Marine Pollution Bulletin xxx (2014) xxx–xxx

Contents lists available at ScienceDirect

Marine Pollution Bulletin

journal homepage: www.elsevier.com/locate/marpolbul

An approach to bioassessment of water quality using diversity measures based on species accumulative curves

Guangjian Xu [a], Wei Zhang [b], Henglong Xu [a,*]

[a] College of Marine Life Science, Ocean University of China, Qingdao 266003, China
[b] College of Fisheries, Ocean University of China, Qingdao 266003, China

ARTICLE INFO

Article history:
Available online xxxx

Keywords:
Species diversity
Bioassessment
Microperiphyton
Species-accumulative curves
Marine ecosystems

ABSTRACT

Traditional community-based bioassessment is time-consuming because they rely on full species-abundance data of a community. To improve bioassessment efficiency, the feasibility of the diversity measures based on species accumulative curves for bioassessment of water quality status was studied based on a dataset of microperiphyton fauna. The results showed that: (1) the species accumulative curves well fitted the Michaelis–Menten equation; (2) the β- and γ-diversity, as well as the number of samples to 50% of the maximum species number (Michaelis–Menten constant *K*), can be statistically estimated based on the formulation; (3) the rarefied α-diversity represented a significant negative correlation with the changes in the nutrient NH_4–N; and (4) the estimated β-diversity and the *K* constant were significantly positively related to the concentration of NH_4–N. The results suggest that the diversity measures based on species accumulative curves might be used as a potential bioindicator of water quality in marine ecosystems.

1. Introduction

Microperiphyton is a primary component of periphytic microfauna, and plays an important role in mediating the flux of both matter and energy from plankton to benthos in most aquatic ecosystems (Fischer et al., 2002; Kathol et al., 2009; Norf et al., 2009; Xu et al., 2011, 2014a, b, c; Zhong et al., 2014). Because they respond rapidly to environmental changes, are easily sampled and allow standardization for spatial and/or temporal comparisons, the microperiphyton has successfully be used as a useful bioindicator of water quality status in aquatic environments (Gold et al., 2002; Khatoon et al., 2007; Risse-Buhl and Küsel, 2009; Morin et al., 2010; Zhang et al., 2012; Xu et al., 2014a, b). However, traditional community-based monitoring programs are time-consuming because they rely on the both identification and enumeration of all species within the community. In order to improve bioassessment efficiency, the potential of species diversity measures based on the species accumulative curve (SAC) was explored to confirm the feasibility as a useful bioindicator of water quality status.

In this study, the feasibility of the SAC-based diversity measures for evaluating water quality status was studied, based a dataset of microperiphyton communities. Our aim was to establish a methodology based on the SACs. The main points for this objective were: (1) to extract the α-, β- and γ-diversity measures and the relevant parameter based on the SACs; (2) to reveal their relationships with the environmental conditions; and (3) to develop a method allows removing the influence of sampling effort on species diversity information in marine ecosystems.

2. Materials and methods

2.1. Data collection

Microperiphyton communities were collected from four sampling stations in coastal waters, near Qingdao, northern China, each with different levels of water quality (Fig. 1: Xu et al., 2014a). A total of 40 samples were collected monthly at the four stations from August 2011 to July 2012 (Fig. 1). Microscopy glass slides, each with an area of 2.5 × 7.5 cm, were used as artificial substrates for collecting the microperiphyton. For each sampling at each station, 20 glass slides, as two replicates of the sample with 10 slides each, were immersed at a depth of 1 m below the water surface and exposed for 14 days in order to allow colonization by microperiphyton species. Thus, a total of 960 glass slides were examined during the study period. The slides were then retrieved, transferred into Petri dishes with the *in-situ* sea water from the station, placed in a cooling box, and transported to the laboratory for identification (Xu et al., 2009).

* Corresponding author. Tel./fax: +86 532 8203 2082.
E-mail address: henglongxu@126.com (H. Xu).

http://dx.doi.org/10.1016/j.marpolbul.2014.11.041
0025-326X/

Species identification was conducted following the methods described by Xu et al. (2014a). Protargol staining was carried out for species identification where necessary (Song et al., 2009). Identifications were performed using keys and guides references such as Song et al. (2009). Although the glass slide substrates used in this study were colonized by a range of microperiphyton organisms, including bacteria, fungi, algae, and micrometazoa, we have restricted our taxonomic analyses to ciliated protozoa.

The environmental factors, nitrate nitrogen (NO_3–N), nitrite nitrogen (NO_2–N), ammonium nitrogen (NH_3–N), soluble reactive phosphate (SRP) and COD were measured according to the "Standard Methods for the Examination of Water and Wastewater" (APHA, 1992). The measurements of water temperature (T), pH, salinity (Sal) and dissolved oxygen (DO) were recorded using WTW Multi 3500i sensor. Transparency (Tra) was measured *in situ* using a transparent scale.

2.2. Data analyses

The SACs were modeled by the asymptotic Michaelis–Menten equation:

$$\gamma_n = \gamma_{max}/(1 + K/n) \quad (1)$$

where γ_n is the accumulative species number at nth sample; γ_{max} is the predicted maximum accumulative species number; n is the number of samples; K is a constant, i.e., the number of samples to 50% of the predicted maximum accumulative species number (Flather, 1996; Xu et al., 2014b). The fitness of the equation was tested using the SIGMAPLOT (Xu et al., 2012). Before analysis, the SACs were rarefied using the software package EstimateS v8.2 (Colwell et al., 2004; Mao et al., 2005; Clarke et al., 2011).

The α-, β- and γ-diversities were extracted from SACs: the α-diversity equates to the average number of species, which is mathematically identical to the first point on the SAC, and the final point on the SAC is the total number of species recorded, or the γ-diversity (Crist and Veech, 2006). The β-diversity, as the difference in species richness between the first and last points, was calculated according to the equation developed by Ricotta (2008):

$$\beta = 1 - \alpha/\gamma \quad (2)$$

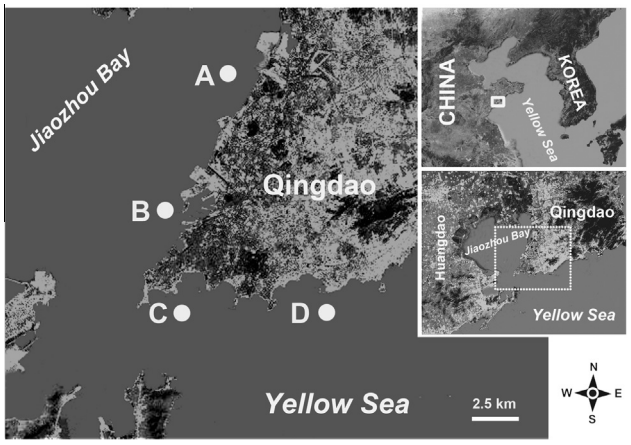

Fig. 1. Sampling stations in coastal waters of the Yellow Sea, near Qingdao, northern China. A: station A, heavily stressed area in Jiaozhou Bay, the pollution being mainly in the form of organic pollutants and nutrients from domestic sewage and industrial discharges from several rivers; B: station B, moderately polluted area Jiaozhou Bay by minor discharges from a small river entering the bay; C: station C, slightly polluted area near the mouth of Jiaozhou Bay and relatively distant from the rivers entering the bay; D: station D, relatively clean area which was outside the bay and distant from the river discharges.

where α is α-diversity, β is β-diversity and γ is γ-diversity (Ricotta, 2008).

Thus, the β-diversity and the sampling effort influence can be predicted through the equation that was derived from the Eqs. (1) and (2):

$$\beta_n = 1 - \alpha/\gamma_{max}(1 + K/n) \quad (3)$$

where β_n is β-diversity and at nth sample.

The correlation analyses between species diversity measures and environmental variables were carried out using the statistical program SPSS v16 at the 0.05 level (Xu et al., 2011). Data were log-transformed before analysis.

3. Results

3.1. Environmental variables

The average values of each environmental factor at the four sampling stations are summarized in Table S1. Salinity ranged from 28.7 to 29.3 psu, with the lowest at station A and the highest value at station B. The pH ranged from 8.13 to 8.28 among the four stations. The values of transparency ranged from 2.0 to 3.6 m, with the highest at station D and the lowest at station A. The values of DO were generally >7.5 mg L^{-1} at all stations, with the highest at station D and the lowest value at station A. Nutrients NO_3–N and SPR were usually lowest at station C and highest at station A, and the NH_4–N decreased from station A to D in concentration (Table S1). The lowest were measured at station C, and the highest values of COD and NO_2–N at stations B and D. Note that the transparency and the values of DO had an increasing trend, while NH_4–N had a generally decreasing trend, from the more polluted areas (A and B) to the less polluted ones (C and D).

3.2. Observed species richness and SACs

The average and accumulative species number recorded in the microperiphyton communities at each sampling station are summarized in Table 1. A total of 144 species were recorded, which occurred in low average number at station A and in high richness at the other three stations (Table 1). However, in terms of accumulative species number, the high values occurred at stations B and C and low at the other two stations (Table 1).

The SACs for all communities at each station were shown in Fig. 2. The curves indicated that the number of accumulative species number (i.e., γ-diversity) in the communities at each station increased with the increase of sampling effort (number of samples) from each initial value (i.e. α-diversity) (Fig. 2). Linear regression revealed that all four SACs were well fitted to the Michaelis–Menten equation ($R^2 > 0.99$; $P < 0.05$) (Fig. 3).

3.3. Diversity based on SACs

The rarefied α-diversities in microperiphyton communities at each station were summarized in Table 2. The values of both α-diversity showed an increasing trend from station A to D (Table 2).

Table 1
Observed average species number and accumulative species number of microperiphyton fauna at four stations in coastal waters of the Yellow Sea during the study period.

S	St. A	St. B	St. C	St. D
AvS	31	36	35	35
AcS	103	115	111	101

AcS: accumulative species number; *AvS*: average species number. St. A–D: stations A–D.

Please cite this article in press as: Xu, G., et al. An approach to bioassessment of water quality using diversity measures based on species accumulative curves. Mar. Pollut. Bull. (2014), http://dx.doi.org/10.1016/j.marpolbul.2014.11.041