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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 ( $56.59 \pm 12.91$  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 ( $n = 8$ ;  $56 \pm 11$  years) were included for comparison. Samples were transported on ice and immediately refrigerated at  $4^{\circ}\text{C}$  until processed.  $10\mu\text{l}$  per sample was inoculated onto Luria-Bertani (LB) agar plates in duplicates and incubated aerobically at  $37^{\circ}\text{C}$  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  $2,500 \pm 967$  CFU/mL and  $286 \pm 181$  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*