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Production sources and food web of a macrophyte-dominated region in Lake Taihu, based on gut contents and stable isotope analyses

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ABSTRACT

We estimated the food web linkages among primary producers, invertebrates and fish in a macrophyte-dominated region of a eutrophic lake (Lake Taihu) by analyzing gut contents and C and N stable isotope ratios. Observation of the gut contents reflected a variety of feeding modes among fish species that consume a diverse assortment of prey, with limited dietary overlap. Basal food sources were distinguishable based on their $\delta^{13}C$ isotopic signatures, and wide seasonal variations of isotope values were observed in the lake biota with a general trend towards enriched $\delta^{13}C$ and $\delta^{15}N$ values in summer and depleted values in winter. This pattern could be explained by a combination of environmental (e.g., irradiance and nutrient inputs) and biotic (e.g., availability of food sources and plasticity in prey item choice) features. We adopted a paired (gut contents and stable isotopes) approach to reconstruct diets that used known food items as end members in the isotopic mixing model analysis and diagrammed the food web structure of Lake Taihu describing the organic matter pathways from primary producers to predators of the upper trophic levels. Our surveys also corroborate the finding that phytoplankton were the most important primary source of organic matter for fauna within this macrophyte-dominated lake region, whereas macrophytes also made a sizeable contribution for several invertebrate and fish species, especially in winter.

Introduction

In recent years, several theoretical and empirical studies have emphasized the importance of understanding trophic interactions in lacustrine communities as an essential step in restoring the water quality and aquatic ecosystem functions (Carpenter and Kitchell, 1993; Fry, 2006). Over a range of nutrient concentrations, the communities of shallow lakes can be dominated either by aquatic plants and have clear water, or by phytoplankton and have turbid water (Canfield et al., 1984). Anthropogenic nutrient loads to shallow limnetic waters have been linked to shifts from macrophytes- to algae-dominated communities in many regions of the world, yet the influence that these shifts have on the structure of aquatic food webs remains unclear. In contrast to algae-dominated lakes, lakes dominated by macrophytes are species-rich with complex structure and food webs (Jeppesen et al., 1998). As a consequence, describing the food web by characterizing trophic relationships, the main food sources of consumers and the energy pathways among the components in complex macrophyte-dominated aquatic systems is difficult, especially only using traditional gut content analysis (Jones and Waldron, 2003).

Gut content analysis is considered to be a standard practice for identifying carbon sources and fish trophic relationships (Hyslop, 1980). This technique has several inherent limitations such as providing only a short-term (hours to days) pattern of mass transfer, the requirement of high sampling frequency and considerable taxonomic expertise (Vander Zanden et al., 1997). These limitations have led to increasing emphasis on stable isotope analysis as a tool to assess the ultimate food sources and aquatic food web structure (Peterson and Fry, 1987; Post, 2002). This method is based on the premise that predators are enriched in heavy isotope forms compared to their prey in a predictable way (Minagawa and Wada, 1984). Whereas gut contents can provide a taxonomic resolution of recent consumption, stable isotopic compositions integrate the signatures of different prey consumed over much longer periods of time. However, gut content analysis can provide direct evidence of an organism's prey items that may be difficult to achieve by stable isotope analysis. Peterson (1999) also suggested that stable isotope analysis is most effectively used in combination with other

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techniques such as gut content analysis. A number of relatively detailed food web studies combined using gut contents and stable isotope analyses have been published in estuaries (Pasquaud et al., 2008), rivers (Davis et al., 2012), lakes (Jones and Waldron, 2003) and marine systems (Drazen et al., 2008). But, many of these studies have aimed at identifying the sources of energy for a species or a group of species, comparing trophic position of consumers and understanding ontogenetic dietary shifts, rather than detailing relationships among the aquatic community as a whole, especially any seasonal variations in food web structure.

Lake Taihu is situated in the Changjiang (Yangtze) delta, the most industrialized area in China with high population density, urbanization, and economic development. Lake Taihu is characterized by its shallowness (mean depth = 1.9 m) and large surface area (2338 km^2) (Qin et al., 2007). Since the 1980s, however, eutrophication and algal blooms have occurred because of the deterioration of water quality. Recently, algal blooms have extended their coverage and persist throughout the summer, which affects the imbalance of food web and the ecosystem functions of the lake (Liu et al., 2011; Qin et al., 2006). Within Lake Taihu, there are significant differences in environmental conditions between different lake regions which have different nutrient levels and distribution of macrophytes. The eastern region of the lake is fully covered by a submersed macrophyte community; whereas, all other lake areas are characterized by the absence of macrophytes and by occurrence of cyanobacteria-dominated algal blooms (Wu et al., 2007) (Fig. 1). In marked contrast to lakes dominated by phytoplankton, macrophyte-dominated lakes are species-rich and complex, both in terms of food sources and biotic interactions (Jeppesen et al., 1998). Although some authors have found that submerged macrophytes may be an important food source in a few plant-dominated aquatic ecosystems, whether aquatic consumers rely primarily for sustenance upon macrophytes or phytoplankton has been often debated (France, 1996; Vizzini and Mazzo, 2003). Moreover, algal blooms occurring in Lake Taihu during summer seem to have a strong influence on the competitive balance between macrophytes and algae, and may be one of the prime determinants of seasonal variations of this lake food web. Despite the high biotic diversity and ecological importance of Lake Taihu, stable isotope data on food webs in this region are still scarce (Mao et al., 2012). Little is known about the role of trophic interactions in the community structure and dynamics of Lake Taihu compared with other aquatic communities (Jones and Waldron, 2003; Wang et al., 2011). In this study, we examined gut contents in combination with stable carbon and nitrogen isotopes to trace and compare the main food sources and trophic links of dominant consumers in a macrophyte-dominated region of this shallow, eutrophic lake. We also tested the hypothesis that seasonal variations of environmental conditions, particularly the higher occurrences of algal blooms in the warm period of the year, influenced the contributions of production sources and these relationships. Therefore, the overall aim of the present study is to evaluate to what extent these two methods can provide us with knowledge of the structure and functioning of the Lake Taihu aquatic food web.

Methods

Study site

Lake Taihu (119°08′–121°55′E and 30°05′–32°08′N), the third largest freshwater lake (surface area of 2338 km^2; average depth of 1.9 m) in China, is located in the Yangtze Delta plain, on the border of the Jiangsu and Zhejiang provinces (Qin et al., 2007). This lake is an important resource for drinking water, fisheries and vegetation, and about 35 million people inhabit the 36,500 km^2 watershed of Taihu Lake.

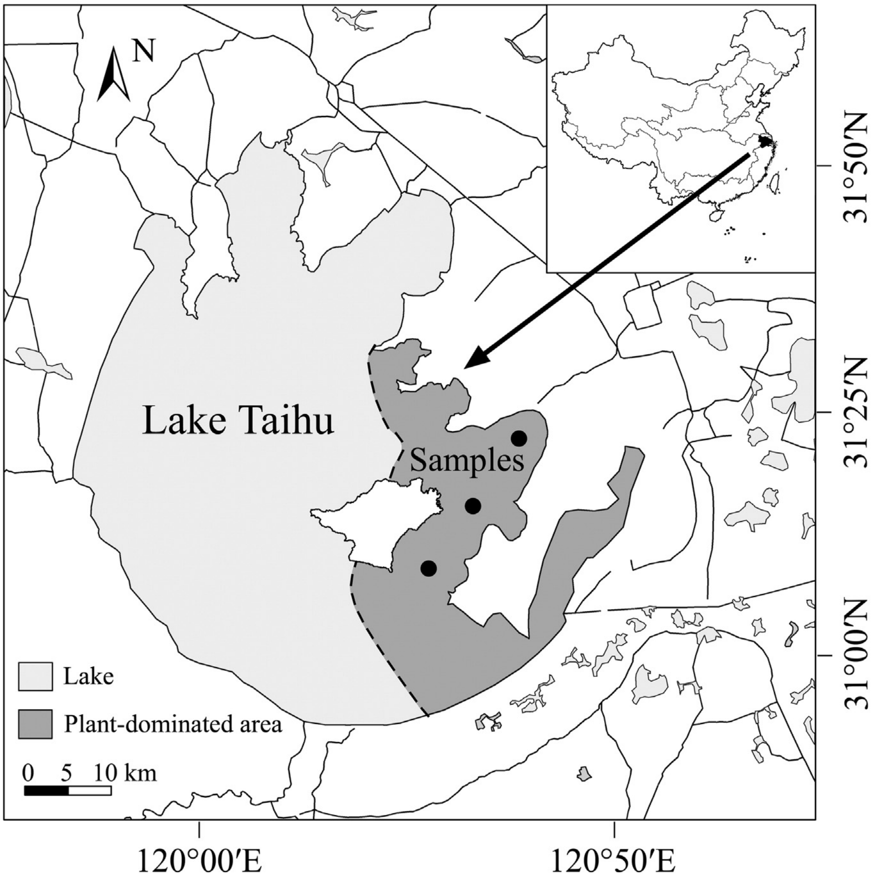

Fig. 1. Map of the Lake Taihu showing macrophyte-dominated area and sampling sites.

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