Isotopes in Amino Acids: What we still may learn about biosynthetic pathways and fluxes

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For over 50 years, the stable isotope community has been making compound specific isotope measurements on amino acids, simple molecules all organisms make, and that can be stable for thousands of years in fossil materials and soils. John Hayes' review paper in 2001 concentrated on the enzymatic pathways that could be attributed to the wide range of isotope fractionations in amino acids that had been measured at that time. This talk will jump off from Hayes' interpretations using new data generated in this century.

Stable isotope measurements of amino acids are determined by fluxes of metabolites through biosynthetic pathways in addition to the specific enzyme pathways involved in their synthesis. For higher organims, the sources of carbon, nitrogen, and hydrogen from amino acids in the diet can also have a strong influence on the isotopic composition of amino acids in the consumer, which has been used for various applications that have extended compound specific isotope analyses in amino acids to many different fields.

Although there has been much progress in understanding how these isotopic signatures can be used for biogeochemistry, there are major opportunities that still exist for breakthroughs including intramolecular and positional isotope measurements, enzymatic studies, and microbiome directed synthesis. In particular, stronger understanding of why certain amino acids considered to be "source" amino acids have nitrogen isotope signatures that remain virtually unchanged needs careful examination. Last, hydrogen isotope measurements in amino acids, coupled with carbon and nitrogen isotopic compositions, have the potential to expand this field even further.