

Lipidomic analysis of ADNI cohort

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Contents	
Page 1	Lipid extraction
Page 1	Liquid chromatography mass spectrometry
Page 1-2	Data analysis and run details

Summary

Targeted lipidomic analysis was carried out on the ADNI in the same manner done on the AIBL (Australian Imaging, Biomarker & Lifestyle Study of Ageing) cohort.

Targeted lipidomic analysis

Lipid extraction

Pre aliquoted 10µL of plasma was mixed with 100µL of butanol:methanol (1:1) with 10mM ammonium formate which contained a mixture of internal standards. Samples were vortexed thoroughly and set in a sonicator bath for 1 hour maintained at room temperature. Samples were then centrifuged (14,000 x g, 10 min, 20°C) before transferring the into sample vials with glass inserts for analysis.

Liquid chromatography mass spectrometry

Analysis of plasma extracts was performed on an Agilent 6490 QQQ mass spectrometer with an Agilent 1290 series HPLC system and a ZORBAX eclipse plus C18 column (2.1x100mm 1.8µm, Agilent) with the thermostat set at 60°C. Mass spectrometry analysis was performed in positive ion mode with dynamic scheduled multiple reaction monitoring (MRM).

The solvent system consisted of solvent A) 50% H₂O / 30% acetonitrile / 20% isopropanol (v/v/v) containing 10mM ammonium formate and solvent B) 1% H₂O / 9% acetonitrile / 90% isopropanol (v/v/v) containing 10mM ammonium formate. The following mass spectrometer conditions were used; gas temperature, 150°C, gas flow rate 17L/min, nebulizer 20psi, Sheath gas temperature 200°C, capillary voltage 3500V and sheath gas flow 10L/min. Isolation widths for Q1 and Q3 were set to “unit” resolution (0.7 amu).

Data analysis and run details

- Run was divided into two batches of approximate equal size (total of 824 samples), each batch took approximately one week to analyse.
- Mass spectrometry results were integrated using Agilent software (MassHunter B9.00)

Each batch contained:

Plasma QC samples (PQC, n=21-23) a pooled plasma from six healthy individuals (Baker Lab)

AIBL QC samples (A_QC, n= 10) pooled plasma QC from the AIBL samples that can be used to align with the AIBL dataset. NIST 1950 QC samples (NIST, n=10) NIST 1950 plasma that can be used to align with future cohort analyses.

In total 5 samples had no available plasma sample during the extraction process (E0052, E0290, E0363, E0530, E0796) and a further 4 samples were found to be watery and had abnormally low lipid values (E0488, E0110, E0739, E0142).

- Raw area of each analyte was normalised to its respective internal standard.
- A total of 579 lipids were examined.
- Correction factors were applied to some species, mainly to species without class specific internal standards.
- Pooled plasma quality control samples (PQC) were used to align the dataset in two steps:

Linear correction – To account for differences in signal drift between analytes and standards over time, a linear regression was fitted across the quantitative data for each analyte for all the PQCs in each batch. This was used correct the signal for each sample to the median sample.

Median centering – To account for signal differences between the two batches, the median concentration of each analyte for the PQCs was used to align the two batches.

Version Information 1

Dataset Information

This methods document applies to the following dataset(s) available from the ADNI repository:

Dataset Name	Date Submitted
Meikle Lab – Lipidomics Database	19 th April 2018

References

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