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On the trophic level estimates based on nitrogen isotopic compositions of amino acids

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Recently, nitrogen isotopic composition of amino acids has been proposed to be useful for estimating more precise trophic positions of organisms (e.g., McClelland and Montoya, 2002; Chikaraishi et al., 2009). The significant 15N-enrichment (~8.0 per mil) in glutamic acid (Glu) provide a scope for defining trophic position, whereas little isotopic changes (~0.4 per mil) in phenylalanine (Phe) provide information of nitrogen sources at the base of the food web. Based on the general trends observed in various organisms, Chikaraishi et al. (2009, in press) established equations obtaining precise trophic level (TL) of organisms, employing the following equation:

(Aquatic) TL = (d15N(Glu) ? d15N(Phe) ? 3.4) / 7.6 + 1
(Terrestrial C3) TL = (d15N(Glu) ? d15N(Phe) ? 7.0) / 7.6 + 1
(Terrestrial C4) TL = (d15N(Glu) ? d15N(Phe) + 0.6) / 7.6 + 1

The resulting error (< +/-0.2) is much smaller than that in traditional estimates based on bulk isotope analysis. Furthermore, this method is applicable to formalin-fixed samples. Although the number of the reports is still limited, the amino acid method potentially provides a powerful tool for the food web study in the future.
This method has recently been demonstrated to be applicable for microbial processes based on the laboratory culture experiments of various microbes (Yamaguchi et al., in prep.). In this presentation, I will summarize the principles, applications, and limitations of this tool, and then discuss the potential utility for the paleontological application.

Keywords: amino acid, nitrogen isotopic compisition, trophic level