

## A mechanistic metabolic model of nitrogen stable isotope dynamics in trophic processes

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Stable isotope analysis of nitrogen and carbon have been a powerful tool used for identifying trophic structure of ecosystems. Our previous studies suggested that the ratios of trophic fractionation of carbon and nitrogen isotopes ( $\Delta^{15}\text{N}/\Delta^{13}\text{C}$ ) throughout food chain are similar in various ecosystems (Aita et al. 2011, Wada et al. 2013), although the general mechanisms determining isotopic incorporation rates and discrimination factors are not understood mechanistically yet. On the other hand, recent studies revealed the  $^{15}\text{N}$  enrichment factor for trophic processes varies among amino acids from which new method of estimation of the trophic level of animal samples (e.g., Chikaraishi et al. 2009).

Based on these observations, we developed a simple dynamic model of the isotopic fractionation in nitrogen metabolic processes that are common to animals composing most grazing food chains. Particularly, we focused on and incorporated the transamination and deamination processes of two classes of amino acid, essential and non-essential, respectively into the model. With this model we investigated how  $\delta^{15}\text{N}$  signatures of the two amino acid classes and whole-body change. Preliminary 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. Based on this model we will discuss possible negative feedback processes in isotopic enrichment for nitrogen to explain the commonly observed trophic-step  $^{15}\text{N}$ -enrichment factor through many food chains.

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