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An approach to analysis of colonization dynamics in community functioning of protozoa for bioassessment of marine pollution

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ABSTRACT

Biological trait analysis is a powerful tool to summarize the spatial/temporal patterns of community functioning and ecosystem process at taxon-free resolutions. To identify the optimal colonization period with high homogeneity in functional patterns of protozoa for bioassessment, 1-month baseline colonization survey was conducted in coastal waters of the Yellow Sea. A fuzzy-coding functional trait system was used to summarize the functional structure of protozoan communities during the colonization process. The functional patterns showed a low homogeneity during the early stage (3–7 days), followed by a stable stage (10–14 days) with high homogeneity, and the last stage (21–28 days) with high heterogeneity. The functional richness showed a low variability, while the functional evenness and divergence generally showed a decreasing trend during the whole colonization process. Furthermore, the functional dispersion and RaoQ indices generally leveled off only during the stable stage. These results suggest that it is necessary to determine the optimal exposure time period with high homogeneity of community functioning for bioassessment using protozoan colonization in marine ecosystems.

1. Introduction

Biological trait analysis (BTA) is a powerful tool to summarize community functioning and ecosystem process in response to environmental changes at taxon-free resolutions (Micheli and Halpern, 2005; Schleuter et al., 2010; Dimitriadis et al., 2012; Wan Hussin et al., 2012). Based on this approach, the community structures and biodiversity measures were characterized by the species trait distribution and the range of species functional categories characterize the in functional space (Bremner et al., 2003; Mason et al., 2005; Petchey and Gaston, 2006; Villéger et al., 2008, 2010; Gusmao et al., 2016). Compared with traditional analysis in species space, the BTA has an advantage in monitoring programs by reducing "signal to noise" ratios in multiple species space, and thus has been progressively used as a useful tool for bioassessment (Bremner et al., 2003, 2006; Hewitt et al., 2008; Mouchet et al., 2010; Wong and Dowd, 2015).

As primary grazers, protozoa play an important role in the functioning of microbial ecosystems in aquatic environments (Finlay and Esteban, 1998). They have been successively used as useful bioindicator for bioassessment in a verity type of aquatic ecosystems because of their sensitivity to environmental changes (Norf et al., 2009; Kathol et al., 2011; Zhang et al., 2012; Xu et al., 2014; Zhong et al., 2014). However, the previous work was commonly carried out based on species-abundance data, and thus subjected to influence from high "signal to noise" ratios (Wey et al., 2009; Kathol et al., 2011; Zhang et al., 2012; Xu et al., 2014). Recently, although several works on the trophic-functional structure and body-size spectrum have reported, however, as regards to understandings on functional patterns of protozoan communities using multiple biological traits, little information was known (Tillin et al., 2006; Paganelli et al., 2012; Zhang et al., 2012; Xu et al., 2016).

In this study, we attempted to address the colonization dynamics in community functioning of protozoa in coastal waters of the Yellow Sea. Our aims of this study were: (1) to reveal the temporal variability in functional trait distribution of protozoan communities during the colonization process; (2) to summarize the behaviour of functional diversity measures; and (3) to identify the optimal colonization period with high homogeneity of com-

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Fig. 1. Sampling area in coastal waters of the Yellow Sea, near Qingdao. Arrow, sampling site.

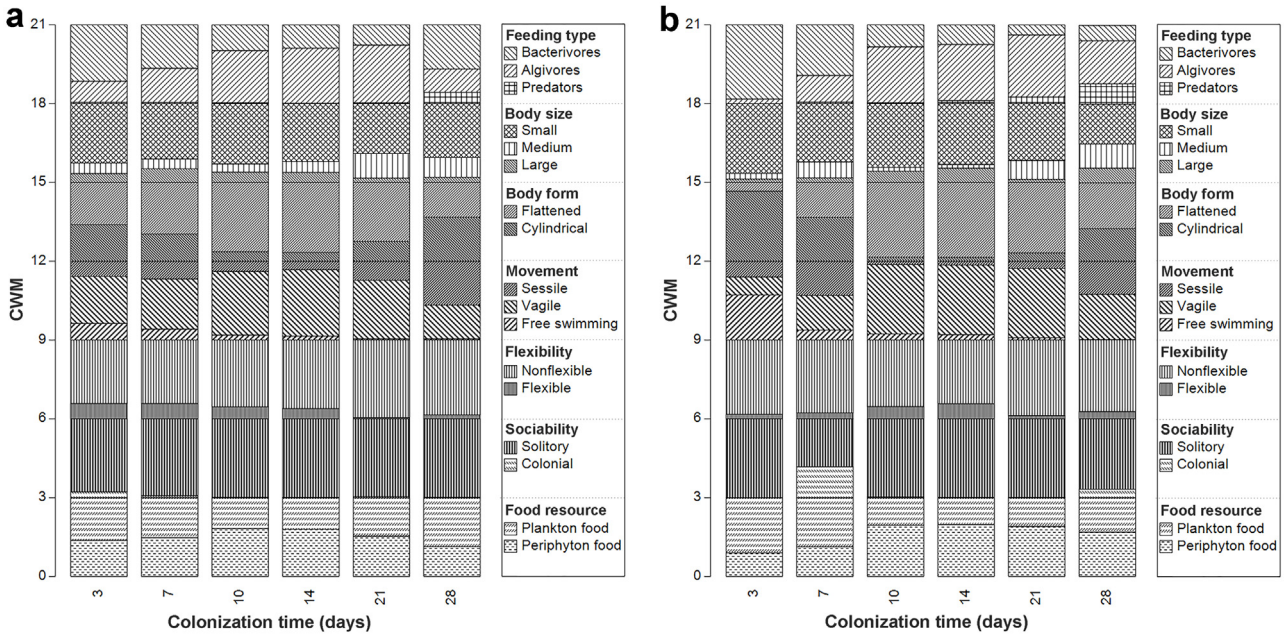

Fig. 2. Temporal variations in community-level weighted means of multiple functional traits of protozoan communities during the colonization process at two depths of 1 (a) and 3 m (b).

munity functioning for bioassessment, using protozoa, in marine ecosystems.

2. Materials and methods

2.1. Data collection

The study site was located in the harbor of the Olympic Sailing Center at Qingdao, northern China (Fig. 1). This was a typical coastal area of the Yellow Sea, with an average depth of ~8 m and an average tidal range of 3 m (Fig. 1).

For the 1-month baseline survey, a total of 240 glass slides were used to collect the ciliates at two depths (1 and 3 m) below the water surface. Seven PVC frames holding 120 slides were immersed at each depth. A total of six sampling events were carried out at intervals of 3, 7, 10, 14, 21 and 28 days after immersion. On each sampling occasion, ten randomly selected slides were collected as an independent sample from one PVC frame at each depth (Xu et al., 2014).

Species identification was carried out based on published keys and guides such as Song et al. (2009). The enumeration of protozoan individuals was performed according to the methods described by Xu et al. (2014).