other genes studied did not show statistically significant correlation with the parameters studied.

Differential expression of the genes in diseased individuals compared to healthy controls indicates their involvement in the disease process. However, further in-depth analyses of a larger population are needed to validate these preliminary results and to link expression patterns to biochemistry and pathophysiology of the disease.

*Financial assistance given by the National Research Council of Sri Lanka (NRC-11-059) and the Institute of Fundamental Studies, Kandy, Sri Lanka is acknowledged.*