



FEATURE ARTICLE

Estimation of predator–prey mass ratios using stable isotopes: sources of errors

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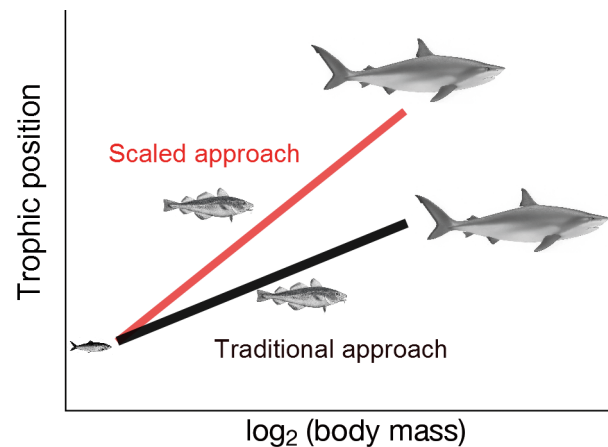
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ABSTRACT: In aquatic systems, the ratio of predator mass to prey mass (PPMR) is an important constraint on food web structure, and has been correlated with environmental stability. One common approach of estimating PPMR uses nitrogen stable isotopes ($\delta^{15}\text{N}$) as an indicator of trophic position, under the assumption that the discrimination between diet and tissue is constant with increasing diet $\delta^{15}\text{N}$ (an additive approach). However, recent studies have shown that this assumption may not be valid and that there is a negative trend between the $\delta^{15}\text{N}$ of the diet and the discrimination value (a scaled approach). Here, we estimated PPMR for a simulated food web using both the traditional additive approach and the improved scaled approach, and then tested our predictions with isotope samples from a North Sea food web. Our simulations show that the additive approach yields incorrect estimates of PPMR, and these biases are reflected in North Sea PPMR estimates. The extent of the bias is dependent on the baseline $\delta^{15}\text{N}$ and trophic level sampled, with the greatest differences for samples with low baseline $\delta^{15}\text{N}$ sampled at lower trophic levels. The scaled approach allows for the comparison of PPMR across varying $\delta^{15}\text{N}$ baselines and trophic levels, and will refine estimates of PPMR.

KEY WORDS: Body size · Diet-dependent discrimination factor · North Sea · Size spectra · PPMR · Food webs · Size structure

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Schematic showing potential difference in estimates of predator–prey mass ratio (PPMR) between traditional and scaled approaches: trophic level ~ body mass slope is greater and PPMR estimates are lower under the scaled approach.

Image: E. Hertz

INTRODUCTION

Body size is of critical importance in ecology, reflecting key ecological processes including metabolism and feeding interactions (Elton 1927, Peters 1983, Brown et al. 2004). Aquatic communities are size structured, with individual organisms generally feeding on prey smaller than themselves (Jennings et al. 2001, Barnes et al. 2010). The mean predator–prey mass ratio (PPMR) reflects constraints on community size structure (Trebilco et al. 2013) and is correlated

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with the general food web properties of food chain length and stability (Jennings & Warr 2003). Empirical sub-community estimates of PPMR vary by over an order of magnitude, from approximately 100 in the North Sea (Jennings & Mackinson 2003) to over 7000 in the Western Arabian Sea (Al-Habsi et al. 2008), although it is unclear whether this variability reflects methodological biases or real food web differences.

PPMR can be estimated using direct observations of the size of prey in predator stomach contents or indirectly through stable isotope analysis (Jennings et al. 2002, Barnes et al. 2010). Although stomach contents allow identification of prey types and direct measurement of predator and prey body masses, this approach is limited because stomach contents reflect only recent feeding events, do not represent assimilated material, and can be biased by differences in digestibility amongst prey items (Polunin & Pinnegar 2002). Given these limitations, stable isotope analysis of nitrogen ($\delta^{15}\text{N}$) has been increasingly employed to estimate PPMR (Jennings et al. 2002, Al-Habsi et al. 2008). In this approach, for a community spanning several orders of magnitude in mass, each sampled body mass class is assigned a biomass-weighted mean $\delta^{15}\text{N}$ value that is used as a proxy for trophic position (TP, Jennings et al. 2002). Assuming a linear relationship between TP and body mass class, the slope (b) is then used to estimate PPMR:

$$\text{PPMR} = n^{(\Delta^{15}\text{N}/b)} \quad (1)$$

where n reflects the log base used to bin mass values (often 2), and $\Delta^{15}\text{N}$ is the assumed change in $\delta^{15}\text{N}$ between predator and prey, known as the isotope discrimination value (Fig. 1).

When using $\delta^{15}\text{N}$ to determine TP, the isotope discrimination value ($\Delta^{15}\text{N}$) is assumed to be a constant value, typically 3.4‰ (Minagawa & Wada 1984, Vander Zanden & Rasmussen 1999, Post 2002). However, recent laboratory experiments and syntheses of published data have shown that this is not necessarily the case. Instead, there appears to be a significant negative linear relationship between the $\delta^{15}\text{N}$ of an organism's diet (hereafter dietary $\delta^{15}\text{N}$) and the $\Delta^{15}\text{N}$ experienced by that organism (Caut et al. 2008, 2009, Dennis et al. 2010, Hussey et al. 2014). At low dietary $\delta^{15}\text{N}$ values (e.g. <6‰), the $\Delta^{15}\text{N}$ experienced by an organism can be significantly higher than 3.4‰; at high dietary $\delta^{15}\text{N}$ values (e.g. >12‰), the $\Delta^{15}\text{N}$ can be significantly lower than 3.4‰; and at very high dietary $\delta^{15}\text{N}$, the $\Delta^{15}\text{N}$ may even become negative (Dennis et al. 2010, Hussey et al. 2014). Consequently, estimation of PPMR from stable isotope data

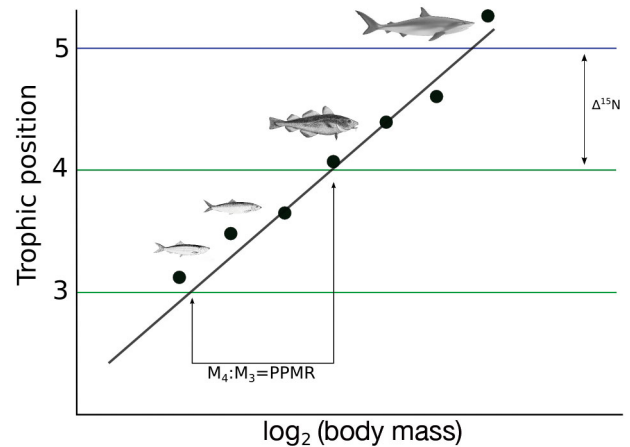


Fig. 1. Relationship between trophic position and log body mass (M) in a size-structured food web. The slope (b) of a linear regression between trophic position and body mass is used to calculate the ratio of body sizes at successive trophic positions (e.g. $M_2:M_3$), thus giving an estimate of community predator-prey mass ratio (PPMR). Eq. (1) accounts for the difference between trophic positions ($\Delta^{15}\text{N}$) and transforms the logged mass values (n)

may be systematically biased if one assumes a constant $\Delta^{15}\text{N}$ of 3.4‰.

Here, we examined to what extent estimates of PPMR would be affected by systematic differences in $\Delta^{15}\text{N}$ with increasing dietary $\delta^{15}\text{N}$. We estimate TP and PPMR for simulated $\delta^{15}\text{N}$ data, first using the traditional assumption of a constant discrimination of 3.4‰ and second using a correction for variable discrimination values depending on dietary $\delta^{15}\text{N}$. We then tested our approach with stable isotope estimates from a North Sea food web (Jennings & Warr 2003). Comparison of these 2 approaches reveals that the traditional approach underestimates PPMR at low dietary $\delta^{15}\text{N}$ (4–9‰) and overestimates PPMR at high dietary $\delta^{15}\text{N}$ (10–17‰).

MATERIALS AND METHODS

PPMR estimation

To assess the extent of bias in PPMR estimation, we estimated the TP of an organism in 2 distinct ways. First, we assumed that $\Delta^{15}\text{N}$ is constant across dietary $\delta^{15}\text{N}$ at a value of 3.4‰. In this additive approach, the TP of an organism is calculated as

$$\text{TP}_{\text{additive}} = \text{TP}_{\text{base}} + \frac{\delta^{15}\text{N}_{\text{fish}} - \delta^{15}\text{N}_{\text{base}}}{\Delta^{15}\text{N}} \quad (2)$$

where $\Delta^{15}\text{N}$ is 3.4‰, $\delta^{15}\text{N}_{\text{fish}}$ is the $\delta^{15}\text{N}$ value of the organism, and $\delta^{15}\text{N}_{\text{base}}$ is the $\delta^{15}\text{N}$ value of a baseline

consumer (Cabana & Rasmussen 1996, Post 2002). Second, we varied $\Delta^{15}\text{N}$ systematically with the dietary $\delta^{15}\text{N}$ using the scaled approach developed by Hussey et al. (2014). In this scaled approach, $\Delta^{15}\text{N}$ declines systematically with dietary $\delta^{15}\text{N}$, and TP is calculated using a $\delta^{15}\text{N}$ enrichment model, based on a formulation of the von Bertalanffy growth equation:

$$\text{TP}_{\text{scaled}} = \frac{\log(\delta^{15}\text{N}_{\text{lim}} - \delta^{15}\text{N}_{\text{base}}) - \log(\delta^{15}\text{N}_{\text{lim}} - \delta^{15}\text{N}_{\text{fish}})}{k} + \text{TP}_{\text{base}} \quad (3)$$

where $\delta^{15}\text{N}_{\text{lim}}$ and k are parameters from Hussey et al.'s (2014) meta-analysis. In both approaches, PPMR is then estimated using Eq. (1). After conversion of $\delta^{15}\text{N}$ to TP, the equation to estimate PPMR becomes

$$\text{PPMR}_{\text{TP}} = n^{(1/b)} \quad (4)$$

Simulated data

To explore how PPMR estimates differ between the additive and scaled approaches, we simulated $\delta^{15}\text{N}$ values for a theoretical community of individuals ranging in body mass from 4 to 10^6 g, binned into \log_2 mass classes ranging from 2 to 20. We parameterised the simulations with values to reflect biologically realistic isotope values for aquatic communities. $\delta^{15}\text{N}$ increased sequentially for each mass class by a random number drawn from a normal distribution (mean = 0.34, standard deviation = 0.05), representing the generally positive increase of $\delta^{15}\text{N}$ with mass class observed in other studies (e.g. Jennings et al. 2001, Al-Habsi et al. 2008). The initial $\delta^{15}\text{N}$ (at log mass class 2) spanned a range of values of primary consumers, increasing from $\delta^{15}\text{N}_{\text{base}}$ values of 4 (Chiba et al. 2012, Hussey et al. 2014) to 11 (El-Sabaawi et al. 2012). We examined 2 theoretical communities. First, we performed the simulations for a low $\delta^{15}\text{N}$ community, where the initial $\delta^{15}\text{N}$ was similar to $\delta^{15}\text{N}_{\text{base}}$. Second, since trophic level estimates vary depending on the baseline trophic level (Mancinelli et al. 2013, Hussey et al. 2014), and as the study design and sampling gears used in some previous studies sampled communities beginning at a trophic level of 4 (Jennings & Warr 2003), we also ran the simulations with initial $\delta^{15}\text{N}$ at 6 above $\delta^{15}\text{N}_{\text{base}}$ to explore the effects of sampling these higher trophic level organisms (e.g. Jennings et al. 2002).

TP_{base} for all simulations was 2.5 following Jennings & Warr (2003), although our results are robust to other biologically plausible TP_{base} values, as TP_{base} is a constant in both methods of estimating TP (Eqs. 2

& 3). We show that the robustness of our simulation results does not depend on the PPMR value by repeating our simulations for communities with low PPMR (e.g. Jennings et al. 2002) and high PPMR (e.g. Al-Habsi et al. 2008; see Supplement at www.int-res.com/articles/suppl/m516p001_supp.pdf, Figs. S1 & S2). All simulations were repeated for 10 000 replicates. All analyses were conducted in R (version 3.0.2) (R Core Team 2013), and the code used to generate the analyses is available on GitHub (<https://github.com/baumlab/ppmr-isotopes>).

North Sea data

We then reanalysed the North Sea stable isotope data from Jennings & Warr (2003) to determine the extent to which the biases evidenced from our simulations affect PPMR estimates in real food webs. Stable isotope estimates were extracted from fish sampled by an otter trawl at 74 sites in the North Sea. Detailed sampling methods are described in Jennings & Warr (2003). We compared PPMR estimates from the additive and scaled approaches, and divided sites into high ($>7\%$) and low ($<7\%$) $\delta^{15}\text{N}_{\text{base}}$ samples to determine how estimates of PPMR varied with $\delta^{15}\text{N}_{\text{base}}$. We used an integer value between the median and midpoint of the dataset (median = 5.8, midpoint = 7.6, cut off = 7‰) to compare equivalent ranges of $\delta^{15}\text{N}_{\text{base}}$ while accounting for skewed sampling at low $\delta^{15}\text{N}_{\text{base}}$.

RESULTS AND DISCUSSION

Our analyses show that the assumption of a constant $\Delta^{15}\text{N}$ of 3.4‰ can result in vastly different estimates of PPMR than when one employs a more realistic scaled approach. The extent of this bias depends on 2 factors: the $\delta^{15}\text{N}_{\text{base}}$ value and the trophic level of the sampled community. For a low $\delta^{15}\text{N}$ community, the additive approach overestimated PPMR by over 1000 at low $\delta^{15}\text{N}_{\text{base}}$ values ($\delta^{15}\text{N}_{\text{base}} = 4\text{--}8\%$), but underestimated PPMR by approximately 500 at high $\delta^{15}\text{N}_{\text{base}}$ values ($\delta^{15}\text{N}_{\text{base}} = 8\text{--}11\%$; Fig. 2a). In the scaled approach, initial $\Delta^{15}\text{N}$ is much larger than 3.4‰ at low $\delta^{15}\text{N}_{\text{base}}$ values, producing lower trophic level estimates, a correspondingly lower b and higher PPMR estimates (Fig. 1). As $\delta^{15}\text{N}_{\text{base}}$ increases to 8‰, $\Delta^{15}\text{N}$ approaches 3.4‰ such that PPMR estimates converge, while at $\delta^{15}\text{N}_{\text{base}}$ greater than 8‰, $\Delta^{15}\text{N}$ decreases below 3.4‰, trophic level estimates increase, and PPMR decreases (Fig. 2a).

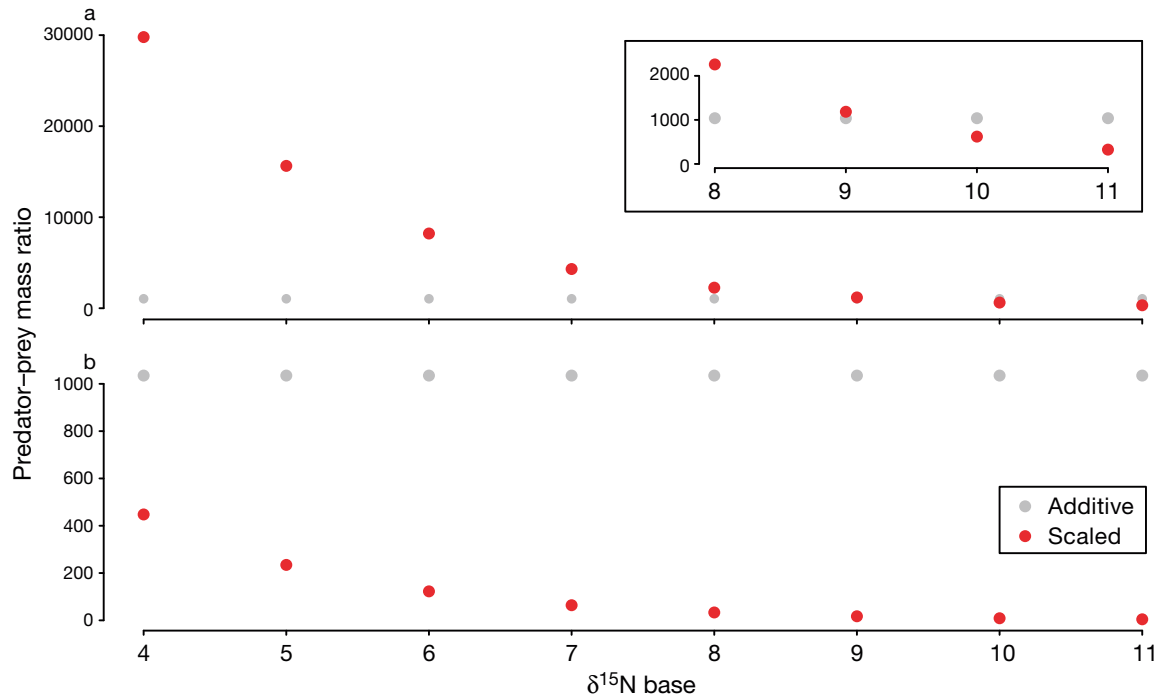


Fig. 2. Predator–prey mass ratio (PPMR) estimates calculated from additive and scaled estimates of trophic level across a range of $\delta^{15}\text{N}_{\text{base}}$ (4–11‰). (a) PPMR estimates for a low $\delta^{15}\text{N}$ community (initial $\delta^{15}\text{N}$ similar to $\delta^{15}\text{N}_{\text{base}}$), inset with $\delta^{15}\text{N}_{\text{base}}$ 8–11‰ at smaller PPMR scale to highlight differences between estimates. (b) PPMR estimates for a high $\delta^{15}\text{N}$ community (initial $\delta^{15}\text{N}$ at 6 above $\delta^{15}\text{N}_{\text{base}}$). Note the different scales on the y-axes. In both sample types, PPMR is approximately 1000 under the additive approach

For a high $\delta^{15}\text{N}$ community, additive PPMR estimates are overestimated by approximately 400 when $\delta^{15}\text{N}_{\text{base}}$ is 4‰, and by 1000 when $\delta^{15}\text{N}_{\text{base}} > 7$ ‰ (Fig. 2b). When higher trophic level organisms are sampled (corresponding with higher $\delta^{15}\text{N}$), the scaled approach estimates of PPMR decrease with increasing $\delta^{15}\text{N}_{\text{base}}$ (Fig. 2b). Since the largest difference between the scaled $\Delta^{15}\text{N}$ and the additive $\Delta^{15}\text{N}$ occurs where the dietary $\delta^{15}\text{N}$ is lowest, by sampling at high $\delta^{15}\text{N}$ the differences are muted (Fig. 2b). Results are qualitatively similar for a range of PPMR estimates under the additive approach (see Figs. S1 & S2 in the Supplement at www.int-res.com/articles/suppl/m516p001_supp.pdf) and show that because of the inverse relationship between $\Delta^{15}\text{N}$ and dietary $\delta^{15}\text{N}$, the estimate of PPMR depends strongly on the $\delta^{15}\text{N}_{\text{base}}$ value.

The scaled approach diverges markedly from the additive one when $\delta^{15}\text{N}_{\text{base}}$ is especially large or small. When dietary $\delta^{15}\text{N}$ is between approximately 5 and 13‰, however, bias in PPMR estimates between the scaled and additive approach is negligible (e.g. Fig. 2, Hussey et al. 2014). The subsequent deviation in PPMR estimates is generally smaller if the body mass – $\delta^{15}\text{N}$ relationship is entirely contained in this range. However, if the dietary $\delta^{15}\text{N}$ falls at the boundaries of

this range, the difference between methods is more apparent, with the scaled approach predicting $\Delta^{15}\text{N}$ values double of the additive approach at low $\delta^{15}\text{N}$, and less than half at high $\delta^{15}\text{N}$ (Caut et al. 2009, Hussey et al. 2014).

Jennings & Warr (2003) analysed isotope data of North Sea food webs with the additive approach and reported a mean community PPMR of 424:1. We reanalysed these data using the scaled approach and found mean North Sea PPMR equal to 430:1 (Fig. 3a), despite our simulations predicting a greater bias at similar $\delta^{15}\text{N}_{\text{base}}$ (North Sea data: 4.5–10.7‰, mean = 6.3‰) and $\delta^{15}\text{N}$ (North Sea data: 8–18‰, mean = 12.8‰) values (Fig. 2b). To explore these disparate results, we disaggregated the North Sea into low and high $\delta^{15}\text{N}_{\text{base}}$ sites. We then found strong support for the model prediction (Fig. 3b,c). At sites with $\delta^{15}\text{N}_{\text{base}} < 7$ ‰, additive PPMR was 331:1, whereas scaled PPMR was only 187:1. At sites with $\delta^{15}\text{N}_{\text{base}} > 7$ ‰, additive PPMR was 3915:1 and scaled PPMR was 255:1. As predicted by the high $\delta^{15}\text{N}$ model (Fig. 2b), scaled PPMR is consistently lower than additive PPMR, and the difference increases with $\delta^{15}\text{N}_{\text{base}}$.

The similar scaled and additive estimates for the full North Sea community were driven by the inclusion of the largest mass class (13.5), which was sampled only at 4 low $\delta^{15}\text{N}_{\text{base}}$ sites ($\delta^{15}\text{N}_{\text{base}} = 4.5$,

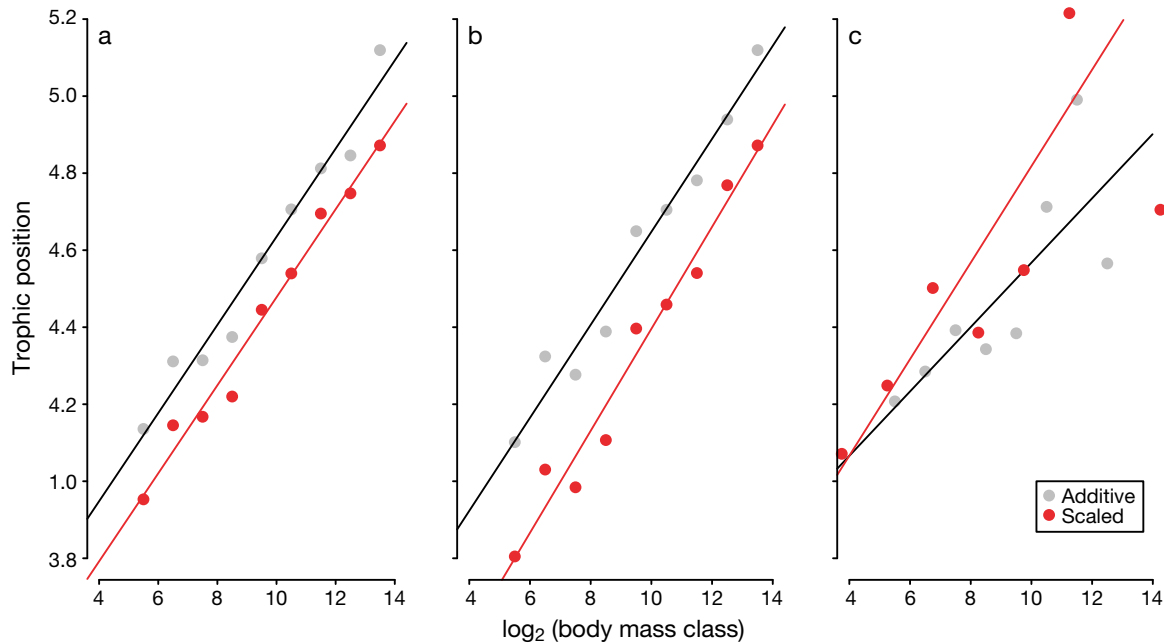


Fig. 3. Trophic level estimates from additive and scaled approaches for North Sea fish data from Jennings & Warr (2003). Estimated trophic position presented for: (a) the full community, (b) sites where $\delta^{15}\text{N}_{\text{base}} < 7\text{‰}$, (c) sites where $\delta^{15}\text{N}_{\text{base}} > 7\text{‰}$

4.8, 5.2, 5.5). For a single mass class sample, at low $\delta^{15}\text{N}_{\text{base}}$ the level of discrimination is greater than at high $\delta^{15}\text{N}_{\text{base}}$ and the corresponding scaled TP is lower. In the full community analysis, the TP estimate at mass 13.5 was necessarily lower relative to other mass classes (where each other $\delta^{15}\text{N}_{\text{base}}$ estimate reflected the full range of $\delta^{15}\text{N}_{\text{base}}$), contributing to a lower slope and thus greater scaled PPMR estimate. When sample sizes are equivalent across $\delta^{15}\text{N}_{\text{base}}$ values and mass classes (Fig. 2b,c), scaled PPMR is lower than additive PPMR, thus reflecting our predictions. Note that in splitting sites by their $\delta^{15}\text{N}_{\text{base}}$ value, our approach is not indicative of the overall North Sea community PPMR but instead allows us to explore variation in PPMR across a range of $\delta^{15}\text{N}_{\text{base}}$.

Although the underlying mechanism is not understood, the inverse relationship between $\Delta^{15}\text{N}$ and dietary $\delta^{15}\text{N}$ has been demonstrated by a number of controlled laboratory experiments (Caut et al. 2008, Dennis et al. 2010) as well as meta-analyses of published data from across an array of aquatic organisms (Caut et al. 2009, Hussey et al. 2014). Many factors can affect $\Delta^{15}\text{N}$, including diet quality (Robbins et al. 2010), temperature (Power et al. 2003), and type of nitrogen excretion (Vanderklift & Ponsard 2003). However, these other factors do not vary consistently with body size and thus would not cause a systematic change in $\Delta^{15}\text{N}$. The systematic change in $\Delta^{15}\text{N}$ with dietary $\delta^{15}\text{N}$, and thus body size, demands further investigation.

Previous PPMR estimates have been calculated across the range of $\delta^{15}\text{N}$ values where we expect substantial differences between the scaled and additive approaches. According to our simulations, the additive PPMR estimates of both Jennings et al. (2008a) (PPMR = 109:1, for $\delta^{15}\text{N}$ of 7.5–14‰) and Al-Habsi et al. (2008) (PPMR = 7792:1, for $\delta^{15}\text{N}$ of 14.1–19‰) may be substantially biased toward overestimating the true community PPMR value. Such biases have important implications for food web studies. As PPMR are used to build fisheries size spectra (Andersen & Beyer 2006, Blanchard et al. 2009), to describe food web structures (Cohen et al. 2003, Bascompte et al. 2005) and to discern general community properties (Riede et al. 2011, Trebilco et al. 2013), the interpretations we draw from such studies depend on the accuracy of PPMR estimates. In the aquatic size spectrum (a relationship between body size and abundance of individuals in a community), the slope is strongly constrained by PPMR and by the efficiency of energy transfer across trophic levels (Jennings & Mackinson 2003). If PPMR is overestimated, the spectrum slope will be underestimated, affecting, for example, the reliability of size spectra as indicators of ecosystem health (Petchey et al. 2010).

Stable isotope analyses have vastly advanced our understanding of the importance of size in food webs (Jennings et al. 2002, 2008b). Here, we demonstrate that isotope-based PPMR estimates are sensitive to systematic differences in the discrimination factor.

Adopting the scaled approach to studies of trophic position and PPMR in real food webs will ensure improved comparisons of food web properties across habitats with varying nitrogen baselines, and across a full range of trophic positions.

Acknowledgements. We thank Simon Jennings for providing the North Sea community stable isotope data and for providing comments on an earlier draft of the manuscript. We acknowledge support from The Leverhulme Trust (to J.P.W.R.), NSERC Strategic Project Grant (to A.M. and M.T.) and NSERC Discovery Grants (to A.M. and J.K.B.).

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