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Culturable bacterial pathogens in midstream urine of chronic kidney disease patients in Vavuniya, Sri Lanka: A preliminary study

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Background: Contribution of the midstream urine microbiome to chronic kidney disease (CKD) is clinically relevant, yet it's understudied**.**

Objectives: To identify bacteria from midstream urine of CKD patients with comorbidities of diabetes mellitus (DM), hypertension (HT) and other causes, in Vavuniya.

Methods: A total of seventeen (n = 17) midstream clean-catch urine samples were collected from CKD patients (56.59 ± 12.91 years) at the District General Hospital, Vavuniya, belonging to CKD + HT (n = 8), CKD + DM (n = 2), CKD + HT + DM (n = 3) and causes of CKD other than DM and HT (n = 4). Non-CKD healthy controls (n = 8; 56 ± 11 years) were included for comparison. Samples were transported on ice and immediately refrigerated at 4°C until processed. 10µl per sample was inoculated onto Luria-Bertani (LB) agar plates in duplicates and incubated aerobically at 37°C for 24 hours. Morphologically different bacterial colonies were subcultured in LB broth to obtain pure isolates, which underwent gram staining, and biochemical analyses for preliminary identification.

Results: Mean colony count for CKD subjects was 2,500 ± 967 CFU/mL and 286 ± 181 CFU/mL for controls. The CKD + HT + DM group had the highest mean colony count. In total, 24 bacterial isolates were obtained from the patients' urine of which 45.8% were gram positive cocci, 37.5% were gram negative rods and bacterial genera Staphylococcus (33%), Streptococcus (12.5%), Pseudomonas (4%), Klebsiella (4%) and Proteus (4%) were identified. *Staphylococcus, Corynebacteria, Proteus, Escherichia,* and *Citrobacter* were found in controls.

Conclusion: Various viable uropathogens in the midstream urine of CKD patients were identified using culture-based tests. This preliminary study is currently ongoing to further identify the midstream urine microbiome in CKD with molecular techniques too, as culture alone is insufficient.

Keywords: *Chronic Kidney Disease, Midstream urine microbiome*