



Comparing trophic structure of a subtropical bay as estimated from mass-balance food web model and stable isotope analysis



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ABSTRACT

The trophic structure of a subtropical bay in Taiwan Strait was analyzed by using two methods: mass balance modeling (Ecopath) and stable isotopic analysis (SIA). Trophic levels (TLs) of main functional groups estimated from the two methods were compared. The Ecopath model was built based on the fishery resource survey in Xiamen Bay in 2009. Specifically, data on species composition, biomass, mortality rates, diet composition and fisheries catches were obtained from the survey in and around the bay. The model consisted of 26 functional groups, including plankton, benthos, fish, cephalopods, shrimps, crabs and marine mammals. TLs of the main functional groups were estimated to be between 2.89 (cephalopods) and 3.94 (congers), with an average of 3.11. Trophic transfer efficiencies from levels II to V were 12.8%, 19.2%, 19.7% and 12.1%, respectively. Catfish (*Tachysurus sinensis* and *Netuma thalassina*) and the fisheries have major trophic impacts on most functional groups in the Xiamen Bay ecosystem. Total system throughput was estimated to be 411 t km⁻² year⁻¹. TLs derived from isotopic analysis were highly correlated with those estimated from Ecopath (Linear regression: $R^2 = 0.696$, $n = 23$, $p < 0.001$). On an average, Ecopath underestimated TLs of the functional groups by about 12.2% compared to those estimated from SIA, with TLs from Ecopath being slightly higher at low TLs and lower at high TLs. This studies support value of using both stable isotopes and Ecopath methods to analyze this food web.

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1. Introduction

Trophodynamic models and stable isotope analysis (SIA) are commonly used approaches to quantify trophic levels in marine food webs (Nilsen et al., 2008). One of the modeling approaches that have been most widely used is Ecopath with Ecosim (Christensen et al., 2008, 2014; Downing et al., 2012). Ecopath allows the application of network analysis to calculate effective trophic levels (TLs) for ecosystem functional groups based on carbon flow between groups and food web relationships derived mainly from laboratory feeding experiments and analysis of stomach contents.

SIA has become a standard approach for understanding trophic interactions (Peterson and Fry, 1987; Post, 2002). Carbon and nitrogen stable isotope ratios, in particular, have been shown to be a valuable source of information to understand animals' sources of diet (e.g., Papiol et al., 2012). By comparing TLs value from Ecopath with TLs estimated from $\delta^{15}\text{N}$ SIA, it is possible to validate the

network model (Deehr et al., 2014). Disagreement in such comparison could indicate an incompletely specified ecosystem model or unaccounted variation in stable isotope concentration due to environmental, metabolic or species-specific parameters (Dame and Christian, 2008).

Several recent studies have shown good agreement between TLs calculated from $\delta^{15}\text{N}$ values and those from food web models (Dame and Christian, 2008) although some studies also show that TLs estimated from Ecopath models are different from $\delta^{15}\text{N}$ -based TLs (Polunin and Pinnegar, 2000; Milessi et al., 2010). For example, Nilsen et al. (2008) shows that TLs from Ecopath are slightly lower than isotope-based estimates and vice versa.

Here, using Xiamen Bay marine ecosystem as a case study, we aim to compare TLs of key functional groups estimated from SIA and Ecopath trophic dynamic modeling. Several quantitative studies on the trophic ecology of Xiamen Bay have been conducted (Huang et al., 2006, 2008; Zhang and Huang, 2009; Du et al., 2012; Liao et al., 2014). However, the system has not been described using a trophic model. Thus, in this study, we develop an Ecopath model for Xiamen Bay marine ecosystem and analyze its trophic structure. We also estimate the TLs of key ecosystem groups using stable isotope

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approach. We then compare the trophic position and trophic levels estimated from the two methods.

2. Materials and methods

2.1. Study area

Xiamen Bay is a subtropical area, located from 24°21' to 24°32'N and from 118°05' to 118°13'E in the southeast coast of China bordering the Taiwan Strait to the east (Fig. 1). The area covers about 1260 km², with water depth ranging from 5 to 31 m. There are 31 islands in the Bay. The outflows of Jiulong River (Compiling Committee of Records of China Bays, 1993) greatly influence plankton dynamics, composition and function of the Bay's food web (Huang et al., 2008). Moreover, Xiamen Bay supports a rich fauna while it is subjected to a variety of anthropogenic activities such as fishing and shipping (Lu et al., 1998; Zhang and Huang, 2009; Du et al., 2012; Liao et al., 2014).

2.2. Mass-balanced trophic dynamic model

Ecopath with Ecosim (EwE) is one of the most widely used food web modeling and network analysis tools for marine, estuaries and freshwater ecosystems around the world. Ecopath was first developed to model coral reef ecosystems (Polovina, 1984). It was then further developed into the Ecopath with Ecosim software package (Christensen and Pauly, 1992; Christensen et al., 2005). This study used EwE version 6.4 that was available at <http://www.ecopath.org/>

Ecopath model is based on the mass balance of energy that goes into and out of the modeled ecosystem. To reduce complexity of the model, species with similar ecological characteristics are usually aggregated into functional groups. The model assumes that total amount produced or consumed by a group is equal to the amounts that go out of the group through predation and fishing mortalities, migrations and biomass accumulations:

$$B_i(P/B)_i EE_i = Y_i + \sum_{j=1}^n B_j(Q/B)_j DC_{ij} + B_i BA_i + E_i \quad (1)$$

where, B is biomass, P the production, EE the ecotrophic efficiency, Y the fishery catch, i and j are prey and predator groups, Q is consumption, DC the diet composition, BA the biomass accumulation and E the net immigration. The model achieves mass balance by solving Eq. (1) simultaneously for all functional groups in the model. Thus, one of the input parameters B , P/B , Q/B or EE for each functional group should be left to be estimated by the model.

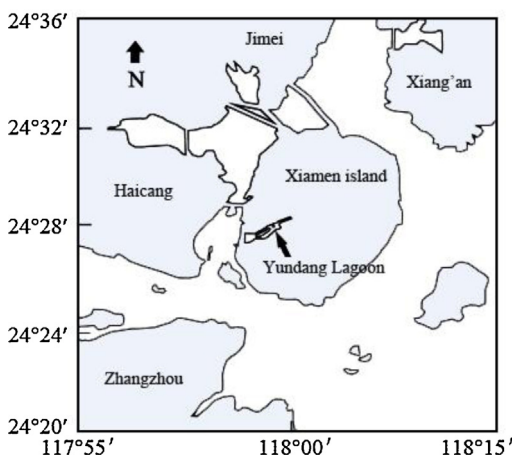


Fig. 1. Study area of the Xiamen Bay.

An Ecopath model representing the state of Xiamen Bay marine ecosystem in 2009 was developed. The model area is 1260 km². The biomass flows within this area was assumed to be closed. We aggregated major species occurring in Xiamen Bay into 26 functional groups according to their ecological characteristics. Input parameters were based on data collected from the fishery resources surveys in 2009, fishery statistics, published literature and reports on diet compositions and FishBase (www.fishbase.org). Specifically, biomass estimates for most functional groups were based on survey data and published literature, while P/B was based on estimated total mortality rates and other publications. Q/B of fish and non-fish groups was based on data from FishBase and published literature. Catch is based on Fujian statistical yearbook (Yang, 2009). Diet composition matrix of the model is based on survey data and published literature (Yang, 2001a,b; Huang et al., 2008; Cheng et al., 2009). As biomass and diet composition are most uncertain among the input parameters, they were adjusted to achieve mass-balance of the model.

2.3. Stable isotopes processing

The SIA was performed on 23 species/groups, including marine mammals, cartilaginous fish, bony fish, mollusks, crustaceans, benthos and zooplankton. All the muscles samples were freeze-dried at -40 °C, ground into powder and sieved with 120 meshes. The $\delta^{15}\text{N}$ signals of samples were measured using an isotope ratio mass spectrometer (IRMS) attached to a Flash EA1112 HT Elemental analyzer. The ratio of $^{15}\text{N}/^{14}\text{N}$ was detected by IRMS, and then compared with the international standards (Pee Dee Belemnite and atmospheric N_2), after which $\delta^{15}\text{N}$ was calculated using the following equation:

$$\delta^{15}\text{N}(\text{‰}) = \frac{(R_{\text{sample}} - R_{\text{standard}})}{R_{\text{standard}}} \times 1000 \quad (2)$$

The detection limits were 0.2‰ for $\delta^{15}\text{N}$. R represents the $^{15}\text{N}/^{14}\text{N}$.

2.4. Comparison between Ecopath and isotope results

TLs of each organism were estimated according to Post (2002):

$$\text{TL}_{\text{consumer}} = \text{TL}_{\text{basis}} + \frac{(\delta^{15}\text{N}_{\text{consumer}} - \delta^{15}\text{N}_{\text{basis}})}{\text{TEF}} \quad (3)$$

where, TL_{basis} is the trophic position of a primary consumer used to estimate the TLs of other consumers in the food web (Vander Zanden and Rasmussen, 1999; Post, 2002), and is assumed to be equal to 2. $\delta^{15}\text{N}_{\text{consumer}}$ is the value measured for consumers. $\delta^{15}\text{N}_{\text{basis}}$ is $\delta^{15}\text{N}$ of organisms that are herbivores and are sessile or have very limited mobility. In the present study, *Ruditapes philippinarum* was identified as the most important species that makes up the total organic matter at the base of the food web. TEF is the $\delta^{15}\text{N}$ trophic enrichment factor for the difference between a source and its consumer, and 3.4 parts per thousand (ppt) is the average $\delta^{15}\text{N}$ enrichment per trophic level (Vander Zanden and Rasmussen, 2001).

TLs estimated by the Ecopath model were plotted against the corresponding TLs estimated by SIA and their correlation was tested using the Spearman-rank correlation coefficient test (Zar, 1999).

3. Results

3.1. Ecopath outputs and sensitivity

The basic input such as biomass, landings, P/B , Q/B , diet composition and estimated outputs like TLs, mortality rates and ecotrophic efficiency from the Xiamen Bay model in 2009 are summarized in Table 1 and Table 2. The flow diagram of the balanced trophic model

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