Professor Hookeun Lee at Lee Gil Ya Cancer and Diabetes Institute (LCDI), College of pharmacy, Gachon University utilizes proteomics and metabolomics platforms to explore novel biomarkers from human diseases.

The proteomics laboratory at LCDI serves as the Agilent’s reference laboratory for complete glycol-proteomics and biomarker discovery workflows.

Professor Lee is focusing on delivering solutions for personalized drugs for individual and development of automated sample preparation workflow’s to handle large number of clinical samples. This can only be possible with the collaboration of Agilent to provide access to the latest technologies to Gachon University like automated sample preparation platform Assay-Map Bravo, and LC-MS/MS coupled Q-TOF and MRM machines from Agilent.

Automation of the entire proteomic pipeline after sample preparation to process for LC-MS/MS can result in minimal loss of sample information. The assay bravo can handle 384 samples at a time for trypsinization which can drastically reduce the time required for analysis.

With the platforms, his recent researches focus on establishment of high-throughput dual omics analysis of proteomics and metabolomics. This has been enabled by recently released Mass Profiler Professional software, in which quantitative proteomic and metabolomics data were efficiently correlated and analyzed.

As a one of study, we used this automated trypsinization protocol to apply combined phospho- and glycoproteome analysis in necprocalcinosis tissue of phytate-fed rats.

By using 1 mg of protein from kidney tissue lysates from normal and disease rats, we concurrently identified 437 glycosites/358 phosphosites and 468 glycosites/369 phosphosites in normal and disease kidneys, respectively, by liquid chromatography/tandem mass spectrometric analysis.

Compared with individual PTM analyses, the combined PTM analysis clearly provides more broad implications for PTMs related to the pathological status and discovery of biomarker candidates. Furthermore, the combined protocol thoroughly showed its advantages in enrichment efficiency and biological interpretation compared with current methods.

Using Agilent chip-cube nano LC-QTOF MS system, intensity based label-free quantification of peptides were carried out for quantitative proteome analysis. High reproducibility and sensitivity of the LC-MS system induced to analyze specific signal pathways enrichments from the proteome quantifications.

**RELATED INFORMATION:**
