



An approach to analysis of functional redundancy in protozoan communities for bioassessment in marine ecosystems



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ABSTRACT

It is necessary to detect how much ecological redundancy or response units (RUs) exist in communities for reducing the “signal-to-noise” ratios of the observed full species data in community-based ecological research and monitoring programs. To reveal the functional redundancy in ciliated protozoan communities in marine ecosystems for both ecological research and monitoring programs, a multivariate approach (peeling procedure) was used to identify the response units to the environmental changes using a dataset of biofilm-dwelling ciliates from coastal waters of the Yellow Sea, northern China. From the full 141-species dataset, three subsets with sufficient information of the whole community (correlation coefficient >0.75) were identified as response units (RUs 1–3) at three levels of functional redundancy, which comprised 20, 26 and 27 species, respectively. These response units appeared to be interchangeable between functional equivalents on both spatial and temporal scales. In terms of relative abundance, RU1, which predominated the ciliate communities over 1-year period, and RU2, which occurred only in warm seasons (except winter) with a peak in summer, presented a decreasing trend, while RU3, which distributed all four seasons with two peaks in summer and autumn, increased with the increase of pollution level. Furthermore, high proportions of bacterivores were found in RU1 during warm seasons and represented an increase trend, while high relative abundances of algivores occurred in RUs 2 and 3 appeared to be decreasing along the pollution gradient. These results demonstrated that the ciliated protozoan assemblages have high functional redundancy in response to environmental changes in marine ecosystems.

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1. Introduction

Community-based bioassessment is commonly subject to a strong “signal-to-noise” ratio due to functional redundancy of full species dataset (Clarke, 1993; Clarke and Warwick, 1998; Xu et al., 2014a,b). A number of investigations have revealed that many species are interchangeable between functional equivalents in a community (Clarke and Warwick, 1998; Gray et al., 1998; Zhong et al., 2014; Zhang and Xu, 2015). This implies that there is considerable structural and functional redundancy in response to environmental changes (Menge et al., 1994; Chapin et al., 1995; Frost et al., 1995; Clarke and Warwick, 1998). Thus, it is necessary to detect how much ecological redundancy or response units exists in communities for outlining the functional compensation and for reducing the “signal to noise” ratios of the observed full species data in community-based ecological research and monitoring programs.

As a primary contributor to the functioning of microbial food webs, ciliated protozoa have been used as bioindicator of water quality due to their simple life cycle and sensitive to environmental contaminations in aquatic ecosystems (Sime-Ngando et al., 1995; Coppellotti and Matarazzo, 2000; Xu et al., 2014a,b). However, community response assessment of these organisms has been traditionally conducted based on full species-abundance dataset, and thus are laborious with a significant limit in use (Coppellotti and Matarazzo, 2000; Xu et al., 2014a,b). Although the functional redundancy has been well exploited on macrobenthos, studies on how the functional redundancy is structured in protozoan communities, little information was known (Clarke and Warwick, 1998; Gray et al., 1998).

In this study, a multivariate approach, peeling procedure, was used to identify a response units from a full set of species, based on a dataset of biofilm-dwelling ciliates, which was collected in coastal waters of the Yellow Sea, near Qingdao, northern China from August 2011 to July 2012. The aims of this study was: (1) to identify the levels of functional redundancy, (2) to reveal how the response units structured and changed on temporal and temporal scales, and (3) to indicate how the trophic-functional structures were estab-

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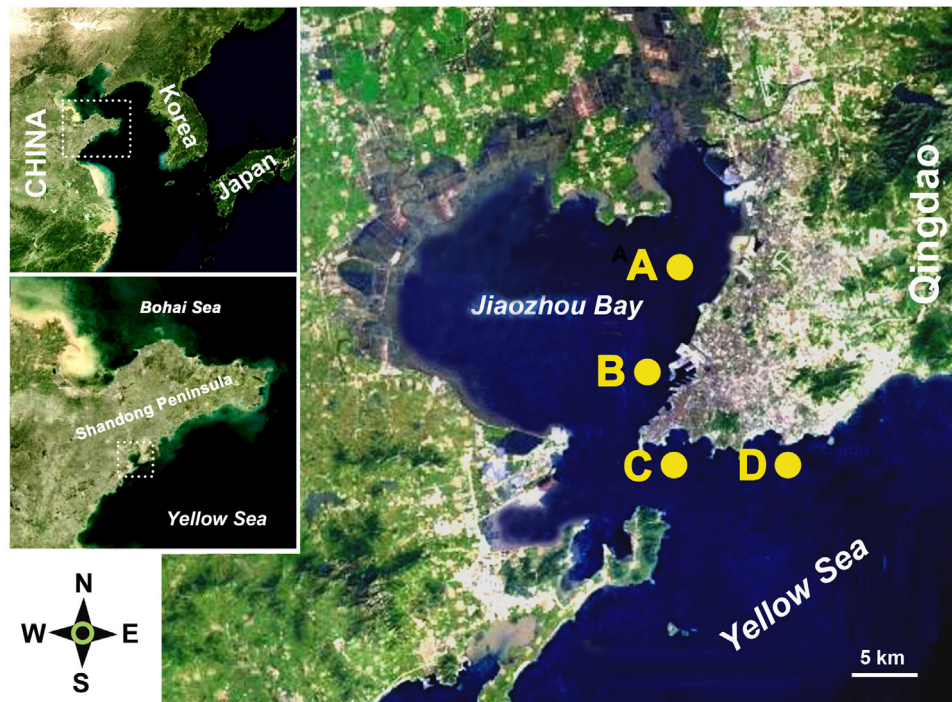


Fig. 1. Sampling stations in coastal waters of the Yellow Sea, near Qingdao, northern China. A: station A, heavily polluted area in Jiaozhou Bay by domestic sewage and industrial discharges from several rivers; B: station B, moderately polluted area Jiaozhou Bay by minor discharges from a small river;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

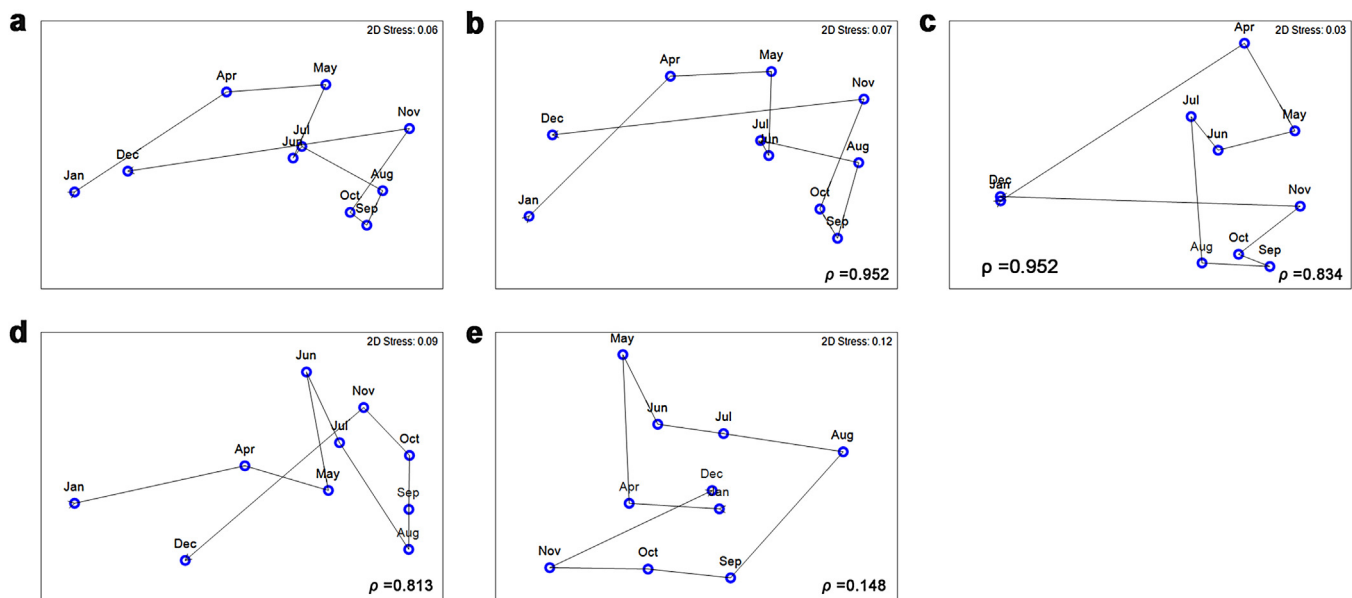


Fig. 2. Non-metric MDS ordinations for samples in coastal waters of the Yellow Sea, showing the remarkable extent to which the overall community pattern (a), a complex mixture of seasonal and pollution signals during a 1-year cycle, is producible by a succession of three small, mutually exclusive subsets of species (b–d), generated by the peeling procedure (see text), after which the pattern (e) breaks down. ρ is matching coefficients to the overall community pattern.

lished in each response unit of the ciliate communities in coastal ecosystems.

2. Materials and methods

2.1. Dataset collection

A total of 40 samples were collected monthly, using glass slide method, at a depth of 1 m from coastal waters of the Yellow Sea,

northern China, during 1-year period of August 2011–July 2012. Four sampling stations were selected within a pollution gradient: station A, a heavily polluted area; station B, a moderately polluted area; station C, a slightly polluted area; and station D, a clean area (Fig. 1, A–D).

A total of 141 ciliate species were identified in the 40 samples following the published keys such as Song et al. (2009), Fan et al. (2010) and Jiang et al. (2010). Trophic-functional groupings of biofilm-dwelling ciliate species, which comprised bacterivores

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