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GLOBAL PROTEOMICS CONFERENCE

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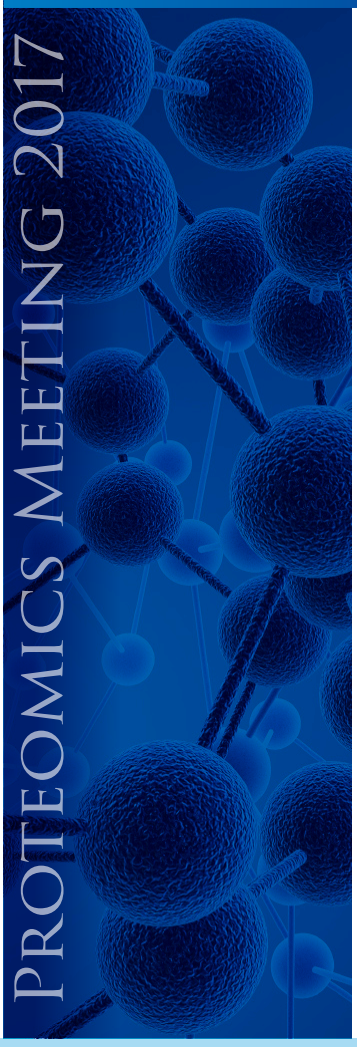

Development and validation of targeted metabolomics for clinical applications

Metabolome, representing a vast array of analytes, is the ultimate functional equivalent of the genome and can be studied through small molecules (<1500 Da) identification and quantification. The global metabolome influences the individual phenotype through environment and clinical interventions. Metabolomics has been shown to identify relevant biomarkers responsible for/or associated with complex phenotypes in diverse biological systems. Combining metabolomics with genomics, transcriptomics and proteomics studies provides a higher level of understanding of the mechanism and the pathophysiology of many diseases and related clinical interventions. Metabolomics plays a major role in clinical practice as it represents >95% of the clinical laboratories routine work load. However, many of these metabolites require different analytical platforms and many clinically relevant metabolites are still not amenable to detection using routinely available assays. Mass spectrometry (MS) coupled with liquid chromatography (LC) is a robust and important analytical tool, where two almost universal techniques merge to accommodate the chemical diversity of the metabolome. Herein, we introduce the establishment of a comprehensive targeted metabolomics method for a panel of 225 metabolites using liquid chromatography tandem mass spectrometry. The sensitivity, reproducibility and molecular stability of each targeted metabolite were assessed under experimental conditions. Quantification of metabolites by peak area was linear, with minimal deviation (R2=0.98). Inter and intraday precision had an average coefficient of variation <20%. The method reported here is robust for the extraction of the maximum number of metabolites from different types of tissues and bio-fluids.

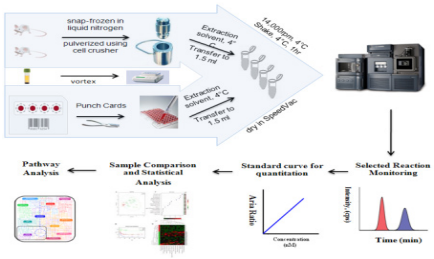

Figure-1: Workflow for targeted LC-MS/MS analysis of metabolites extracted from Dried Blood Spot (DBS), plasma, whole blood and tissues. Tissue samples were frozen on dry ice, stored at -80 oC and crushed in a crucible on liquid nitrogen just prior to extraction.

References

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Biography

Anas M Abdel Rahman has completed his PhD in Bioanalytical Chemistry in Proteomics at Memorial University of Newfoundland, Canada. In 2014, he was appointed as an Associate Scientist at the Research Center of King Faisal Specialist Hospital and as an Assistant Professor at School of Medicine at Al Faisal University. His current scientific interests are related to signaling pathways controlling the metabolic reprogramming in cancer. He has several publications in the field of proteomics and metabolomics.

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