

Liquid Extraction Surface Analysis Imaging of Lipids and Proteins in Human Liver Analysed by High Resolution Mass Spectrometry

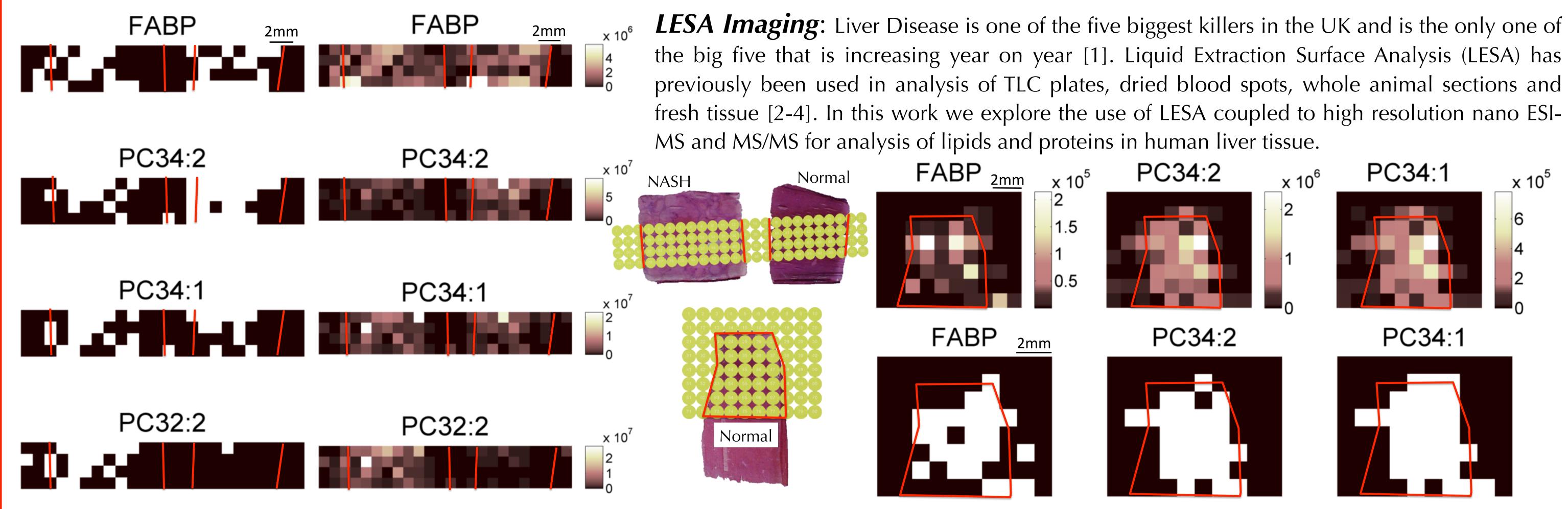
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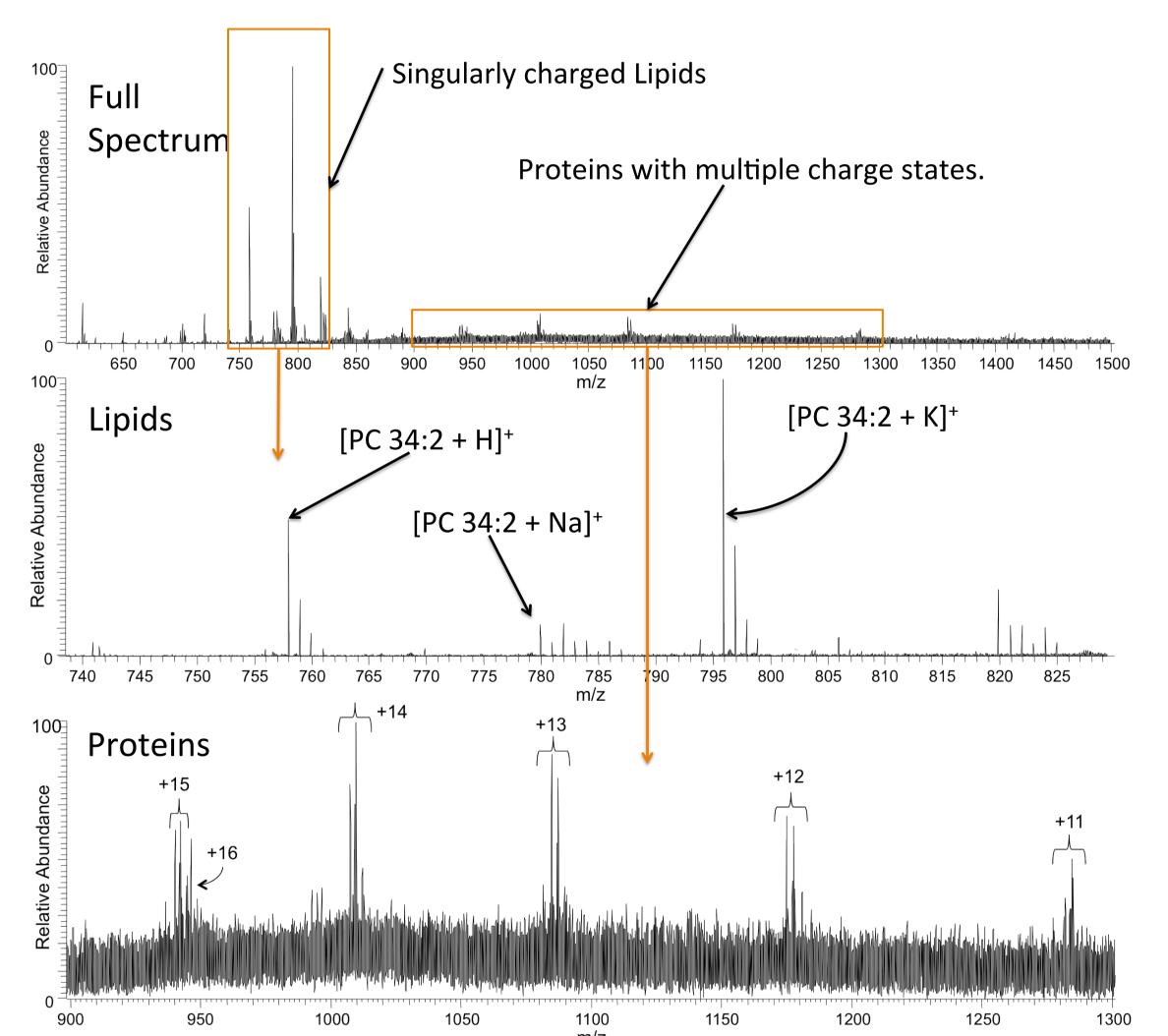
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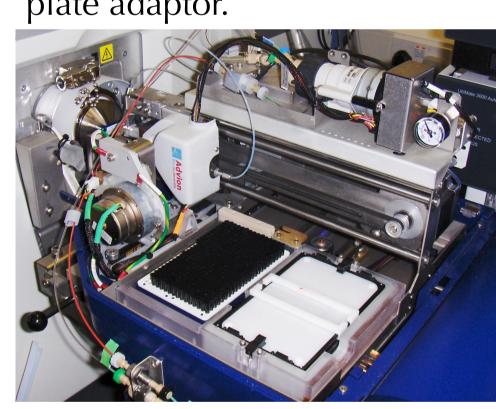


Lipid and protein Images were created using LESA sampling (Advion) coupled to high resolution MS. Images shown as relative intensity and in binary form. **LESA sampling:** 0.8μ L of 70% methanol_(ac) 0.1% Formic Acid, of which 0.5μ l was dispensed from a height of $0.2 \,\mathrm{mm}$ onto a 10 μ m thick tissue section. $0.5 \,\mu$ L was re-aspirated after 10 s delay and electrosprayed into a LTQ Orbitrap velos (Thermo) (tip voltage: 1.75kV, gas pressure: 0.3 psi, capillary temperature: 250°C). **MS Method:** Spectra acquired (resolution: 100,000 at m/z 400), ~25 scans (3 mins) for normal only and ~15 scans (2 min) for normal and non-alcoholic steatohepatitis (5 co-added microscans per scan). The AGC target was 1 X 10⁶ with a max fill time of 2s.

Repeat extractions from a single location revealed changes in species detected. Protocol as for imaging, but with an increased solvent volume of 3.5 μ L, of which 3 μ l was dispensed and re-aspirated.

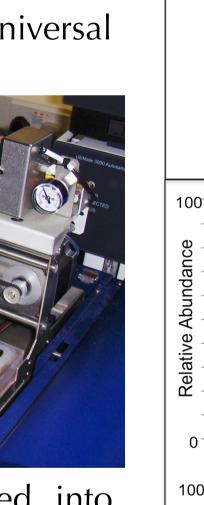


LESA sampling (using a conductive pipette tip) from a glass slide held In a universal



The solution is injected into the mass spectrometer by chipbased nano-ESI (Advion Nanomate) [5].

plate adaptor.



20000

1st Analysis - Lipids

770 775 780 785 790 795 800 805 m/z 3rd **Analysis** - Lipids

PC34:2 Adducts

Two unknown Species

Extraction

Choline head group **104.1070 №** 1374.74398 4000000 3000000 2000000 1st Analysis - Proteins 3rd Analysis - Proteins

Lipid and

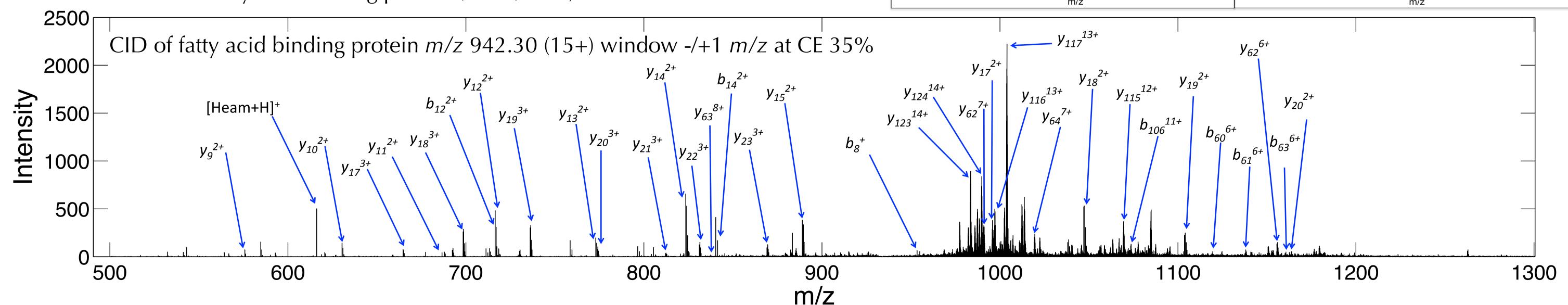
Protein

4.000.000

3,000,000

671.11957

Lipid and Protein detection in a single spectrum. One of these proteins has been fully characterised as liver fatty acid binding protein (FABP) – 14,111 Da.



Aceyl-SFSGKYQLQSQENFEAFMKAIGLPEELIQKGKDIKGVSEIVQNGKHFKFTITAGSKVIQNEFTVGEECELETMTGEKVKTVVQLEGDNKLVTTFKNIKSVTELNGDIITNTMTLGDIVFKRISKRI **Red** = Covered by B fragments only **Blue** = Covered by Both B and Y fragments **Green**= Covered By Y fragments only 100% Coverage of the entire protein

Principal Findings:

- Lipids and proteins readily detected in tissue by LESA-MS.
- Direct analysis of tissue via LESA-MS can be used to construct ion images of lipids and proteins in thin tissue sections.
- High mass accuracy and high mass resolving power of the Velos Orbitrap enables identification of numerous constituents directly in tissue.
- Repeat analysis of the same area enables the detection of additional ions following the removal of salts and other abundant molecules.

References: [1] British Liver Trust www.britishlivertrust.org.uk/home/about-us/ media-centre/facts-about-liver-disease.aspx accessed 10/04/12. [2] Edwards, R. L.; Creese, A. J.; Baumert, M.; Griffiths, P.; Bunch, J.; Cooper, H. J. Analytical Chemistry 2011, 83, 2265. [3] Eikel, D.; Vavrek, M.; Smith, S.; Bason, C.; Yeh, S.; Korfmacher, W. A.; Henion, J. D. Rapid Communications in Mass Spectrometry **2011**, 25, 3587. [4] Walworth, M. J.; Stankovich, J. J.; Van Berkel, G. J.; Schulz, M.; Minarik, S. Rapid Communications in Mass Spectrometry 2012, 26, 37. [5] Kertesz, V.; Van Berkel, G. J. Journal of Mass Spectrometry 2010, 45, 252.

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