ADNI Alzheimer's Disease Neuroimaging Initiative

ADMC Lipidomics Meikle Lab Longitudinal Data Matrix

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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^{o}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 5µM medronic acid 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^{o}C, gas flow rate 17L/min, nebulizer 20psi, Sheath gas temperature 200^{o}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 batches of 486 samples each.
- Mass spectrometry results were integrated using Agilent software (MassHunter B10.00)

Each batch contained:
Plasma QC samples (PQC, n = 20) a pooled plasma from six healthy individuals (Baker Lab)

NIST 1950 QC samples (NIST, n=9) NIST 1950 plasma that can be used to align with future cohort analyses.

- Raw area of each analyte was normalised to its respective internal standard.
- A total of 781 lipids were examined.
- Correction factors were applied to some species, mainly to species without class specific internal standards.
- NIST 1950 QC samples were used to align the dataset in two steps:

Median centering – To account for signal differences between the batches and the two studies (divided into ADNI1 longitudinal and ADNI2/GO), the median concentration of each analyte for the NIST1950 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
ADMCLIPIDOMICSMEIKLELABLONG.csv	20/10/2020

References

About the Authors

This document was prepared by Kevin Huynh and Peter Meikle, Baker Heart and Diabetes Institute, Metabolomics laboratory. For more information please contact **Prof. Peter Meikle** at **+61 (0)3 8532 1770** or by email at **Peter.Meikle@baker.edu.au. .**

Methodology describing the lipidomics platform has been published here;
Huynh, Kevin, et al. "High-throughput plasma lipidomics: detailed mapping of the associations with cardiometabolic risk factors." Cell chemical biology 26.1 (2019): 71-84.