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RESEARCH ARTICLE

An approach to determining potential surrogates for analyzing ecological patterns of planktonic ciliate communities in marine ecosystems

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Abstract
Introduction In order to identify a potential surrogate of planktonic ciliate communities for marine bioassessments and evaluating biological conservations, the different taxonomic/numerical resolutions and taxa as surrogates were studied in Jiaozhou Bay, northern China during a 1-year cycle (June 2007–May 2008).
Materials and methods Samples were collected biweekly from a depth of 1 m at each of five sites. A range of physicochemical parameters were also measured in order to determine water quality.
Results The genus- and family-level resolutions maintained sufficient information to evaluate the ecological patterns of the ciliate communities in response to environmental status. The non-loricate oligotrichous ciliate assemblages in both abundance and occurrence may be used as a surrogate of planktonic ciliate communities. Heavy data transformations were an optimal strategy for the species level of planktonic ciliates, while mild data transformations were for the higher. The ordination patterns based on species biomass, occurrence, and biomass/abundance ratio matrices were significantly consistent with that of species abundance data.
Conclusion The results suggest that the use of simplifications at both taxonomic and numerical resolutions are time-efficient and would allow improving sampling strategies of large spatial/temporal scale monitoring programs and biological conservation researches in the marine ecosystem with a relative paucity of scientists.

Keywords Bioassessment · Taxonomic sufficiency · Numerical resolution · Planktonic ciliate · Marine ecosystem

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1 Introduction

Ciliated protozoa are an important component of microplankton communities and have long been considered as primary mediators of energy transfer from pico- and nanoplanktonic production to higher trophic levels in the functioning of microbial food webs (Sherr and Sherr 1987; Dolan and Coats 1990; Stoecker and McDowell-Cappuzzo 1990; Sime-Ngando et al. 1995; Kchaou et al. 2009; Jiang et al. 2011a, b; Xu et al. 2011a, b). With their short life cycle and more rapid responses to environmental changes than any other eukaryotic organisms, special attentions have been increasingly focused on ciliated protozoa as a useful bioindicator of marine bioassessments and biological conservations in recent decades (Coppellotti and Matarazzo 2000; Corliss 2002; Xu et al. 2002, 2009a, b; Ismael and Dorgham 2003; Jiang et al. 2011a, b). So far, monitoring programs using ciliated protozoan communities have traditionally been based on the species abundance data (Coppellotti and Matarazzo 2000; Xu et al. 2002; Jiang et al. 2011a, b). However, the identification of ciliates at species level requires a skilled taxonomic expertise and is laborious and thus limits the use of ciliated protozoa for monitoring researches, especially by the environmental agencies that are often dealing with large scales in a limited time span (Lovell et al. 2007; Bertasi et al. 2009; Liu et al. 2010; Shao et al. 2010; Yu et al. 2010; Xu et al. 2011a, b).

The development of fast and cost-effective procedures for marine bioassessments and biological conservations has become a pressing issue for marine ecologists as anthropogenic impacts increase rapidly and dramatically worldwide in recent years (Warwick 1988; Xu et al. 2002; Terlizzi et al. 2003; Tataranni et al. 2009). For this purpose, taxonomic sufficiency has been received increasing attentions in terms of its basic concept that anthropogenic impacts can be detected using coarse taxonomic resolutions without a significant loss of information, thus avoiding long and difficult precise taxonomic identifications and saving time and costs (Ellis 1985; Vanderklift et al. 1998; Olsgard and Somerfield 2000; Pagola-Carte et al. 2002; Dauvin et al. 2003; Mendes et al. 2007; Puente and Juanes 2008; Bertasi et al. 2009). The other technique is to identify either a sufficient numerical resolution or a taxonomic/ecological group as a surrogate of the whole species assemblages (Olsgard and Somerfield 2000; Bertasi et al. 2009; Carneiro et al. 2010; Xu et al. 2011a). Otherwise, data transformations have been known to affect the results of multivariate analyses by weighting the relative contributions to results of abundant and rare taxa (Stark et al. 2003; Anderson et al. 2005; Xu et al. 2011a). Although the effectiveness of taxonomic/ecological surrogates has been reported on metazoan, phytoplanktonic, and periphytic protozoan assemblages, such studies have yet to be carried out on planktonic ciliate communities for marine bioassessments and biological conservations (Bertasi et al. 2009; Carneiro et al. 2010; Xu et al. 2011a).

In this study, the dataset of planktonic ciliate communities, which was collected biweekly at five sampling sites in Jiaozhou Bay near Qingdao, northern China, during a 1-year cycle (June 2007–May 2008), was analyzed. Our study asks the following questions: (1) are the ordination patterns of planktonic ciliate communities independent of the taxonomic and numerical resolutions used (abundance, biomass, occurrence, and biomass/abundance ratio matrices), so that simplification of sample processing (aggregation to higher taxonomic levels and/or the use of occurrence and biomass/abundance ratio data); (2) can the non-loricate oligotrich assemblages be a surrogate of whole planktonic ciliate communities; and (3) do data transformations influence the bioassessments and biological conservations?

2 Materials and methods

2.1 Study area

Jiaozhou Bay (35°58′ N~36°18′ N, 120°04′ E~120°23′ E) is a typical semi-enclosed bay in the western part of the Yellow Sea, with an area of 390 km^2 and an average depth of about 6 to 7 m. It connects the South Yellow Sea via a narrow mouth (width: about 2.5 km). More than ten small seasonal streams empty into the bay with varying water and sediment loads, notably the Yang River, Dagu River, Moshui River, Baisha River, Licun River, and Haipo River (Fig. 1). Most of these rivers have become discharge

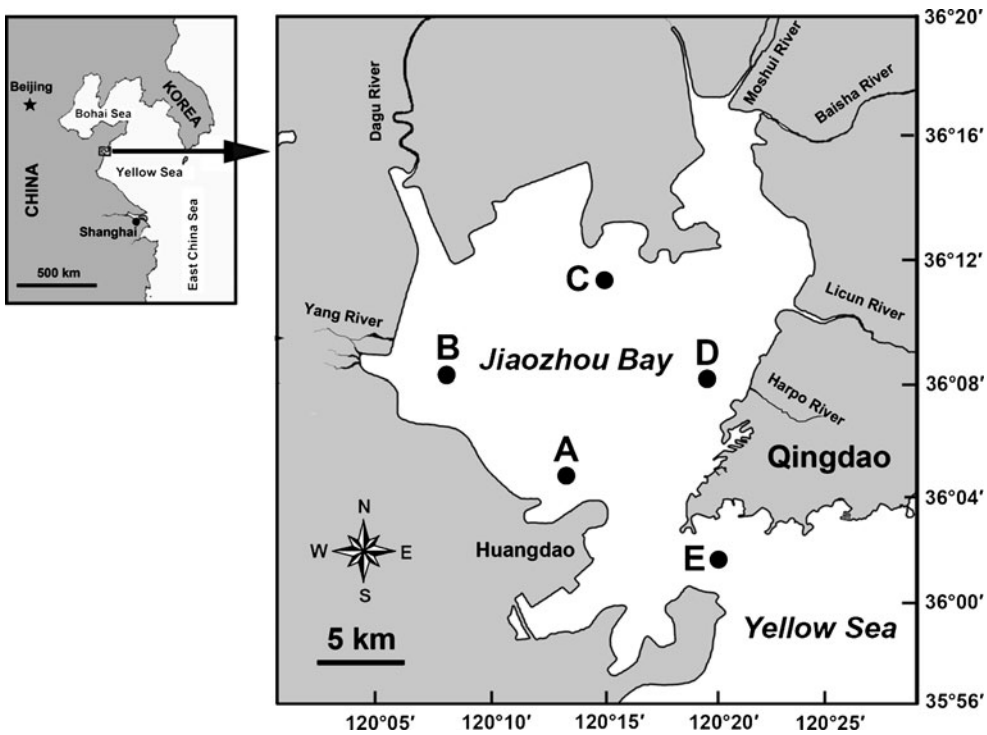

Fig. 1 Map of the sampling stations in Jiaozhou Bay, northern China

trenches for industrial and urban living wastes from Qingdao city and important sources of external nutrients entering Jiaozhou Bay. In recent decades, deterioration in water quality within Jiaozhou Bay has led to serious concern within both the social and scientific communities (Shen 2001; Liu et al. 2005, 2008).

Five sampling sites in Jiaozhou Bay were selected as study areas (Fig. 1). Site A was located near Huangdao, which was slightly stressed by pollutants from inshore waters due to tidal circulation. Site B near both mouths of Dagu and Yang rivers was selected as a severely stressed area polluted by organic pollutants, nutrient, and heavy metals from domestic sewage and industrial discharge. Site C was located at the middle-north part of this bay where the sources of heavy pollution mainly come from mariculture activities and inshore water by tidal circulation. Site D was moderately stressed by both domestic and heavy-metal pollutants from Haipo and Licun rivers. Site E was located at the mouth of this bay, which was the cleanest area (Fig. 1).

2.2 Data collection

A total of 120 samples were collected biweekly at the five sampling sites in Jiaozhou Bay from June 2007 to May 2008. All water samples were collected at a depth of 1 m. For quantitative studies and for the identification of ciliates, 1,000-ml water samples were fixed with acid Lugol's iodine solution to a final concentration of 2% (*v*/*v*).

The measurements of concentrations of dissolved inorganic nitrogen (DIN; sum of NO_3-N, NO_2-N, and NH_3-N), soluble reactive phosphate (SRP), and chlorophyll *a* (chl *a*) were carried out in the same scheme as Jiang et al. (2011a, b). Water temperature, salinity, pH, and dissolved oxygen (DO) were recorded in situ with appropriate sensors (WTW) at a depth of 1 m.

Enumeration and re-fixation with Bouin's fixative for protargol staining were performed according to Montagnes and Humphrey (1998). Species identification of ciliates was based on the published references to keys and guides such as Song et al. (1999, 2003), Fan et al. (2010), and Pan et al. (2010). The taxonomic scheme used was according to Lynn (2008).

2.3 Data analysis

For assessing both the taxonomic and numerical sufficiency of the whole planktonic ciliate communities, the planktonic ciliate abundance matrix (PAM), planktonic biomass matrix (PBM), occurrence (presence/absence) matrix (P/A-M), and the biomass/abundance ratio matrix (B/A-M) were constructed. The PAM, PBM, and P/A-M were subjected to aggregate to the levels of genus, family, order, and class before analyses. For assessing the efficiency of the primary components as a surrogate of the whole planktonic ciliate communities, the non-loricate oligotrich abundance matrix (OAM) and the loricate tintinnid abundance matrix (TAM) were separately computed. Each of these was analyzed after aggregating abundances at the levels of genus, family, order, and class. For assessing the correlations between temporal and spatial variations in each potential surrogate of planktonic ciliate communities and the changes of environmental variables, the biotic and abiotic matrices were changed into both temporal and spatial matrices according to the month and site ordination, respectively. Thus, a total of 48 data matrices were constructed, including both the biotic and abiotic data.

Bray–Curtis similarities of all abundance and biomass matrices were computed based on the data that were subjected to a sequence of transformations (none, square root, fourth root, and logarithmic) for gradually down-weighting the dominant taxa, whereas the Sørenson similarities were resulted from the presence/absence data at various taxonomic levels. Additionally, the Spearman correlation matrix of the biomass/abundance ratios was computed from the log-transformed data, while the dissimilarity matrices of abiotic variables on Euclidean distance were established from the log-transformed/normalized data (Clarke and Gorley 2006). The relationships between pairs of similarity matrices were analyzed using the Spearman rank correlation coefficients (ρ values) which were computed by the submodule RELATE (Somerfiled and Clarke 1995; Clarke and Gorley 2006). All multivariate analyses were carried out using the PRIMER package version 6.1 (Clarke and Gorley 2006). Correlation analyses between planktonic ciliate numbers of species and those of higher taxonomic levels were conducted using the statistical program SPSS 16.0.

A cost/benefit (*C*/*B*) ratio was calculated for each dataset in order to objectively select the taxonomic level with the minimal loss of information and the least taxonomic effort according to the equation:

$$CB_L = (1 - r_L)/[(S - t_L)/S]$$

where CB_L is the cost/benefit ratio at taxonomic level L, r_L is the Spearman correlation coefficient between taxonomic level L and species level, t_L is the number of taxa at taxonomic level L, and S is the number of species (Karakassiss and Hatziyanni 2000).

The cost/benefit ratio ranges between 0 and 1. Values equal to 0 show a high correlation between the species level and any of the other groups, which means that the loss of information is the lowest.

3 Results

3.1 Physical–chemical parameters

The ranges of physical–chemical parameters at the five sampling sites for a 1-year cycle were summarized in Table 1. Among these variables, temperature and pH showed minor differences at all sampling stations during the 1-year cycle (Table 1). Salinity ranged during 29.46–31.29 with lowest average values at site B and highest at site A. The concentration of DO was commonly higher than 8 mg l^{-1} at all five sites, with the minimum average value at site D but the maximum at site B. However, the high concentrations of chl *a* occurred in sites A and C, the lowest in site B. Furthermore, the concentrations of NO_3-N, NO_n-N (sum of NO_3-N and NO_2-N) and combination of NO_n-N and SPR basically showed high values in sites B and C but low in sites E and A although DIN, SRP, and sum of DIN and SRP presented maximum values at site D mainly due to the most primary contributor NH_3-N (Table 1).

3.2 Numerical resolution and taxonomic aggregation

The taxonomic composition of the dataset in terms of numbers of species, genera, families, orders, and classes is listed in Table 2. The levels of concordance between the abundance matrix (PAM) and the other numerical matrices (PBM, P/A-M, and B/A-M) at species resolution as well as the matrices from planktonic ciliate abundance data at higher taxonomic levels, under all types of data transformations, were summarized in Fig. 2. It was shown that the correlations presented higher values than 0.75 between the PAM and the other three numerical resolutions, although the ρ values increased with the increased severity of data transformations (Fig. 2a). However, high-rank correlations between PAM similarity matrices at species level and those at higher taxonomic ranks were found for none and square root transformed data. It should be noted that the correlation coefficients presented higher values than 0.75 at the taxonomic resolutions up to family level under none and square root transformations (Fig. 2b). Otherwise, congruency analyses revealed that planktonic ciliate number of species was significantly correlated with those of genus (ρ=0.845; P<0.001) and family (ρ=0.735; P<0.001; Fig. 3).

3.3 Non-loricate oligotrichs and loricate tintinnids

The taxonomic composition of non-loricate oligotrich and tintinnid assemblages in terms of the numbers of species, genera, families, orders, and classes is summarized in Table 2. The matching correlations between the PAM-species similarity matrices and those for OAM and TAM at different taxonomic aggregation levels, under all data transformations, are shown in Fig. 4a. The results showed that the correlation coefficients represented higher than 0.75 only at the species-level resolution of the OAM (Fig. 4a). Furthermore, congruency analyses revealed that the species number of oligotrich assemblage was significantly correlated with that of whole planktonic ciliate communities (ρ= 0.941; P<0.001; Fig. 4b). However, it should be noted that no significant correlation was found between TAM and PAM at any taxonomic levels and under any data transformations.

3.4 Cost/benefit analysis

The cost/benefit (*C*/*B*) ratios for the dataset are summarized in Fig. 4. The PAM at species level was compared to the matrices of the higher taxonomic levels and of oligotrich assemblages at all taxonomic levels, respectively. The *C*/*B* ratios represented minimal values at the species-level resolution of OAM due to the high correlation coefficients with PAM-species matrix, but the decrease of the taxon numbers was only 50% compared with the number of species (Fig. 5; Table 2). At the genus and family levels of PAM, the numbers of taxa correspondingly decreased of 67% and 78%, but the *C*/*B* ratios were acceptably low, respectively (Fig. 4; Table 1). Otherwise,

Table 1 Physicochemical parameters of the five sampling sites in Jiaozhou Bay during the 1-year cycle from June 2007 to May 2008 (mean values for a total of 24 samples from each sampling site)

Parameters	Site A	Site B	Site C	Site D	Site E
Tem (°C)	14.50±8.17	14.09±9.32	14.84±9.17	14.93±8.43	14.04±9.05
pH	8.22±0.23	8.13±0.62	8.22±0.24	8.08±0.21	7.85±0.77
Sal (psu)	31.48±0.89	30.02±3.31	30.47±1.87	30.78±1.37	29.99±3.39
Chl *a* (μg l^{-1})	1.01±2.24	1.05±1.29	1.60±1.85	1.18±1.32	1.00±1.32
DO (mg l^{-1})	8.46±1.67	8.79±1.87	8.69±1.42	7.94±2.02	8.55±1.60
NH_4-N (mg l^{-1})	0.14±0.08	0.18±0.12	0.22±0.15	0.60±0.41	0.19±0.16
NO_3-N (mg l^{-1})	0.42±0.25	0.47±0.27	0.45±0.31	0.40±0.30	0.39±0.25
NO_2-N (mg l^{-1})	0.02 ±0.02	0.04 ±0.05	0.06±0.06	0.04±0.03	0.04±0.05
SRP (mg l^{-1})	0.19±0.15	0.26±0.17	0.17±0.12	0.22±0.16	0.15±0.16

Tem temperature, *Sal* salinity, *DO* dissolve oxygen, *SRP* soluble active phosphate, sum of NO_3-N and NO_2-N, dissolved inorganic nitrogen

Table 2 Number of taxa at each taxonomic resolution level for all planktonic ciliates, oligotrichs, and tintinnids in the planktonic ciliate communities collected at five sites in Jiaozhou Bay during a 1-year cycle of June 2007–May 2008

Tax-Num	Site A	Site B	Site C	Site D	Site E	Total
All planktonic ciliates						
Species	41	37	47	41	45	64
Genus	14	12	17	16	15	21
Family	9	8	12	11	10	14
Order	4	4	7	7	5	9
Class	2	2	3	4	2	4
Non-loricate oligotrichs						
Species	28	26	26	23	28	32
Genus	9	8	8	9	9	10
Family	4	4	4	4	4	4
Order	2	2	2	2	2	2
Class	1	1	1	1	1	1
Tintinnids						
Species	10	10	16	13	13	23
Genus	3	3	4	3	3	4
Family	3	3	3	3	3	3
Order	1	1	1	1	1	1
Class	1	1	1	1	1	1

the severity of the data transformation played a significant role in determining the analyzing results. The lower values were obtained from the mild (e.g., none, square root) transformed data at the levels of genus and family and the heavy (e.g., presence/absence, fourth root, and logarithmic) transformed species abundance data of oligotrich assemblages (Fig. 4a).

3.5 Effects of taxonomic and numerical resolution on linking environmental variables

Spearman correlation coefficient values between ecological patterns of planktonic ciliate communities and the temporal/spatial changes of physicochemical variables were summarized in Table 3. Results showed that (1) the temporal/spatial variations in planktonic ciliate communities at all four numerical (abundance, biomass, P/A, and B/A ratio) resolutions at species level were significantly correlated with the changes of physicochemical variables and (2) the variations in abundances of planktonic ciliate communities, at least family-level resolution, were significantly associated with the environmental changes. It should be noted that some lower resolutions (e.g., PAM up to class level under square root transformation, P/A-M/OAM up to genus level) also significantly related to the abiotic data although they represented lower than 0.75 in ρ values with the PAM.

4 Discussion

So far, numeral studies on taxonomic sufficiency with benthic organisms have suggested that identification to the level of genus or family may be adequate for bioassessment and biological conservation issues (Olsgard and Somerfield 2000; Dauvin et al. 2003; Waite et al. 2004; Khan 2006; Heino and Soininen 2007). This approach has also been used for other taxonomic groups, e.g., vascular plants, ants, spiders, Coleoptera, Diptera and Acari, Nemathelminthes, macromycetes, phytoplankton, and periphyton (Somerfiled and Clarke 1995; Cardoso et al. 2004; Heino and Soininen 2007; Lovell et al. 2007; Carneiro et al. 2010; Xu et al. 2011a).

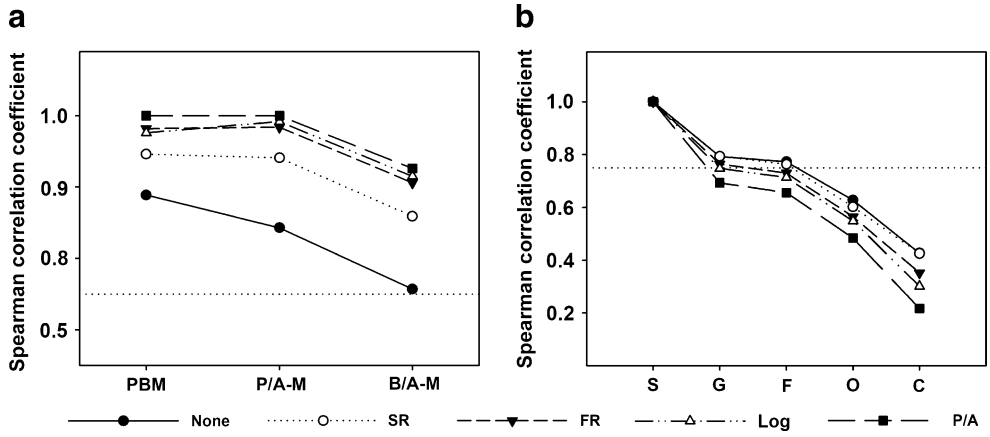

Fig. 2 Correlations between the planktonic ciliate abundance matrix and each of the planktonic ciliate biomass matrix (*PBM*), presence/absence matrix (*P/A-M*), and biomass/abundance ratio matrix (*B/A-M*) at species-level resolution (**a**) as well as the matrices from planktonic ciliate abundance data at higher taxonomic levels (**b**), under all types of data transformation. *S* species, *G* genus, *F* family, *O* order, *C* class, *None* untransformed, *SR* square root, *FR* fourth root, *Log* logarithmic, *P/A* presence/absence; *horizontal dotted line*, ρ=0.75

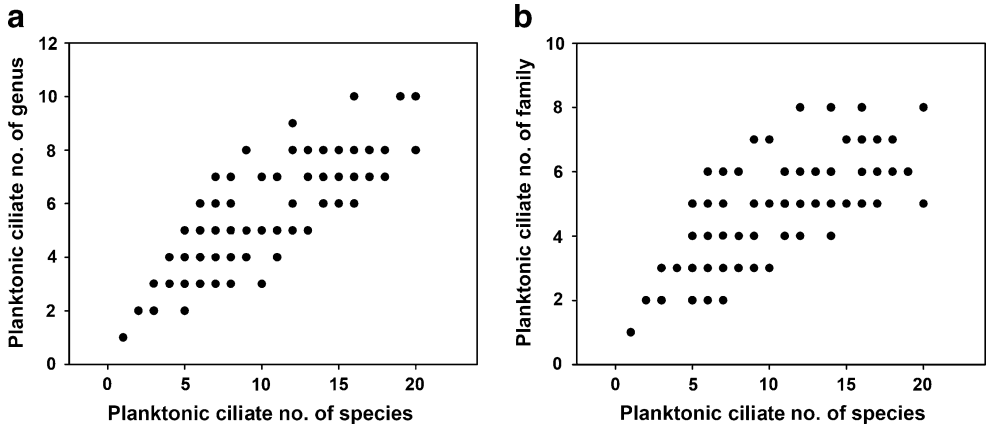

Fig. 3 Congruency between planktonic ciliate number of species and those of genus (**a**) and family (**b**)

The use of genus or family as surrogates for species-level identification offers many advantages: (1) genus- or family-level identification can be more reliable since species-level identification is complex and laborious and (2) the identification of ciliate species to genus- or family-level can be less time-consuming, reducing the costs of monitoring programs, in particular the large temporal/spatial scale bioassessment and biological conservation issues (Heino and Soininen 2007; Carneiro et al. 2010; Xu et al. 2011a). Lovell et al. (2007) proposed that a ρ value of greater than 0.75 should be used as minimal level of congruency for an optimal surrogate. In this study, the ρ values between PAM and the other numerical matrices (PBM, P/A-M, and B/A-M) at species level as well as the taxonomic matrices up to family level (PAM) remained higher than 0.75. With the acceptable cost/benefit ratios and significant correlations with abiotic data, the genus and family levels under mild data transformations may obtain the sufficient information for evaluating ecological patterns of planktonic ciliate communities in response to the environmental changes. The results demonstrate that the genus- and family-level resolutions are sufficient in analyzing the ecological patterns of planktonic ciliate communities.

In the present study, the oligotrich assemblages represented higher correlations (ρ>0.75) with the patterns of PAM-species matrices. The lowest cost/benefit ratios showed significant disturbances of the severity of data transformations to the effectiveness of the surrogates, i.e., the best results may be obtained under the fourth root, logarithmic, and presence/absence transformations at species level. Furthermore, it should be addressed that the oligotrich ciliate assemblage represented lowest *C*/*B* ratio values at the species level under P/A data transformation. This suggests that the oligotrichous ciliate assemblage is a good surrogate for planktonic ciliate communities in detecting their ecological patterns by presence/absence data at species level (Xu et al. 2009b).

Based on our data, the loss of information can be negligible when one uses presence/absence resolution of whole planktonic ciliate communities, even the presence/absence data of oligotrichs. This may be due to the fact that the ciliate communities were predominated by the non-loricate oligotrichous ciliates, but not by a few ciliate species (Jiang et al. 2011a, b). This supports the suggestion that the analyses of planktonic ciliate community patterns can be done at coarse level taxonomic and numerical resolution (Carneiro et al. 2010).

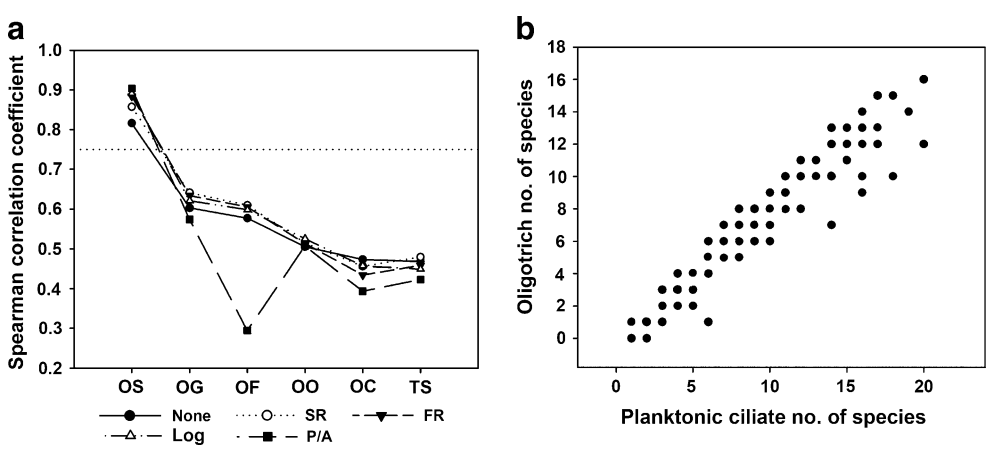

Fig. 4 Correlations between the planktonic ciliate abundance matrix at species resolution and the matrices from oligotrich abundance data at different taxonomic levels (**a**), under all types of data transformation, and congruency between planktonic ciliate and oligotrich number of species. For all abbreviations, see Fig. 2

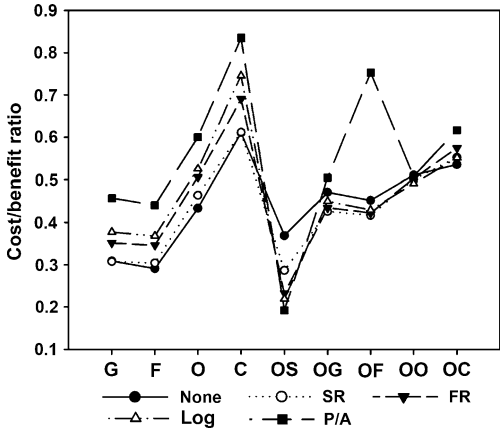

Fig. 5 Cost/benefit ratios for different taxonomic levels for the planktonic ciliate abundance matrix and the oligotrich abundance matrices at different aggregation levels and under different data transformations. For all abbreviations, see Fig. 2

Biomass is always considered to be of paramount importance to analyses of ecological patterns of a community in both freshwater and marine ecosystems (Beaver and Crisman 1982; Zhang and Wang 2001; Jiang et al. 2011a, b). Since the biomass was commonly calculated according the biovolume of the cells, the ordination patterns based on biomass were almost mirrored by those based on abundance. Otherwise, the body-size patterns are one of the tools capable of assessing ecosystem changes due to environmental impacts (Sheldon et al. 1972). Several studies have shown that natural aquatic communities tend to have inherent patterns of body-size spectrum and its normalized variant (Sheldon et al. 1972; San Martin et al. 2006; Kamenir et al. 2010). In our study, both the biomass and the body-size (i.e., biomass/abundance ratio) patterns of planktonic ciliate communities were found to be significantly correlated with the abundance matrices. These findings were consistent with the previous evidence that ciliate assemblages are strongly related to eutrophication status in terms of species body size and biomass (Beaver and Crisman 1982, 1989). However, the two numerical resolutions may not be cost-effective for monitoring researches as the estimation of biovolume (using microscopy methods) is commonly very time-consuming (Zhang and Wang 2001; Jiang et al. 2011a, b). For this numerical resolution, the use of counter

Table 3 Spearman correlation coefficient values between the ecological patterns of planktonic ciliate communities and changes of physicochemical variables on Bray–Curtis similarity matrices from PAM/PBM and OAM under a range of data transformations, Sørenson similarity from P/A-M at various taxonomic levels, and Spearman correlation matrices from B/A-M

Tansf	Taxa	PAM		PBM		OAM		B/A-M	
		Temp	Spat	Temp	Spat	Temp	Spat	Temp	Spat
None	S	**0.578**	**0.733**	**0.380**	**0.709**	**0.537**	0.370	–	–
	G	**0.564**	**0.564**	0.333	**0.624**	0.301	0.321	–	–
	F	**0.538**	0.539	0.258	**0.564**	0.228	0.321	–	–
	O	0.270	0.394	0.073	0.358	0.142	0.527	–	–
	C	0.218	0.394	0.067	0.345	0.255	–	–	–
SR	S	**0.625**	**0.588**	**0.492**	**0.685**	**0.576**	**0.479**	–	–
	G	**0.612**	**0.576**	**0.453**	**0.576**	**0.494**	0.261	–	–
	F	**0.532**	**0.685**	0.308	**0.685**	0.273	0.200	–	–
	O	0.237	**0.612**	0.095	0.503	0.192	0.327	–	–
	C	0.153	**0.697**	0.099	0.527	0.255	–	–	–
FR	S	**0.652**	**0.552**	**0.581**	**0.661**	**0.536**	**0.576**	–	–
	G	**0.619**	0.479	**0.532**	**0.564**	**0.554**	**0.600**	–	–
	F	**0.432**	**0.612**	0.296	0.673	0.235	0.176	–	–
	O	0.115	0.661	0.089	0.491	0.205	0.527	–	–
	C	0.019	**0.806**	0.076	**0.745**	0.255	–	–	–
Log	S	**0.652**	**0.515**	**0.539**	**0.709**	**0.526**	**0.515**	**0.364**	**0.479**
	G	**0.616**	**0.576**	**0.501**	**0.612**	**0.560**	0.212	–	–
	F	**0.394**	**0.661**	0.290	**0.685**	0.231	0.018	–	–
	O	0.054	0.576	0.093	0.430	0.258	0.527	–	–
	C	0.005	**0.673**	0.082	0.358	0.267	–	–	–
P/A	S	**0.647**	**0.486**	**0.647**	**0.486**	**0.423**	**0.652**	–	–
	G	**0.451**	**0.527**	**0.451**	**0.527**	0.359	0.578	–	–
	F	0.095	0.280	0.095	0.280	0.110	0.110	–	–
	O	0.057	0.466	0.057	0.466	0.091	0.110	–	–
	C	0.110	0.308	0.110	0.308	0.072	–	–	–

Values are the correlation coefficient ρ, significant tests ($P<0.05$) are in bold

S species, *G* genus, *F* family, *O* order, *C* class, None untransformed, *SR* square root, *FR* fourth root, *Log* logarithmic, *P/A* presence/absence, *Tansf* transformation, *Temp* temporal pattern, *Spat* spatial pattern, *PAM* planktonic ciliate abundance, *PBM* planktonic biomass matrices, *OAM* oligotrich abundance matrices, *P/A* presence/absence matrices, *B/A-M* biomass/abundance ratio matrices

programs may be an alternative to reduce sample processing time and to obtain reliable and more ecologically relevant information in monitoring programs (San Martin et al. 2006; Kamenir et al. 2010).

In summary, the present study has demonstrated that (1) the genus- and family-level resolutions maintained sufficient information to evaluate the temporal/spatial patterns of ciliate communities in response to environmental impacts; (2) the non-loricate oligotrichous ciliate assemblages in both abundance and presence/absence may be used as a surrogate of planktonic ciliate communities; (3) heavy data transformations were an optimal strategy for the species level of planktonic ciliates, while mild data transformations were for the higher; and (4) the ordination patterns based on species biomass, presence/absence, and biomass/abundance ratio matrices were significantly consistent with that of species abundance data. These results suggest that the use of some simplifications at both taxonomic and numerical resolutions are time-efficient and would allow improving sampling strategies of large spatial/temporal scale monitoring programs and biological conservation researches in the marine ecosystem with a relative paucity of scientists. However, it should be noted that further studies on a range of marine environments and over long time periods are needed in order to verify this conclusion.

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