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New methods for the compound specific analysis of underivatized amino acids

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The isotopic analysis of amino acids has become an important area of application in a range of geoscientific, palaeo-ecological and biochemical disciplines including in particular palaeodietary reconstruction and environmental forensics (Dunn et al., 2011; Raghaven et al., 2010; Lynch et al., 2011; Godin and McCullagh, 2011). Commercialisation of an interface between liquid chromatography and isotope ratio mass spectrometry in 2004 has enabled the analysis of non-volatile, soluble compounds without the need for derivatization (via GC-C-IRMS), providing exciting new analytical possibilities (Krummen et al., 2004).

One of the major problems facing LC-IRMS for δ^{13}C analysis is the development of efficient and robust methods. Chromatographic restrictions on mobile phase composition and flow rates, combined with the need for baseline resolution, are analytically challenging but imperative for accurate isotopic analysis. Since the introduction of LC-IRMS a number of research groups have been working on separation methods in particular but, although suitable for resolving the majority of amino acids, current protocols are extremely time consuming, with recently published methods taking over 4 hours per sample (Smith et al., 2009). The low sample throughput of these methods is directly affecting research efficiency. For example, we are currently trying to better understand what palaeodietary information is represented by individual amino acid δ^{13}C values from bone collagen and hair keratin, and this work has been significantly hampered by a lack of sample throughput.

Recognizing the need for larger sample sets to better understanding biogenic information represented by amino acid δ^{13}C for palaeodietary reconstruction, high throughput approaches to amino acid LC-IRMS have been investigated and developed. This poster will present unpublished research, developing an analytical protocol which cuts analysis time for amino acids dramatically. This approach is based on mixed-mode chromatography, building on research in the literature, and is applicable to the analysis of amino acids from a wide range of sources. The figure below shows the LC-IRMS chromatogram for a set of standard proteinogenic amino acids using the new protocol and the poster will provide analytical details and demonstration of its application.

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