Trapped Ion Mobility Spectrometry (TIMS) and Parallel Accumulation Serial Fragmentation (PASEF) for Urine Metabolomic Profiling

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Human urine is an easily accessible biofluid that has become a promising sample for non-invasive discovery of biomarkers. Urine metabolomics could reveal metabolic differences in response to a specific disease or therapeutic intervention. Urine is mainly free from interfering proteins or lipids but complicated by the presence of metabolic breakdown products from a wide range of by-products derived from diet, drugs, environmental contaminants, endogenous waste and bacterial metabolites, many of which are poorly characterized. Therefore, a robust method for metabolite identification is essential to maximize the potential of utilizing urine as a diagnostic specimen. Here, we evaluate the potential of improving traditional LC-MS workflows for urine metabolomics by implementing trapped ion mobility (TIMS) with parallel accumulation serial fragmentation (PASEF) technology.