Salivary and Urinary Metabolomics Study in IgA Nephropathy Patients

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Introduction: Immunoglobulin A Nephropathy (IgAN) is the most common primary glomerulonephritis, often leading to end-stage kidney disease in 20–40% of cases. Despite extensive research on urinary and serum metabolomics, salivary metabolomics remains unexplored. This study investigates metabolomic alterations in IgAN using both salivary and urinary analyses and examines potential correlations between these biofluids.

Methods: Metabolomic profiling was performed using liquid chromatography-high resolution mass spectrometry (LC-HRMS) on saliva and urine samples from 16 IgAN patients and 13 matched controls. Data were processed using TidyMass and MetaboAnalyst, with metabolite annotation via HMDB, MassBank, and MoNA. Pathway analysis was conducted using the KEGG database, with statistical significance set at $p < 0.05$ or FDR < 0.05.

Results: Salivary analysis identified 42 metabolites, with four significantly altered in IgAN patients. Picric acid, Buphedrone, and Deoxyadenosine were elevated, while N-Acetylneuraminic acid was reduced, implicating ABC transporters, purine metabolism, and neurotransmitter pathways. Urinary analysis revealed 138 metabolites, with 14 significantly altered, primarily affecting the pentose phosphate pathway. No significant correlation was observed between urinary and salivary metabolomic profiles.

Conclusion: Though urinary and salivary metabolomes showed distinct alterations, our study only supported N-Acetylneuraminic acid as a potential IgAN biomarker.

Keywords: urine, saliva, LC-MS/MS, pathway analysis, N-Acetylneuraminic acid