

A metabolic model of stable isotope dynamics

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Carbon and nitrogen stable isotope analysis have been a powerful tool used for identifying food-web structures. Our recent study suggested that the ratios of trophic fractionation of carbon and nitrogen isotopes ($\Delta\delta^{15}\text{N}/\Delta\delta^{13}\text{C}$) throughout food chain are similar in various ecosystems (Wada et al. 2013), although the general mechanisms determining isotopic incorporation rates and discrimination factors are poorly understood.

Here, we developed a mechanistic model of the isotopic fractionation in metabolic processes that are common to animals composing most grazing food chains. Particularly, we calculate fluxes of carbon and nitrogen stable isotopes within an organism by following fluxes of molecules involved in some of physiological reactions: the synthesis of amino acids and their carbon skeletons, the rates of which are governed by energy-producing systems such as glycolysis, the TCA cycle, and oxidative phosphorylation, that is, the ratio of the rate of amino-acid syntheses to that of energy-yielding processes. The active metabolic pathways above are assumed to be changed by the conditions of supply (diet quantity and quality) and demand (growth rate).

The model result suggests that the instant isotopic composition of animals are sensitive to the change of their diet composition and growth rate, but on the other hand, the isotopic composition converges as the integrating period becomes long. With further temporal scaling-up, in turn, the isotopic compositions of animal body reflect the spatio-temporal variability due to their life history, migration and foraging patterns. This gives mechanistic insight to what information we can acquire from the observation.