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Mass spectrometry in regenerative medicine to promote translational resources to be implemented into personalized heathcare

Ilgar S Mamedov
LLC Chromsystemslab, Russia

A mass spectrometer detects the mass of ionized molecules. Many of these molecules are compounds found in biological fluids and are integral intermediates of clinical biochemistry. Metabolites are the substrates and products of the chemical reactions that constitute life. As such, they comprise an enormously heterogeneous mixture of compounds and compound classes (e.g., sugars, amino acids, lipids, organic acids and biogenic amines). This alone leads to significant issues with the provision of metabolomics, as technological methods ideal for the characterization of amino acids are likely to be not enough for the characterization of steroids. Despite this, most metabolomics platforms now detect hundreds to thousands of compounds, covering the majority key biochemical pathways. Good design of experiments is absolutely needs to a successful metabolomics analysis sample. For example, clinical samples are likely to be extremely variable and often even small changes in metabolite concentration are of interest and thus hundreds to thousands of samples per state may be required for sufficient statistical power. In contrast, well-defined cell culture experiments (for example, where cells are exposed to drug treatments) may be characterized by low variability and the effects may be large, so a handful of replicates may be sufficient. Whether one is performing a targeted or untargeted metabolomics analysis, the process of data analysis for MS is relatively unchanged. Statistical analysis is performed and the dataset is put about, regarding biochemical pathways, or in clinical studies, stratified with respect to clinical outcomes and patient data. When performing any analysis, it is critical to have a good understanding of the raw data, the statistics to be applied, the fundamentals of biochemistry and the biological question to be addressed. Generally, metabolomics can provide the greatly useful information in the medical field, the discovery of disease biomarkers, the finding of novel therapeutic agents and the examination of pathogenesis mechanisms behind various diseases. The present report describes a new method of diagnostics of illnesses of an exchange purines and pyrimidines with the use of HPLC the data is presented to combinations with electro spray mass spectrometry. Procedure of the analysis from pre-analytical stage to interpretation of the data of a liquid chromatography-mass spectrometry, quality assurance of the data of the analysis, mass spectrometer parameters and chromatographic research conditions of purines, pyrimidines and the metabolites is in detail described by the given technique.

Biography

Ilgar S Mamedov has completed his PhD in Dermatology and Biophysics at the Russian State Medical University, Russia. He continued his professional education in Clinical Laboratory Diagnostics at Russian State Medical University during 2003. He was an Associate Professor at the Russian State Medical University and was the Head of Clinical Diagnostic Laboratory at the Moscow Clinical Diagnostic Center. Currently he is the Director of the Chromsystemslab, Russia.

is_mamedov@mail.ru

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