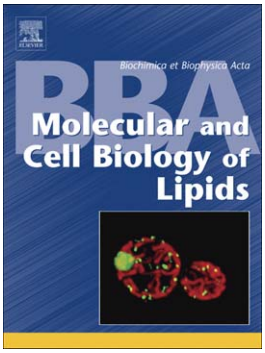

Stable isotope analysis of dynamic lipidomics

Joost Brandsma, Andrew P. Bailey, Grielof Koster, Alex P. Gould, Anthony D. Postle

PII: S1388-1981(17)30042-2
DOI: doi:10.1016/j.bbalip.2017.03.002
Reference: BBAMCB 58125

To appear in: *BBA - Molecular and Cell Biology of Lipids*

Received date: 16 December 2016
Revised date: 7 March 2017
Accepted date: 9 March 2017

Please cite this article as: Joost Brandsma, Andrew P. Bailey, Grielof Koster, Alex P. Gould, Anthony D. Postle, Stable isotope analysis of dynamic lipidomics, *BBA - Molecular and Cell Biology of Lipids* (2017), doi:10.1016/j.bbalip.2017.03.002

Stable isotope analysis of dynamic lipidomics

Joost Brandsma[a], Andrew P. Bailey[b], Grielof Koster[a,c], Alex P. Gould[b] and Anthony D. Postle[a]

[a] Academic Unit of Clinical & Experimental Sciences, Faculty of Medicine, University of Southampton, Southampton, United Kingdom
[b] The Francis Crick Institute, 1 Midland Road, London, United Kingdom
[c] National Institute of Health Research Biomedical Research Unit in Respiratory Medicine, University Hospitals NHS Foundation Trust

Corresponding author:

Professor A.D. Postle
Mailpoint 803, Level F
South Laboratory and Pathology Block
Southampton General Hospital
Tremona Road
Southampton
SO16 6YD
United Kingdom

Tel: +44(0)2381 206161
Email: adp@soton.ac.uk

Abstract
Metabolic pathway flux is a fundamental element of biological activity, which can be quantified using a variety of mass spectrometric techniques to monitor incorporation of stable isotope-labelled substrates into metabolic products. This article contrasts developments in electrospray ionisation mass spectrometry (ESI-MS) for the measurement of lipid metabolism with more established gas chromatography mass spectrometry and isotope ratio mass spectrometry methodologies. ESI-MS combined with diagnostic tandem MS/MS scans permits the sensitive and specific analysis of stable isotope-labelled substrates into intact lipid molecular species without the requirement for lipid hydrolysis and derivatisation. Such dynamic lipidomic methodologies using non-toxic stable isotopes can be readily applied to quantify lipid metabolic fluxes in clinical and metabolic studies *in vivo*. However, a significant current limitation is the absence of appropriate software to generate kinetic models of substrate incorporation into multiple products in the time domain. Finally, we discuss the future potential of stable isotope-mass spectrometry imaging to quantify the location as well as the extent of lipid synthesis.

Keywords
Dynamic lipidomics; stable isotopes; mass spectrometry; lipid metabolism