

DIVERSITY OF MIDSTREAM URINARY BACTERIA IN CHRONIC KIDNEY DISEASE PATIENTS: A PRELIMINARY CULTURE-BASED STUDY

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Introduction: Chronic kidney disease (CKD) is a global disease. Diabetes and hypertension are major risk factors for CKD, while bacterial colonization in the urinary system causes rapid disease progression. **Objectives:** To identify the urinary bacterial diversity in diabetic and hypertensive nephropathy patients rather than identifying urinary infections and study the alteration in bacterial diversity with CKD progression. **Methods:** Mid-stream clean catch urine samples were collected from the study subjects ($n=105$), including diabetic nephropathy (DN), hypertensive nephropathy (HT), CKD with both diabetes and hypertension (HD), other aetiology of CKD (O), and healthy controls (HC). Urine samples were cultured using cystine lactose electrolyte-deficient agar medium, and a panel of biochemical tests was used to identify the bacterial species. **Results:** Bacterial growth was observed in only 31.43% of urine samples. *Escherichia coli*, *Klebsiella* spp., and *Staphylococcus aureus* were predominantly identified in DN patients with the highest mean bacterial load (DN: $>10^5$ CFU mL⁻¹, HT, HD, and O: between 10^4 and 10^5 CFU mL⁻¹ and HC: $<10^4$ CFU mL⁻¹). *Pseudomonas* spp. was the most predominant bacteria isolated from HT, HD, and O CKD study groups. Further, *Escherichia coli* and *Klebsiella* spp. had been predominantly isolated from early-stage (stages 1-3) CKD patients. In contrast, *Pseudomonas* spp. and *Enterobacter* spp. had been isolated from late-stage (stages 4-5) CKD patients. **Conclusions:** The findings suggest that diabetes predisposes to urinary bacterial colonization in CKD, while greater bacterial diversity is associated with increased disease progression. Further validation is required with a large cohort before clinical application.

Keywords: Chronic kidney disease, Diabetes, Hypertension, and Urinary bacteria

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