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Complimentary LC- and GC-mass spectrometry techniques provide broader coverage of the metabolome

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The metabolome is difficult to characterize; there is a wide dynamic range of concentrations of metabolites, which are chemically and structurally diverse with various polarities and sizes. Thus creating a single analytical method for all of these components is challenging. Metabolomics researchers therefore often require the use of both GC/MS and LC/MS technologies to provide comprehensive coverage of the analytes in biological systems. Here we highlight the value added in using both GC/MS and LC/MS analyses for untargeted metabolomics as an integrated workflow by interrogating a well-established rat model for diabetes, obesity and cardiovascular disease effects.

Data was acquired on a TripleTOF® 5600+ system (AB SCIEX). Serum from the Zucker rat model was taken from 7-9 week old lean (n=10), fatty (n=10) and obese rats (n=10). It was observed that there were many lipids changes amongst the three groups of rats (lean, fatty and obese). Using LC/MS data alone we were only able to generate statistical models using discriminant analyses.However combining the LC/MS and the GC/MS data into Expressionist MSX software from Genedata we were able to generate PCA models with clear differences between the samples groups using non-discriminant analysis. From the combined data set, we built correlation networks and grouped metabolites together. From our results we can observe which metabolites were more amenable to GC and LC and where there was an overlap. The overlap gave an extra level of confidence to our biological interpretation and validated our results.

Biography

Fadi A Abdi is a Sr. Global Market Manager for Lipidomics and Metabolomics at AB SCIEX. He completed his doctorate studies in Biochemistry and Biophysics at the University of Houston in 1999. He served as Postdoctoral research associate at Harvard medical school during 1999-2000 on study of the molecular mechanisms involved in HIV RNA packaging and the development of HIV DNA vaccines. He also served as Postdoctoral Research Associate at Los Alamos National Laboratory during 2000-2002 on development of new applications for the study of SNPs in DNA using stable isotopes in MALDI-TOF-MS and ESI-MS.

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