A Novel Lipid Screening Platform Allowing a Complete Solution for Lipidomics Research

INTRODUCTION

A major challenge in lipid analysis is the many hundreds and near-isotopic isomers present in highly complex samples that confound identification and accurate quantitation. This problem coupled with complex sample preparation procedures limits the ability to generate a comprehensive solution that addresses these difficulties and provides a simplified approach for analysis. A novel lipidomics platform was developed that simplifies sample preparation, automated methods, and automated data processing through a streamlined workflow process, using a unique internal standard labeling protocol, a novel screening tool (calibrated mobility, specificity, and novel lipid data analysis software).

MATERIALS AND METHODS

Applying the tool for simple sample extraction and preparation, a serum matrix was used following the protocols provided. A QTRAP ® System with Select Mass ® Technology was used for targeted profiling of over a thousand lipid species from different blood classes. Two methods covered two lipid classes: one injection with Select Mass Technology Q1 and another with the Select Mass Technology tuned Q1. The lipid species were measured using MM1 and positive ion detection, which is capable on the QTRAP ® platforms for internal standards targeted across lipid classes (Lipidyzer TM -avanti internal standards).

Samples were quantified using software accompanying the full solution which incorporates the novel labeled internal standards available as a kit (over Meristem standards across 12 classes), developed for this platform (Lipidyzer TM).

RESULTS

Figure 1. The Lipidyzer TM Platform allows users to access comprehensive data quality and confidently, while expert analysis services provide you with the assurance to gain accurate biological insight.

Figure 2. Comprehensive Coverage of Complex Lipid Metabolism. Just one of the benefits offered by the Lipidyzer TM Platform. The Lipidyzer TM platform overcomes the partial/isobaric ion challenge often seen in the lipidomics field, allowing only a few FA species are measured across lipid classes in question.

Figure 3. Repeatability Data of TAG Species. The Lipidyzer TM platform for the MS/MS mass chromatogram data for the retention ion mode. CVQ (ranged from 0.6% to 24% for each lipid class. This figure highlights a subset of the lipid classes that can be separated.

Figure 4. Differential Mobility Spectrometry (DMS). A comprehensive volatile CO2 scan in the retention ion mode. CVQ ranged from 0.6% to 24% for each lipid class. This figure highlights a subset of the lipid classes that can be separated.

This system allows for:

1. Quantitative results for each lipid class as a ratio of individual species.
2. More accurate composition was obtained competitively from lipid metabolite species data.
3. Accurate lipid species compositional data was compared with reference data generated by alternative methods.

Table 1. Full Coverage of Complex Lipid Metabolism. The Lipidyzer TM Platform fully elucidates the class and fatty and composition of each lipid metabolite species. The classes covered include comprehensive coverage of complex lipid metabolites.

<table>
<thead>
<tr>
<th>Lipid Class</th>
<th>Relative Concentration (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cholesterol</td>
<td>10.0%</td>
</tr>
<tr>
<td>Cholesteryl</td>
<td>20.0%</td>
</tr>
<tr>
<td>Free Fatty</td>
<td>15.0%</td>
</tr>
</tbody>
</table>

REFERENCES

3. TRADMARKS/LICENSING

For Research Use Only. Not for use in diagnostic procedures.

For Research Use Only. Not for use in diagnostic procedures. The trademarks mentioned herein are the property of the holder and any use of such trademarks is subject to license agreement.© 2015 AB Sciex.

TRADEMARKS/LICENSING