Can Urinary HNF1B Expression Be A Biomarker For Multicystic Dysplastic Kidney?

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Although HNF1β is known to be as a transcription factor in many stages of renal embryonic development, it is important to investigate the level of expression in renal-derived cells in urine to understand its effect on epigenetic control. Thirty nine patients (0-21 years) with multicystic dysplastic kidney followed up from Marmara University School of Medicine, Pediatric Nephrology were included. After isolation of DNAs from blood, DNA molecules were subjected to methylation-sensitive and methylation-dependent endonuclease cleveage, methylated and unmethylated DNA fractions in the promoter region of the HNF1β gene were detected by real-time PCR. In patients with HNF1β methylation, urinary HNF1β expression of isolated renal cells was analyzed. Of all patients, 10.26% of them had HNF1β methylation. Among them one patient had a disappereance/decrease of the cysts. In one patient, cysts did not show any size change. HNF1β gene expression analysis was performed from urine samples of patients with HNF1β methylation and the group with methylated HNF1β had lower expression level compared to control group. Herein, the analysis of urinary HNF1β gene expression using a non-invasive method was performed for the first time in patients with HNF1β promotor methylation with Multicystic Dysplastic Kidney. The use of a more easily applicable, non-radical method instead of histopathological analysis of biopsy specimens will provide significant diagnostic advantage for these patients. Although no statistically significant relationship was found, this is the first study in this field, that gives opportunity to elucidate the pathogenesis of the disease. Our results are preliminary findings to evaluate the downstream effects of HNF1β methylation and in addition these results provide hope about repairing the meachanisms involved in the pathogenesis.

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