Advancing Early Detection of Kidney Cancer (Year 2): A Novel Automated Workflow for Proteomic Profiling of Urinary Extracellular Vesicles

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Renal Cell Carcinoma (RCC) is the deadliest urological disease in the world, accounting for more than 200,000 deaths annually. Detection before metastasis can improve 5-year survival rates drastically, from 16% to 92%. However, current diagnostic methods for RCC are high-cost, impractical for early diagnosis (MRI, CT), and invasive (tissue biopsies). Extracellular vesicles (EVs) are emerging as a promising source of disease biomarkers for non-invasive early-stage diagnoses, but a bottleneck in EV sample processing restricts their immense potential in clinical applications. Existing methods are limited by low EV yield and integrity, slow processing speeds, low sample capacity, and poor recovery efficiency. I aimed to address these issues with a high-throughput, automated workflow for EV isolation, EV lysis, protein extraction, and protein denaturation. The automation can process clinical urine samples in parallel, resulting in protein-covered beads ready for various analytical methods, including immunoassays, protein quantitation assays, and mass spectrometry, the proteomic "gold standard." Compared to the standard manual lysis method for contamination levels, efficiency, and consistency of EV isolation, the automated protocol shows reproducible and superior proteomic quantitation with less than 10% coefficient of variation and 15% greater protein and peptide identification (<0.001 false discovery rate). The automation holds 4X sample capacity, reduces manual labor by 6-10X, and expedites total processing speed by 2-3X. This novel, fully automated workflow represents a practical EV extraction and profiling approach that can benefit both clinical and research applications, streamlining biomarker discovery, tumor monitoring, and early cancer diagnoses.

Awards Won:

Fourth Award of $500