Ion-pairing chromatography and amine derivatization provide complementary approaches for the targeted LC-MS analysis of the polar metabolome

Virag Sagi-Kiss,¹ Yufeng Li,¹ Matthew R. Carey,¹ Sarah J. Grover,¹ Karsten Siems,² Francesca Cirulli,³ Alessandra Berry,³ Chiara Musillo,^{3,4} Ian D. Wilson,¹ Elizabeth J. Want,¹ Jacob G. Bundy*¹

1: Department of Metabolism, Digestion and Reproduction, Imperial College London, South Kensington, London SW7 2AZ, UK

- 2: Analyticon Discovery GmbH, Hermannswerder Haus 17, 14473 Potsdam, Germany
- 3: Center for Behavioral Sciences and Mental Health, Istituto Superiore di Sanità, Rome, Italy

4: Department of Psychology, Sapienza University of Rome, Italy

Table of Contents

Table S1. Settings used for liquid chromatography-mass spectrometry experiments.

Table S2 (XLSX). Retention time data.

Table S3 (XLSX). MS settings for metabolites monitored by final combined method.

Table S4 (XLSX). Metabolite data from LC-MS (AccQ-Tag RPLC).

Table S5 (XLSX). Metabolite data from ¹H NMR spectroscopy.

Table S6 (XLSX). Metabolite data from LC-MS (IPC).

Table S7 (XLSX). Output of statistical analyses for liver samples.

Figure S1. Exemplar chromatograms for ion-pairing chromatography. Some metabolites exhibit sharp, Gaussian peaks; others have poorer peak shape, but can still be analysed if the peaks are well resolved from others.

Figure S2. Comparison of retention times for metabolites with two different ion-pairing reagents, tributylamine (TBA) + acetic acid, vs. diisopropylethylamine (DIPEA) + hexafluoroisopropanol. Metabolites of different chemical classes are indicated on the plot.

Figure S3. Comparison of sensitivity for RPLC-MS vs. IPLC-MS ($n=3, \pm SD$).

Figure S4. Plot of CV_{biol}/CV_{QC} against CV_{QC} for data derived from ion-pairing LC-MS of mouse liver extracts. There is an apparent step in the data at approximately $CV_{QC} = 0.5$. Individual data points represent transitions, rather than metabolites.

Figure S5. Correlations between NMR, AccQ-Tag, and ion-pairing data (for three different transitions) for 2-aminoadipate.

Table S1. Settings used for liquid chromatography-mass spectrometry experiments.

	AccQ-Tag RPLC	RPLC POS	IPC	RPLC NEG
LC unit	ACQUITY Binary Solvent Manager (Waters Corporation) + CTC Pal autosampler	UFLX XR (Shimadzu)	ACQUITY Binary Solvent Manager (Waters Corporation) + CTC Pal autosampler	ACQUITY Binary Solvent Manager (Waters Corporation) + CTC Pal autosampler
Mobile phase A	0.1 % Formic acid water	0.1 % Formic acid water	10mM of tributylamine + 15mM of acetic acid + acetylacetone (0.02% v/v) in water	0.1 % Formic acid water
Mobile phase B	0.1 % Formic acid Acetonitrile	0.1 % Formic acid Acetonitrile	80% methanol and 20% isopropanol	0.1 % Formic acid Acetonitrile
Flow rate	0.6 ml/min	0.4 ml/min	0.4 ml/min	0.4 ml/min
Column temperatu re	50 °C	45 °C	45 °C	45 °C
Column	Waters HSS T3 (1.8 μm, 2.1 x 150 mm)	Waters HSS T3 (1.8 µm, 2.1 x 100 mm)	Waters HSS T3 (1.8 µm, 2.1 x 100 mm)	Waters HSS T3 (1.8 µm, 2.1 x 100 mm)
Injection volume	5 μl	5 μl	5 μl	5 μl
Gradient	0.1 to 12 min from 1% solvent B to 28% solvent B; at a flow rate of 0.6 mL/min. Post- acquisition wash and recovery steps took 2.65 min in total and went up to 100% B, and 1 min at initial conditions for equilibration.	0min 1%; 0.5 min, 1% B; 10 min, 55% B; 11 min, 100% B; 12 min, 100% B; 12.5 min, 1% B; 14.5 min, 1% B.	0-0.5 min: 0% B; 0.5-6 min: 0% B-5%B; 4-6min: 5%B; 6-6.5 min: 5-20% B; 6.5-8.5 min: 20% B; 8.5-14min: 20-55%B; 14-15 min: 55-100% B; 15-17min: 100%B; 17-18min 100-0% B. 3 min at initial conditions before next injection cycle starts.	0min: 99% A; 0.5min: 99%A; 10 min: 45%A; 11min: 0%A; 12 min: 0%A; 12.5min: 99%A; 14.5 min: 99%A. Linear gradient between all times
MS type	Waters XEVO TQ-S (Waters Corporation)	QTRAP 5500 MS/MS system [Applied Biosystem (CA, USA)]	Waters XEVO TQ-S (Waters Corporation)	Waters XEVO TQ-S (Waters Corporation)
Ion mode	POS	POS	NEG	NEG
Source parameter s	capillary voltage, 1.5 kV; source temperature, 150°C; cone voltage: 40 V;	De-clustering, entrance and collision cell exit potentials were set to 30 V, 10 V and 10 V, respectively.	capillary voltage, 1.5 kV; source temperature, 150°C; cone voltage: 40 V;	capillary voltage, 2 kV; source temperature, 150°C; cone voltage: 40 V;
AdditIona l source settings:	desolvation temperature 600°C; desolvation gas flow, 1000 L/h; cone gas flow, 150 L/h; nebuliser gas 7.0 bar; collision gas, 0.15 mL/min.	Curtain gas, 40 psi; collision gas, medium; ionspray voltage, 5500 V; temperature, 550°C; ion source gas 1 and 2, 40 and 60 psi, respectively.	desolvation temperature 600°C; desolvation gas flow, 1000 L/h; cone gas flow, 150 L/h; nebuliser gas 7.0 bar; collision gas, 0.15 mL/min.	desolvation temperature 300°C; desolvation gas flow, 1000 L/h; cone gas flow, 150 L/h; nebuliser gas 7.0 bar; collision gas, 0.15 mL/min.





Figure S1. Exemplar chromatograms for ion-pairing chromatography. Some metabolites exhibit sharp, Gaussian peaks; others have poorer peak shape, but can still be analysed if the peaks are well resolved from others.





Figure S2. Comparison of retention times for metabolites with two different ion-pairing reagents, tributylamine (TBA) + acetic acid, vs. diisopropylethylamine (DIPEA) + hexafluoroisopropanol. Metabolites of different chemical classes are indicated on the plot.



Figure S3

Figure S3. Comparison of sensitivity for RPLC-MS vs. IPLC-MS (n=3, \pm SD).





Figure S4. Plot of CV_{biol}/CV_{QC} against CV_{QC} for data derived from ion-pairing LC-MS of mouse liver extracts. There is an apparent step in the data at approximately $CV_{QC} = 0.5$. Individual data points represent transitions, rather than metabolites.

Figure S5



Figure S5. Correlations between NMR, AccQ-Tag, and ion-pairing data (for three different transitions) for 2-aminoadipate.