LIPIDOMIC PROFILING OF BLADDER CANCER PATIENTS USING A COMPACT LC-oa-TOF

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INTRODUCTION

- **HRMS provides critical information for various Omics studies, affording identification of unique and reliable biomarkers of disease.**
- **Here, we explore the deployment of an easy-to-use, smart, compact benchtop LC-oa-TOF MS coupled with advanced statistical processing for a typical lipidomics workflow.**
- **This feasibility study was performed on plasma samples collected from bladder cancer patients, alongside healthy controls.**

Progenesis QI

EZinfo

Sample Preparation
100µL plasma from healthy control and bladder cancer were protein precipitated with 400µL IPA.
UPLC
System: Acquity UPLC I-Class
Column: UPLC CSH C_{18} (100 x 2.1 mm, 1.7um)
MPA: 60:40 ACN:water, 0.1% formic acid and 10mM ammonium formate
MPB: 90:10 IPA:ACN, 0.1% formic acid
MS
MS System: RDa
Mass Range: 50-2,000 m/z
Ionization Polarity: +/-
Informatics
Instrument Control: UNIFI 1.9.4
Processing: Progenesis QI with EZinfo with HMDB Searching

CONCLUSIONS

· LC-oa-TOF MS provides suitable dynamic range for labelled PC, LPC and SM lipids.

· Markers of significant association with bladder cancer patient samples were tentatively identified as a variety of lipid classes.

· This work has demonstrated a facile workflow for lipidomic profiling utilising a compact LC-oa-TOF MS.

Linearity of MS response for lipid classes afforded by compact LC-oa-TOF MS.

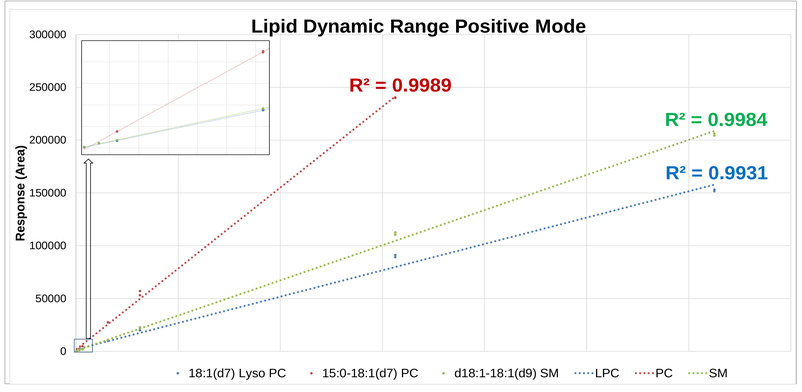
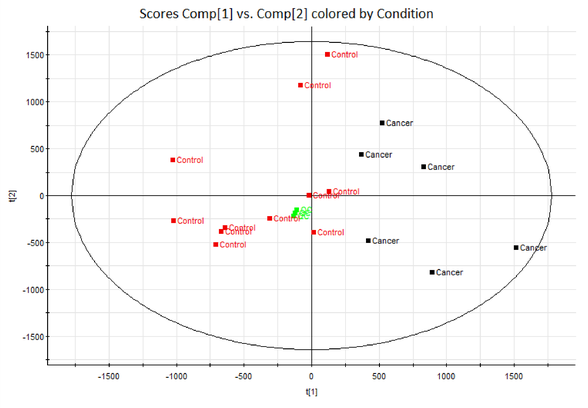
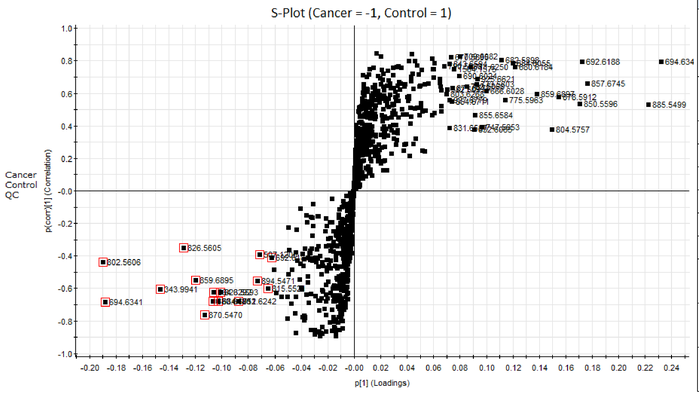


Figure 1: Using the Avanti SPLASH LipidoMIX, MS response is plotted from 40-20,000 ng/mL for 15:0-18:1(d7) PC; 4-40,000 ng/mL for d18:1-18:1(d9) SM; and 0.625-6250 ng/mL for 18:1(d7) Lyso PC. Mass errors were largely < +/- 5ppm for all injections.

Using advanced statistical processing, tentative identifications were proposed based on accurate mass as possible lipids of significance between bladder cancer and control groups.





Upregulated in Cancer Samples				
Tentative ID	RT (min.)	m/z	Adduct	Mass Error (ppm)
LPC(18:2)	1.03	564.3292	M+FA-H	-2.89
PC(38:6)	4.93	850.5597	M+FA-H	-0.81
PC(36:4)	5.13	826.5593	M+FA-H	-1.36
PI(38:5)	5.43	883.5396	M-H	6.08
PC(36:4)	5.87	826.5605	M+FA-H	0.15
PC(34:2)	6.13	802.5606	M+FA-H	0.38
PE(38:4)	7.38	748.5280	M-H2O-H	-0.93
SM(d18:0/24:1)	13.54	859.6895	M+FA-H	-1.8
Cer(d18:1/24:1)	13.59	692.6181	M+FA-H	-2.73
Cer(d18:1/24:0)	14.18	694.6341	M+FA-H	-2.19

Unsupervised PCA → S-Plot → Tentative IDs

Figure 2: Principal component analysis (PCA) from control and bladder cancer patient samples, and S-plot from which markers of interest are selected and then searched against HMDB tentative identification.