

## Precise and sensitive determination of stable isotopic compositions of amino acids

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Amino acids are biologically central and functional organic compounds. Their molecular and stable isotope profiles have been employed as a tool in various fields of studies, particularly for understanding of the trophic energy flow of food web ecology as well as for estimating the origin of amino acid procurers in extraterrestrial samples (e.g., meteorites). One of the most powerful techniques in the stable isotope studies of amino acids is compound-specific isotope analysis (CSIA) by gas chromatography/isotope ratio mass spectrometry (GC/IRMS), which potentially allows a rapid and precise determination of H, C, N, O, and S isotopic compositions of individual amino acids in complex mixture of samples. However, (1) isotopic fractionation and exchange during pretreatment (e.g., hydrolysis, extraction, purification, and derivatization) of samples, (2) chromatographic separation among individual amino acids, and (3) less sensitivity on GC/C/IRMS (i.e., 10-50 nmol of elements is required) are always problematic in CSIA of amino acids.

In the presentation, we will briefly review these issues on CSIA of amino acids, and show current advances in the precise and sensitive determination of C and N isotopic compositions of amino acids (i.e., within 0.4-0.8 permil for a minimum sample amount of 0.5 nmol element), based on the minimizing isotopic fractionation during HPLC purification and derivatization as well as reducing leak and background variation in GC/IRMS instrument. With this method, we can access C and N isotopic signature of wide range of samples including amino acids in bacteria and archea isolated from natural environments as well as amino acid procurers in meteorites.

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