High resolution food web viewed *via* $^{15}N/^{14}N$ of amino acids

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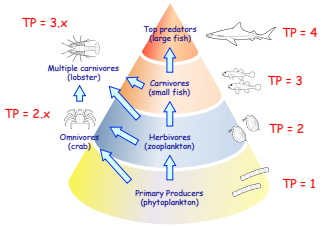
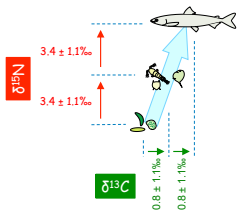
Grazing food web

We often arrange organisms in food-chains according to trophic position (TP), which forms a "food web pyramid" from a broad base of primary producers (TP=1) to a relatively less of herbivores (TP=2) and more-less of carnivores (TP=3), and finally to a few of top predators (TP=4-5). This arrangement is particularly useful, if you want to see the trophic hierarchy and associated energy flow (or energy transfer) in the ecosystem.

【Food web pyramid】



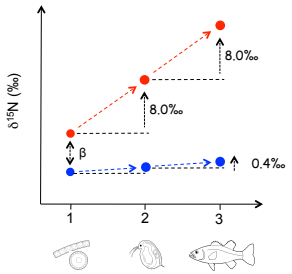
【SIA of bulk tissues】

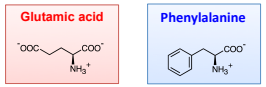


DeNiro & Epstein (1978, 1981), Minagawa & Wada (1984)

$\delta^{15}N$ of amino acids *vs.* TP

A unique offset in $^{15}N/^{14}N$ ($\delta^{15}N$, ‰ vs. Ari) between glutamic acid (Glu) and phenylalanine (Phe) in a single organism enables TP estimates of organisms in food webs. We proposed the following equation to calculate TP of organism (Chikaraishi et al. 2009).



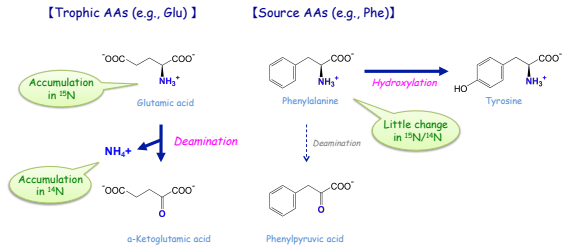


$$TP = \frac{\delta^{15}N_{Glu} - \delta^{15}N_{Phe} + \beta}{7.6} + 1$$

β : −3.4‰ for aquatic (algae, and cyanobacteria)
+8.4‰ for terrestrial (vascular plants)

Possible mechanism

Different metabolic reactions in consumers cause large $\Delta\delta^{15}N$ for Glu but little for Phe.

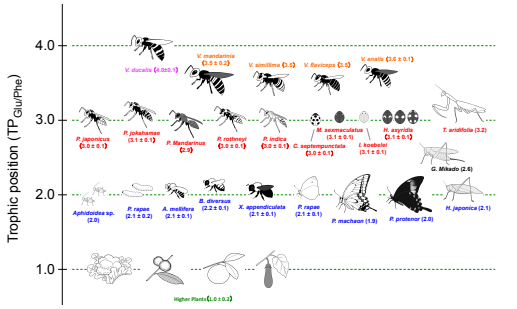


Chikaraishi et al., 2009, 2010

Illustration of trophic hierarchy

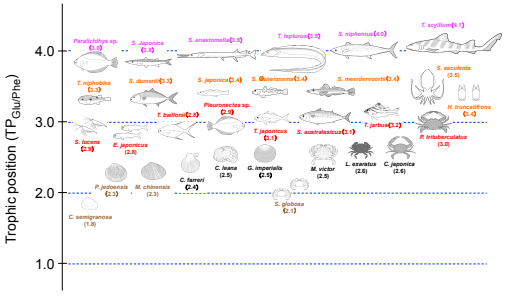
We employed this method to see the trophic structure with high-resolution among approximately >300 free-roaming organisms in coastal and sandy ocean and in terrestrial ecosystems.

【Orange & vegetable farm】



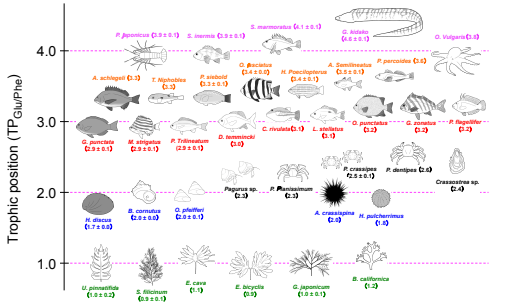
Chikaraishi et al., 2014, *Ecol. Evol.* 4, 2423-2449

【Sandy beach】



Unpublished data (very sorry)

【Stony shore】



Chikaraishi et al., 2004, *Ecol. Evol.* 4, 2423-2449

Advantages of this method

1. TP estimates can be achieved based on $\delta^{15}N$ offset in a pair of amino acids (e.g., Glu & Phe) from a single organism of interest. Unlike the traditional bulk method, this method does not require the characterization of $\delta^{15}N$ of primary producers as the basal resource of food webs.
2. $\delta^{15}N$ of phenylalanine reflects an integrated value for $\delta^{15}N$ of primary producers that are actually eaten by consumers in the studied food web.
3. Very small sample size (0.5-1.0 nmol/amino acid) is required for the $\delta^{15}N$ analysis of amino acids by GC/IRMS.
4. The error in TP estimates is substantially small (1σ=0.12 and 0.17 for for aquatic and terrestrial food webs, respectively).