Acta Limnologica Brasiliensia

Publication of the Brazilian Association of Limnology

Original Article
Acta Limnologica Brasiliensia, 2019, vol. 31, e20
https://doi.org/10.1590/S2179-975X3617
ISSN 2179-975X on-line version

Monitoring simplification in plankton communities using different ecological approaches

Simplificação do monitoramento ambiental de comunidades planctônicas utilizando diferentes abordagens ecológicas

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Cite as: Souza, C. A. et al. Monitoring simplification in plankton communities using different ecological approaches. *Acta Limnologica Brasiliensia*, 2019, vol. 31, e20.

Abstract: Aim: This study aimed to answer: (i) can phytoplankton communities be used as surrogate of zooplankton communities?; (ii) can we use ecological approaches like functional groups (FG) or morphofunctional classification (MBFG) as surrogate for phytoplankton species?; (iii) can we use substitute groups (cladocera, copepod, rotifer or testate amoebae) as surrogate for zooplankton species?; (iv) are the environmental variables' ordination standards concordant with the ordering patterns of phytoplankton and zooplankton species?; and (v) for both communities, is the spatial pattern of ordination maintained using density data or presence/absence of individuals or lower taxonomic resolutions? **Methods:** The study was conducted in 25 water bodies that supply central-pivot irrigation in the Federal District - Brazil (Rio Preto Basin), in October 2012. We evaluated some physical and chemical variables as well as phytoplankton and zooplankton samples. To evaluate correlation among biological groups, numerical and higher taxonomic resolutions, we performed some Mantel and Procrustes analyses. **Results:** Evaluating the use of substitute groups, comparisons between phytoplankton and zooplankton, FG and MBFG classifications and almost all the comparisons between zooplankton groups suggested concordant patterns. However, the values of *r* were low, all below 0.70. Biological analyses with phytoplankton and zooplankton can be performed using presence/absence of individuals without significant loss of information, except for MBFG classification and copepods. Data may also be used at genus or family level for copepods and testate amoebae and only data at genus level for cladocerans and rotifers. Different results were found concerning taxonomic resolution for phytoplankton considering that, while being significant, the *r* value was less than 0.70. **Conclusions:** For environmental monitoring purposes, it is important to sample both phytoplankton

and zooplankton communities because one is not surrogate of the other one, in the same way as phytoplankton density and their functional and morphofunctional approaches. On the other hand, to simplify the environmental monitoring, it is possible to adopt presence/absence species data instead of abundance data for both zooplankton and phytoplankton communities, except for copepods and morphofunctional approach. It is also possible to adopt genera level for zooplankton community and family level for copepods and testate amoebae.

Keywords: reservoir; concordance; substitute groups; numerical resolution; taxonomic resolution.

Resumo: Objetivo: Este estudo pretende responder: (i) as comunidades de fitoplâncton podem ser utilizadas como substitutos de comunidades zooplanctônicas? (ii) podemos utilizar abordagens ecológicas como grupos funcionais (FG) ou classificação morfofuncional (MBFG) como substitutos para espécies de fitoplâncton?; (iii) podemos usar grupos substitutos (cladóceros, copépodes, rotíferos ou amebas testáceas) como substitutos para espécies zooplanctônicas?; (iv) a ordenação das variáveis ambientais é concordante com o padrão de ordenação de espécies de fitoplâncton e zooplâncton?; e (v) para ambas as comunidades, o padrão espacial de ordenação é mantido utilizando dados de densidade ou presença/ausência de indivíduos ou resoluções taxonômicas menores? **Métodos:** O estudo foi conduzido em 25 corpos d'água que fornecem irrigação por pivô central no Distrito Federal - Brasil (Bacia do Rio Preto), em outubro de 2012. Nós avaliamos algumas variáveis físicas e químicas, além de amostras de fitoplâncton e zooplâncton. Para avaliar a correlação entre grupos biológicos, resoluções numéricas e maiores resoluções taxonômicas, realizamos algumas análises de Mantel e Procrustes. **Resultados:** Avaliando o uso de grupos substitutos, as comparações entre fitoplâncton e zooplâncton, as classificações de FG e MBFG e quase todas as comparações entre grupos de zooplâncton sugeriram padrões concordantes. No entanto, os valores de *r* obtidos foram baixos, todos abaixo de 0,70. As análises biológicas com fitoplâncton e zooplâncton podem ser realizadas utilizando dados de presença/ausência de indivíduos sem perda significativa de informação, exceto a classificação MBFG e os copépodes. Os dados também podem ser usados em nível de gênero ou família para copépodes e amebas testáceas e só dados em nível de gênero para cladóceros e rotíferos. Diferentes resultados foram encontrados quanto à resolução taxonômica do fitoplâncton, considerando que, embora significativo, o valor foi menor que 0,70. **Conclusão:** Para fins de monitoramento ambiental, é importante amostrar tanto as comunidades de fitoplâncton como de zooplâncton, porque uma não é substituta da outra, da mesma forma que a densidade do fitoplâncton e suas abordagens funcional e morfofuncional. Por outro lado, para simplificar o monitoramento ambiental, é possível adotar dados de presença/ausência de espécies em vez de dados de abundância para as comunidades de zooplâncton e fitoplâncton, exceto para copépodes e para abordagem morfofuncional. Também é possível adotar nível de gênero para a comunidade zooplanctônica e nível de família para copépodes e amebas testadas.

Palavras-chave: reservatório; concordância; grupos substitutos; resolução numérica; resolução taxonômica.

1. Introduction

In recent decades, the degradation of aquatic ecosystems has occurred quickly and continuously due to multiple environmental impacts from human activities, especially those related to agriculture. This activity causes different environmental impacts such as deforestation, erosion, sedimentation of rivers and reservoirs and the indiscriminate use of fertilizers and pesticides that can easily be leached to water bodies and groundwater (Soldne et al., 2004), changing the water quality.

Multiple changes in hydric ecosystem properties and functions have exerted severe impacts on the wildlife habitat and biodiversity in recent years (Cardador et al., 2015). Therefore, quick and effective assessment of the habitat suitability for species through time is a decisive step in habitat conservation and restoration (Tang et al., 2016). In order to monitor any alterations or disturbances in water ecosystems, it is necessary to establish an effective environmental monitoring system using predictive models that take into account both the environmental conditions and the composition of ecological assemblages (Bennett et al., 2014). For this, simple, fast and low-cost methods should be used. In this context, some methods may provide a way to follow, through summarized information, the possible deterioration of water resources throughout the basin for a certain period, such as the use of surrogate groups and/or different numerical approaches and higher taxonomic resolution (Toledo & Nicollela, 2002).

These approaches are related to the community concordance, that is the degree to which the structure of different communities in a set of sites

are similar to each other (Bini et al., 2008). There is a range of mechanisms that may generate this community concordance, such as the interactions between organisms (when a group is regulated by predation, competition or facilitation, for example) or by similar communities' responses to different environmental variables variations (Paavola et al., 2003).

The use of one or two taxonomic groups as a substitute for another has recently attracted considerable attention (Leal et al., 2010). Thus, if the pattern of community structure is significantly concordant with others, only one may be sampled, providing a possibility of simplifying the biomonitoring program in this location (Johnson & Hering, 2010; Landeiro et al., 2012). For microorganisms this approach (simplification) is an important strategy, because microorganisms quickly respond to environmental changes and are difficult to identify (Machado et al., 2015).

Moreover, the assessment of the biodiversity of microscopic organisms is vital, but it is also a very difficult task in ecology as it is an intensive activity that requires time (Benfield et al., 2007) and skilled labor to ensure that morphological differences are perceived. Thus, the work becomes tiring, expensive and subject to error (Irfanullah, 2006). One option is to use higher taxonomic resolution, which indicates that the organisms can be identified using higher taxonomic levels without undergoing a significant loss of information (Khan, 2006).

Numerical resolution can also be used for this simplification, significantly reducing the time spent on analysis. Typically, quantitative data (abundance or biovolume) should be preferred instead of qualitative data (presence/absence) to contain more information on the response of organisms to environmental gradients (Heino, 2014). However, quantitative and qualitative data have typically reported high correlations (Cushman & McGarigal, 2004; Heino et al., 2010a, b.). In these cases, presence/absence of individuals can replace the abundance data.

However, these practices should be adopted only if the patterns of similarity/correlation between the groups are high (Melo, 2005; Heino, 2010), in order not to lose a significant amount of information. This is an assumption that should be tested and not assumed (Paszkowski & Tonn, 2000; Grenouillet et al., 2008), mainly because the results can vary from region to region (Padial et al., 2012).

In this study, we have worked with phytoplankton and its functional and morphofunctional groups and zooplankton communities (cladocera, copepod, rotifer and testate amoebae). Functional approaches have been widely used (Mutshinda et al., 2016) and they provide reliable predictions of environmental conditions in various aquatic ecosystems, making it easier to understand the impacts on ecosystems (Webb et al., 2010; Brasil & Huszar, 2010) and promote a link between the ecosystem and the community, reducing the difficulty of the communities study in achieving generalizations and predictions (Simberloff, 2004). Classifications based on functional groups (FG) usually provide reliable predictions of environmental conditions in various aquatic ecosystems such as lakes, reservoirs and wetlands (Anneville et al., 2005; Caputo et al., 2008; Becker et al., 2010). They can be more efficient than taxonomic approaches as they may present a strong concordance with data from species, genera and families (Carneiro et al., 2010; Kruk et al., 2010), as well as being more efficient in describing the environmental conditions (Nabout et al., 2006; Becker et al., 2009a, b; Costa et al., 2009). Regarding morphofunctional classification (MBFG) morphological features as the size of the bodies, the presence of flagella or mucilage are shown to provide useful information on the assemblages of phytoplankton (Kruk et al., 2010). The presence of similar structures, sizes or shapes in distant phylogenetically related species can be interpreted as a set of common similar characteristics under strong natural selection (Salmaso et al., 2015).

Therefore, considering the importance and difficulty of microorganism identification at species level, the aim of this study was to evaluate the concordance of higher taxonomic resolution, groups and ecological approaches for phytoplankton and zooplankton species, using density and presence/absence data. To this end, the following questions were asked: (i) can phytoplankton communities be used as surrogate of zooplankton communities?; (ii) can we use ecological approaches as surrogate for phytoplankton species?; (iii) can we use substitute groups (cladocera, copepod, rotifer or testate amoebae) as surrogate for zooplankton species?; (iv) are the environmental variables' ordination standards concordant with the ordering patterns of phytoplankton and zooplankton species?; and (v) for both communities, is the spatial

pattern of ordination maintained using density data or presence/absence of individuals or higher taxonomic resolutions?

2. Material and Methods

2.1. Study area

The Rio Preto Basin is part of the São Francisco basin in Brazil, and it covers an area of 1.045.900 hectares in the states of Goiás, Minas Gerais and the Federal District (DF). In the DF, the basin covers 131.300 hectares, representing 22.5% of its territory, being pre-eminently rural and responsible for about 80% of agricultural production in this region (Carneiro et al., 2007). By being fully within the Cerrado biome, the basin presents strong seasonal climatic variation, with two notably distinct seasons, a dry season, which lasts from April to September, and a rainy season, which lasts from October to March.

In the study area, land use is characterized by intensive farming and mechanized high-technology agriculture, which especially uses intensive-central pivots in the irrigation process (Borges et al., 2007). The use of water in the basin is primarily intended for agricultural activities, particularly irrigation, which accounts for over 90% of the total water used, with the remaining 10% destined for fish farming, pig farming and cattle (Carneiro et al., 2007).

During the dry season, the safe and continuous water supply is uncertain, mainly for irrigation purposes. The water retention and storage process are the way people use to maintain the water supply over time, constructing a barrier transversely to the direction of the flow of the watercourse (Rodrigues et al., 2007). In this study, we selected 25 of these man-made reservoirs that supply central-pivot irrigation, each one regarding a sampling unit (Figure 1). The main differences between sampling sites are related to local environmental variables (Table 1) and the degree of which its border is used or preserved (Table 2).

The sampling period occurred in the beginning of October 2012 because this is the period in which the pivots are heavily used.

2.1.1. Environmental variables

Some physical and chemical variables were determined in the field using portable Digimed equipment: water temperature and conductivity (DM-3P model); pH (DM-2P model); turbidity (DM-TU model) and dissolved oxygen (DM-4P model). Chlorophyll-*a* was determined using a chloroform-methanol method (APHA, 1995), held in the Water Analysis Laboratory of the Faculty of Technology, University of Brasilia. Total phosphorus and ions (Na, K, Ca, Mg, F, Cl, NO_3 and SO_4) were determined using colorimetric methods and ion chromatography (APHA, 1995), respectively, at EMBRAPA´s Water Chemistry Laboratory. The detection limit of this analysis was ≤0.001 $mg.L^{-1}$. Values below this limit were attributed to zero.

Table 1. Mean, Minimum (Min) and Maximum (Max) values, Standard Deviation (SD) and Coefficient of Variation (CV) of environmental variables in water bodies associated with agriculture in the Distrito Federal (Brazil).

Variables	Mean	Min	Max	SD	CV (%)
pH	6.32	4.03	7.75	0.80	0.13
Conductivity ($\mu S.cm^{-1}$)	10.33	2.17	32.10	7.64	0.74
Temperature (°C)	24.50	21.10	28.00	1.80	0.07
Turbidity (NTU)	12.41	1.70	52.10	13.11	1.06
Dissolved Oxxygen ($mg.L^{-1}$)	4.95	3.12	6.15	0.64	0.13
Deph (cm)	247.08	43.00	750.00	175.77	0.71
Clorophill-*a* ($\mu g.L^{-1}$)	2.77	0	22.91	4.62	1.67
Total Phosphorous (P) ($\mu g.L^{-1}$)	0.46	0	5.50	1.14	2.49
Sodium (Na) ($mg.L^{-1}$)	0.39	0	1.07	0.28	0.73
Potassium (K) ($mg.L^{-1}$)	0.19	0	1.33	0.36	1.88
Calcium (Ca) ($mg.L^{-1}$)	1.50	0	6.17	1.63	1.09
Magnesium (Mg) ($mg.L^{-1}$)	0.19	0	0.73	0.24	1.26
Fluoride (F) ($mg.L^{-1}$)	0.05	0	1.14	0.23	4.23
Chlorine (Cl) ($mg.L^{-1}$)	0.39	0.08	1.11	0.32	0.83
Nitrate (NO_3) ($mg.L^{-1}$)	0.16	0	0.72	0.21	1.29
Sulfate (SO_4) ($mg.L^{-1}$)	0.04	0	0.36	0.09	2.35

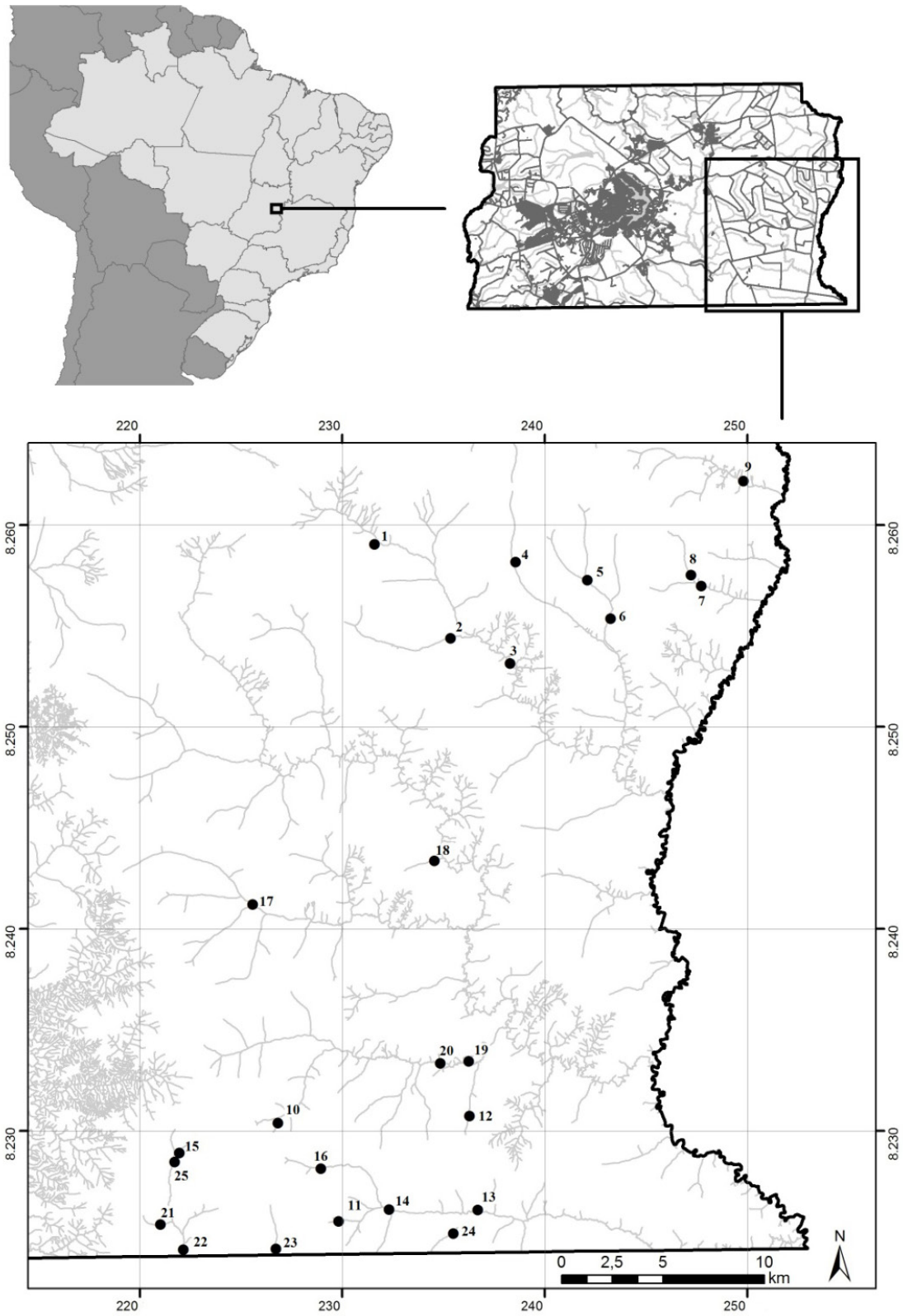

Figure 1. Hydrological map of the Federal District with the sampling sites used in this study.

Table 2. Data related to the perimeter, area, percentage of land use and remnant vegetation of the 25 sampling sites studied.

Sites	Perimeter (m^2)	Area (m^2)	Land Use (%)	Remnant Vegetation (%)
1	176.13	971.65	12.25	87.75
2	30.14	43.74	25.72	74.28
3	28.01	44.52	9.50	90.50
4	559.47	11629.35	39.70	60.30
5	90.76	260.48	9.80	90.20
6	1118.39	22568.46	12.85	87.15
7	1751.75	82652.06	39.88	60.12
8	632.61	8219.29	74.07	25.93
9	1327.08	54131.76	54.55	45.45
10	421.50	9254.90	73.09	26.91
11	258.77	2174.13	12.91	87.09
12	821.90	33230.33	53.35	46.65
13	4979.65	218752.19	50.23	49.77
14	424.07	5327.89	41.21	58.79
15	2844.58	250283.67	27.25	72.75
16	696.77	10735.48	10.17	89.83
17	471.36	9285.36	56.68	43.32
18	52.88	94.25	29.32	70.68
19	62.47	149.51	26.02	73.98
20	38.49	90.46	16.97	83.03
21	619.19	19852.14	26.80	73.20
22	3913.38	362554.46	58.32	41.68
23	905.19	30756.27	21.14	78.86
24	2418.10	99990.26	54.12	45.88
25	2844.58	250283.67	27.25	72.75

2.1.2. Biologic variables

Phytoplankton samples were fixed with acetic acid-modified Lugol solution (Vollenweider, 1974), and its density was estimated according to the method of Utermöhl (1958), using an inverted microscope. Members of the phytoplankton community were classified to the species, genus and family levels according to the taxonomic system proposed by Round (1965), Round (1971) and Round et al. (1990), in addition to their functional (Reynolds et al., 2002; Padisák et al., 2009) and morphofunctional groups (Kruk et al., 2010).

For samples of zooplankton, 300 L of water were filtered using plankton net of 68 μm mesh size. The samples were fixed in 4% formalin and buffered with calcium carbonate. For quantitative analysis, the samples were concentrated to 60 mL, and about 10% of that volume was sub-sampled with a Hensen-Stempell pipette. At least 250 individuals from each zooplankton group were counted per sample using a Sedgewick-Rafter chamber and an optical microscope. Samples that showed few individuals were fully counted. For qualitative analysis, after decantation, aliquots of 2 mL were removed from the bottom of the bottle and read until no new species were found.

The phytoplankton and zooplankton identification was conducted at the lowest possible taxonomic level, and total phytoplankton density was expressed in individuals.mL^{-1} (ind.ml^{-1}) and zooplankton in individuals.m^{-3} (ind.m^{-3}).

2.1.3. Land use variables

The orthophotographs used in this study are scaled of 1:10,000 and are dated from 2009. They were downloaded in the website of the Secretariat of Housing, Regularization and Urban Development – SEDHAB (http://www.sedhab.df.gov.br/mapas_sicad/index_sirgas.htm). The georeferenced points were inserted into the orthophotographs using the program ArcMap 10.1 (ESRI, 2012). The reservoirs were identified, selected and transformed into polygons. Thus, the area and perimeter of each water body was calculated using the Xtools tool (ArcGis extension).

Then, a 50m buffer was performed around each sampling site. We delimitated two classes within the 50m buffer: (i) remnant vegetation, which refers to the vegetation preserved around the reservoirs and (ii) land use, which refers to the land zone used for any anthropic purpose, in order to suppress the local native vegetation. These classes were identified by the process of visual interpretation of the images. Each buffer, already classified, was cropped from the image and transformed into polygons. The area of each class was calculated in m^2 using the Xtools.

2.1.4. Data analysis

To evaluate the correlation between the zooplankton groups (cladocerans, copepods, rotifers and testate amoebae), the groups related to the phytoplankton (species matrices, functional and morphofunctional) and numerical and higher taxonomic resolutions, Mantel and Procrustes tests were performed (Legendre & Legendre, 2012). Previously to the analysis, the biological data were log(x+1) transformed. The matrices of distance required were constructed using the Bray-Curtis index (density data), Jaccard (presence/absence species data) and Euclidean (environmental data and spatial matrix – geographical coordinates). A partial Mantel test was used to evaluate the relationships between environmental variables and the zooplankton groups (cladocerans, copepods, rotifers and testate amoebae), between the groups related to phytoplankton (species, functional and morphofunctional data), controlling for dependence on space. For the Procrustes test were used the scores of the Principal Coordinate Analysis (PCoA).

Significances of all analysis were calculated by 9.999 randomizations. Mantel and Partial Mantel tests were performed using a *mantel* function on *vegan* package (Oksanen et al., 2013), both performed in program R 2.13.2 (R Development Core Team, 2013).

3. Results

In relation to phytoplankton, 89 taxa were identified (Table 3). The taxa found had representatives in 17 of the 40 different functional groups (the most abundant to least abundant: codons Lo, X1, B, E, MP, F, N, W1, J S2, K, Q, P, D, X3, S1, G) and in all the seven morphofunctional groups (the most abundant to least abundant: IV, V, I, II, VII, III and VI). Regarding the zooplankton, 205 taxa were identified, distributed into four groups: 32 cladocerans, 12 copepods including their larval and juvenile forms (nauplii and copepodites), 61 rotifers and 98 testate amoebae (Table 4).

There was concordance between the phytoplankton and zooplankton species in both Mantel and Procrustes tests (Table 5). The density of phytoplankton at the species level is concordant with their FG and MBFG classifications. These two classifications are also concordant with each other. In relation to zooplankton groups, copepods and testate amoebae were the only groups that were not concordant among themselves in both tests. Cladocerans and rotifers were not concordant in Procrustes test. There was concordance between phytoplankton species level and environmental data, but there was no concordance between its morphofunctional group with environmental data in both tests and no concordance between its functional group with environmental data only in Mantel test. In contrast, zooplankton groups are significantly concordant with environmental data, except for the testate amoebae that was not significantly concordant in Mantel test and cladocerans that was not significantly concordant in Procrustes test.

For the numerical resolution (Table 6), the abundance and presence/absence data for species from all groups showed concordant values, the lowest *r* value being 0.53 for MBFG (phytoplankton) in Procrustes test and the largest 0.93 for FG (phytoplankton) and testate amoebae (zooplankton) for Mantel test and for phytoplankton for Procrustes test.

As occurred in relation to the numerical resolution, using higher taxonomic resolution (Table 7) all matrices analyzed were considered concordant, both in comparisons between species and genera data and between species and families data for phytoplankton and zooplankton for both Mantel and Procrustes tests.

4. Discussion

The concordance analysis between communities measures the intensity in which different groups of organisms present spatial and/or similar temporal variation patterns in relation to species richness or compositional similarity (Jackson & Harvey, 1993). One possible explanation for this concordance can be a similar response to environmental gradients. In this case, a high level of concordance is expected between organisms with similar environmental requirements (Grenouillet et al., 2008). However,

Table 3. Phytoplankton species identified in water bodies associated with agriculture in the Distrito Federal (Brazil) and data referring to Mean, Maximum Values (Max), Standard Deviation (SD) and Coefficient of Variation (CV). Values in ind.mL^{-1}.

Class	Order	Family	Taxa	Mean	Max	SD	CV (%)
Bacillariophyceae	Cymbellales	Cymbellaceae	*Placoneis* sp.	2.92	24.41	8.07	2.76
	Eunotiales	Eunotiaceae	*Eunotia* sp1	19.74	97.62	24.68	1.25
			Eunotia sp2	2.12	28.74	7.36	3.47
			Eunotia sp3	10.37	57.48	15.45	1.49
			Eunotia sp4	34.76	217.71	53.05	1.53
			Eunotia sp5	13.24	52.12	18.11	1.37
			Eunotia sp6	3.24	27.46	8.95	2.76
			Eunotia sp7	10.00	122.03	25.57	2.56
			Eunotia sp8	1.18	29.57	5.91	5.00
			Eunotia sp9	8.83	147.60	30.01	3.40
			Eunotia sp10	1.18	29.57	5.91	5.00
	Naviculales	Naviculaceae	*Kobaysiellla* sp.	3.49	29.57	9.65	2.76
			Navicula sp.	1.09	27.21	5.44	5.00
			Nupela sp1	2.07	27.21	7.18	3.47
		Sellaphoraceae	*Sellaphora* sp1	15.69	109.82	29.16	1.86
			Sellaphora sp2	1.09	27.21	5.44	5.00
		Pinnulariaceae	*Pinnularia* sp1	1.10	27.46	5.49	5.00
			Pinnularia sp2	4.14	48.81	12.00	2.90
	Surirellales	Surirellaceae	*Surirella* sp1	2.98	49.60	10.92	3.66
			Surirella sp2	0.99	24.80	4.96	5.00
Chloropyceae	Chlorococcales	Treubariaceae	*Treubaria schmidlei* (Schöed.) Fott & Kovác	0.98	24.41	4.88	5.00
	Chlamydomonadales	Volvocacceae	*Eudorina illinoisensis* (Kofoid) Pascher	3.03	26.06	8.37	2.76
	Chlorococcales	Scenesdesmaceae	*Actinastrum hantzschii* (Lagerheim)	2.25	28.74	7.78	3.46
		Oocystaceae	*Ankistrodesmus falcatus* (Corda) Ralfs	2.13	28.74	7.38	3.47
			Ankistrodesmus fasciculatus (Lundberg) Komárková-Legnerová	0.97	24.21	4.84	5.00
			Ankistrodesmus fusiformes (Corda) Korsikov	6.90	172.43	34.49	5.00
			Ankistrodesmus sp.	3.45	86.22	17.24	5.00
			Ankistrodesmus tortus Komárek & Comas González	13.64	316.13	63.21	4.64
			Kirchneriella sp.	2.20	54.91	10.98	5.00
			Monoraphidium arcuatum (Korshikov) Hindák	25.70	170.84	50.94	1.98
			Monoraphidium contortum (Thuret) Komárková-Legnerová	47.56	402.35	100.67	2.12
			Monoraphidium griffithii (Berkeley) Komárková-Legnerová	184.55	1549.65	335.97	1.82
			Monoraphidium komarkovae Nygaard	5.57	114.96	23.30	4.18

Table 3. Continued...

Class	Order	Family	Taxa	Mean	Max	SD	CV (%)
			Monoraphidium nanum (Ettl) Hindák	4.27	54.91	12.76	2.99
		Chlorococcaceae	*Chlorococcum crenutum* Meneghini	7.42	108.85	23.85	3.21
		Dictyosphaeriaceae	*Dictyosphaerium* sp.	0.99	24.80	4.96	5.00
			Westella botryoides (West) De Wildeman	19.04	329.47	66.28	3.48
		Hidrodictyaceae	*Pediastrum* sp.	1.09	27.21	5.44	5.00
		Radiococcaceae	*Coenochloris asymmetrica* Hindák	2.08	27.21	7.21	3.47
			Radiococcus nimbatus (De Wildeman) Schmidle	15.30	258.65	54.58	3.57
		Scenedesmaceae	*Coelastrum astroideum* De Notaris	3.28	57.48	12.31	3.75
			Coelastrum reticulatum (P.A.Dangeard) Senn	1.15	28.74	5.75	5.00
			Coelastrum sp.	2.30	57.48	11.50	5.00
			Crucigenia quadrata Morren	1.10	27.46	5.49	5.00
			Scenedesmus ellipticus Corda	2.13	28.74	7.41	3.47
			Scenedesmus intermedius Chodat	2.19	27.46	7.57	3.46
			Scenedesmus longispina Chodat	1.15	28.74	5.75	5.00
			Tetrastum triangulare (Chodat) Komárek	38.70	314.77	87.57	2.26
Cryptophyceae	Cryptomonadales	Cryptomonadaceae	*Cryptomonas erosa* Ehrenberg	28.51	341.68	75.71	2.66
			Cryptomonas marssonii Skuja	41.21	173.59	51.37	1.25
			Cryptomonas obovata Czosnowski	14.99	145.05	38.79	2.59
			Cryptomonas pirenoidifera Geitler	62.64	464.16	114.53	1.83
Crysophyceae	Chromulinales	Dinobryaceae	*Dinobryon divergens* O.E. Imhof.	1.05	26.28	5.26	5.00
			Dinobryon elegantissimum Bourrelly	74.96	1873.88	374.78	5.00
			Dinobryon sertularia Ehrenberg	69.22	1508.53	301.02	4.35
		Chromulinaceae	*Chromulina* sp.	4.52	87.03	17.96	3.97
Cyanophyceae	Chroococcales	Chroococcaceae	*Chroococcus minimus* (Keissler) Lemmermann	56.07	390.49	96.21	1.72
			Chroococcus minutus (Kützing) Nägeli	71.09	402.35	102.63	1.44
			Chroococcus turgidus (Kützing) Nägeli	8.93	223.19	44.64	5.00
			Merismopedia tenuissima Lemmermann	65.70	1321.33	266.52	4.06
		Merismopediaceae	*Aphanocapsa* sp.	9.37	75.00	20.85	2.22
		Synechococcaceae	*Aphanothece* sp.	2.10	52.57	10.51	5.00
	Hormogonales	Oscillatoriales	*Oscillatoria redekei* Van Goor	0.98	24.41	4.88	5.00
	Stigonematales	Mastigocladaceae	*Hapalonsiphon* sp.	2.13	28.74	7.38	3.47
	Oscillatoriales	Pseudoanabaenaceae	*Planktolyngbya limnetica* (Lemmermann) Komárková-Legnerová & Cronberg	1.06	26.51	5.30	5.00
			Pseudanabaena limnetica (Lemmermann) Komárek	0.98	24.60	4.92	5.00
			Romeria gracilis (Koczwara)	15.89	146.43	30.73	1.93

Table 3. Continued...

Class	Order	Family	Taxa	Mean	Max	SD	CV (%)
Dinophyceae	Peridiniales	Peridiniaceae	*Peridinium* sp1	56.49	650.02	136.43	2.41
			Peridinium sp2	99.60	848.30	188.92	1.90
			Peridinium sp3	73.77	344.41	83.77	1.14
			Peridinium sp4	0.98	24.41	4.88	5.00
Euglenophyceae	Euglenales	Euglenaceae	*Euglena gracilis* G. A. Klebs	9.92	58.02	19.59	1.97
			Euglena sp.	50.73	367.96	114.26	2.25
			Trachelomonas sp.	10.00	100.00	23.89	2.39
Fragilariophyceae	Fragilariales	Fragilariaceae	*Fragilaria* sp.	0.99	24.80	4.96	5.00
Zygnemaphyceae	Desmidiales	Closteriaceae	*Closterium aciculare* (T. West)	3.20	29.01	8.88	2.77
			Closterium closterioides (Ralfs) A.Louis & Peeters	0.98	24.60	4.92	5.00
		Desmidiaceae	*Cosmarium* sp.	1.04	26.06	5.21	5.00
			Pleurotaenium sp.	8.72	145.28	30.39	3.48
			Staurastrum megacanthum (Lundell)	5.25	49.20	12.89	2.46
			Staurastrum sp1	1.15	28.74	5.75	5.00
			Staurastrum sp2	3.29	54.91	12.05	3.67
			Staurastrum sp3	1.10	27.46	5.49	5.00
			Staurastrum sp4	0.98	24.41	4.88	5.00
			Staurastrum sp5	17.71	442.81	88.56	5.00
			Staurastrum sp6	26.57	664.22	132.84	5.00
			Staurastrum sp7	0.96	24.02	4.80	5.00
			Teilingia granulata (J.Roy & Bisset) Bourrelly	0.98	24.60	4.92	5.00
		Mesotaeniaceae	*Gonatozygon* sp.	0.98	24.60	4.92	5.00

Table 4. Zooplankton species identified in water bodies associated with agriculture in the Distrito Federal (Brazil) and data referring to Mean, Maximum Values (Max), Standard Deviation (SD) and Coefficient of Variation (CV). Values in ind.m-^{3}.

Groups	Family	Taxa	Mean	Max	SD	CV (%)
Cladocerans						
	Bosminidae	*Bosmina hagmanni* (Stingelin, 1904)	343.39	8066.67	1610.56	4.69
		Bosmina longirostris (Müller, 1785)	0.13	3.33	0.67	5.00
		Bosmina tubicen (Brehm, 1953)	320.75	7533.33	1503.66	4.69
		Bosminopsis deitersi (Richard, 1895)	255.48	4293.33	864.02	3.38
	Chydoridae	*Acroperus harpae* (Baird, 1834)	7.78	100.00	21.27	2.73
		Alona cambouei (Guerne & Richard, 1893)	1.47	33.33	6.67	4.55
		Alona davidi (Richard, 1895)	66.61	1600.00	319.59	4.80
		Alona guttata (Sars, 1862)	18.73	316.67	63.98	3.42
		Alona monacantha (Sars, 1901)	3.08	66.67	13.41	4.36
		Alona poppei (Richard, 1897)	26.40	640.00	127.86	4.84
		Alona rustica (Scott, 1895)	0.80	16.67	3.37	4.21
		Biapertura verrucosa (Sars, 1901)	0.53	6.67	1.58	2.95
		Chydorus eurynotus (Sars, 1901)	19.36	388.89	78.14	4.04
		Chydorus sphaericus (Müller, 1785)	0.13	3.33	0.67	5.00
		Disparalona dadayi (Birge, 1879)	17.65	128.57	36.45	2.07
		Leydigiopsis ornata (Daday, 1905)	2.84	71.11	14.22	5.00
	Daphniidae	*Ceriodaphnia cornuta* (Sars, 1886)	0.41	10.26	2.05	5.00
		Daphnia gessneri (Herbst, 1967)	0.53	13.33	2.67	5.00
	Ilyocryptidae	*Ilyocryptus sordidus* (Liévin, 1848)	1.38	17.78	4.37	3.17
		Ilyocryptus spinifer (Herrick, 1882)	4.92	55.56	13.17	2.68
		Ilyocryptus verrucosus (Daday, 1905)	0.13	3.33	0.67	5.00
	Macrothricidae	*Macrothrix elegans* (Sars, 1901)	3.07	53.33	11.05	3.60
		Macrothrix laticornis (Jurine, 1820)	1.04	14.29	3.28	3.16
		Macrothrix squamosa (Sars, 1901)	2.13	53.33	10.67	5.00
		Macrothrix superaculeata (Smirnov, 1982)	2.22	55.56	11.11	5.00
		Streblocerus pygmaeus (Sars, 1901)	0.67	16.67	3.33	5.00
	Moinidae	*Moina micrura* (Kurz, 1874)	1.90	47.62	9.52	5.00
		Moina minuta (Hansen, 1899)	181.47	4233.33	846.26	4.66
		Moina sp.	0.27	6.67	1.33	5.00
	Oxyurella	*Oxyurella ciliata* (Bergamin, 1939)	2.22	55.56	11.11	5.00
	Sididae	*Diaphanosoma birgei* (Korínek, 1891)	354.44	7400.00	1490.94	4.21
		Diaphanosoma spinulosum (Herbst, 1967)	16.13	400.00	79.97	4.96

Table 4. Continued...

Groups	Family	Taxa	Mean	Max	SD	CV (%)
Copepods						
	Diaptomidae	*Diaptomus deitersi* (Poppe, 1891)	0.27	6.67	1.33	5.00
		Notodiaptomus brandorffi (Reid, 1987)	0.13	3.33	0.67	5.00
		Notodiaptomus deeveyorus (Dussart, 1984)	0.13	3.33	0.67	5.00
		Diaptomidae female	12.77	133.33	36.62	2.87
		Diaptomidae juvenile	332.92	4466.67	919.94	2.76
		Diaptomidae nauplii	3694.51	45911.11	9148.13	2.48
	Cyclopidae	*Mesocyclops ogunnus* (Onabamiro, 1957)	0.13	3.33	0.67	5.00
		Microcyclops alius (Kiefer, 1935)	4.44	111.11	22.22	5.00
		Microcyclops ceibaensis (Marsh, 1919)	13.13	166.67	43.80	3.34
		Microcyclops finitmus (Dussart, 1984)	0.13	3.33	0.67	5.00
		Microcyclops sp.	0.67	6.67	1.92	2.89
		Microcyclops anceps anceps (Ricard, 1897)	11.38	277.78	55.51	4.88
		Paracyclops chiltoni (Thomson, 1883)	0.13	3.33	0.67	5.00
		Thermocyclops inversus (Kiefer, 1936)	0.53	10.00	2.08	3.90
		Thermocyclops minutus (Lowndes, 1934)	3.82	55.56	13.42	3.51
		Cyclopidae male	38.75	888.89	177.35	4.58
		Cyclopidae juvenile	256.73	1944.44	486.32	1.89
		Cyclopidae nauplii	768.75	7257.14	1911.57	2.49
Rotifers						
Collothecaceae	Collothecidae	*Collotheca* sp.	28.80	720.00	144.00	5.00
Flosculariaceae	Conochilidae	*Conochilus* sp.	25.78	644.44	128.89	5.00
	Filiniidae	*Filinia longiseta* (Ehrenberg, 1834)	0.13	3.33	0.67	5.00
	Flosculariidae	*Ptygura libera* (Myers, 1934)	659.71	6066.67	1720.75	2.61
		Ptygura pedunculata (Edmondson, 1939)	33.33	833.33	166.67	5.00
	Hexarthridae	*Hexarthra* sp.	1455.51	25000.00	5073.76	3.49
	Testudinellidae	*Pompholyx sulcata* (Hudson, 1885)	0.71	17.78	3.56	5.00
		Testudinella carlini (Bartos, 1951)	1.23	30.77	6.15	5.00
		Testudinella patina (Hermann, 1783)	11.12	141.67	29.30	2.63
Ploima	Asplanchnidae	*Asplanchna sieboldii* (Leydig, 1854)	0.93	23.33	4.67	5.00
	Brachionidae	*Brachionus calyciflorus* (Pallas, 1766)	0.13	3.33	0.67	5.00
		Brachionus dolabratus (Harring, 1914)	0.76	19.05	3.81	5.00
		Brachionus falcatus (Zacharias 1898)	8.86	152.38	31.76	3.59
	Euchlanidae	*Beauchampiella eudactylota eudactylota* (Gosse, 1986)	0.13	3.33	0.67	5.00

Table 4. Continued...

Groups	Family	Taxa	Mean	Max	SD	CV (%)
		Euchlanis lyra (Hudson,1886)	6.00	150.00	30.00	5.00
		Euchlanis meneta (Myers, 1930)	2.67	66.67	13.33	5.00
		Euchlanis sp.	0.76	19.05	3.81	5.00
	Notommatidae	*Cephalodella gracilis* (Ehrenberg, 1832)	6.67	166.67	33.33	5.00
		Cephalodella sp.	7.95	100.00	21.71	2.73
	Brachionidae	*Keratella cochlearis* (Gosse, 1851)	100.89	1250.00	273.07	2.71
		Keratella lenzi (Hauer, 1953)	570.39	12438.10	2480.10	4.35
		Plationus patulus macracanthus (Daday, 1905)	0.67	16.67	3.33	5.00
		Plationus patulus patulus (Müller, 1786)	9.36	166.67	33.95	3.63
		Platyias quadricornis (Ehrenberg, 1832)	8.89	166.67	34.69	3.90
	Epiphanidae	*Microcodides robustus* (Glascott, 1892)	2.04	33.33	7.42	3.63
	Euchlanidae	*Microcodon clavus* (Ehrenberg, 1830)	2.07	33.33	7.49	3.61
	Ituridae	*Itura* sp.	12.04	277.78	55.46	4.60
	Lecanidae	*Lecane bulla* (Gosse, 1851)	66.79	944.44	186.57	2.79
		Lecane curvicornis (Murray, 1913)	2.37	16.67	5.27	2.22
		Lecane elegans (Harring, 1914)	0.13	3.33	0.67	5.00
		Lecane haliclysta (Harring & Myers, 1926)	0.13	3.33	0.67	5.00
		Lecane latissima (Yamamoto, 1955)	0.56	13.89	2.78	5.00
		Lecane leontina (Turner, 1892)	2.79	55.56	11.36	4.07
		Lecane luna (Müller, 1776)	38.53	484.85	110.83	2.88
		Lecane lunares (Sampaio and Lopez, 2000)	19.40	319.44	64.10	3.30
		Lecane (Monostyla) *closterocerca* (Schmarda, 1859)	1.33	33.33	6.67	5.00
		Lecane nana (Murray, 1913)	0.57	14.29	2.86	5.00
		Lecane proiecta (Hauer, 1956)	1.42	35.56	7.11	5.00
		Lecane quadridentata (Ehrenberg, 1832)	1.16	22.22	4.48	3.88
		Lecane signifera (Jennings, 1896)	2.43	25.00	6.83	2.81
		Lecane unguitata (Fadeev, 1925)	1.07	26.67	5.33	5.00
		Lecane ungulata (Gosse, 1887)	3.50	55.56	12.26	3.50
		Lecane venusta (Harring & Myers, 1926)	12.00	300.00	60.00	5.00
	Lepadellidae	*Lepadella patella* (Müller, 1786)	14.10	177.78	39.82	2.82
	Notommatidae	*Notommata* sp.	53.44	1200.00	239.37	4.48
	Scaridiidae	*Scaridium longicaudum* (Müller, 1786)	0.13	3.33	0.67	5.00
	Synchaetidae	*Ploesoma africana* (Wulfert, 1965)	1.51	27.78	5.83	3.86
		Ploesoma sp.	0.93	23.33	4.67	5.00

Table 4. Continued...

Groups	Family	Taxa	Mean	Max	SD	CV (%)
		Ploesoma truncatum (Levander, 1894)	1.00	25.00	5.00	5.00
		Polyarthra vulgaris (Carlin, 1943)	217.47	1571.43	427.24	1.96
		Synchaeta stylata (Wierzejski, 1893)	8.57	214.29	42.86	5.00
	Trichocercidae	*Trichocerca bicristata* (Gosse, 1887)	2.04	47.62	9.52	4.67
		Trichocerca similis (Wierzejski, 1893)	17.73	416.67	83.28	4.70
		Trichocerca sp.	1.93	33.33	6.87	3.55
		Trichotria tetractis (Ehrenberg, 1830)	6.00	150.00	30.00	5.00
	Trichotriidae	*Macrochaetus collinsi* (Gosse, 1867)	44.20	1050.00	209.73	4.75
		Macrochaetus collinsi collinsi (Gosse, 1867)	0.56	13.89	2.78	5.00
		Macrochaetus longipes (Myers, 1934)	8.95	150.00	31.33	3.50
		Macrochaetus sericus (Thorpe, 1893)	1.66	38.10	7.62	4.60
		Macrochaetus subquadratus (Perty, 1850)	0.13	3.33	0.67	5.00
Testate Amoebae						
	Arcellidae	*Arcella arenaria* (Greeff, 1866)	1.11	27.78	5.56	5.00
		Arcella artocrea (Leidy, 1876)	85.69	2111.11	422.00	4.92
		Arcella conica (Playfair, 1918)	37.80	371.43	93.65	2.48
		Arcella costata (Ehrenberg, 1847)	15.13	111.11	31.26	2.07
		Arcella costata angulosa (Perty, 1852)	669.64	15600.00	3111.44	4.65
		Arcella crenulata (Deflandre, 1928)	10.69	166.67	33.85	3.17
		Arcella dentata (Ehrenberg, 1830)	7.27	133.33	26.96	3.71
		Arcella discoides (Ehrenberg, 1843)	28.00	450.00	94.94	3.39
		Arcella excavata (Cunningham, 1919)	38.43	750.00	149.67	3.89
		Arcella gibbosa (Penard, 1890)	91.70	2250.00	449.67	4.90
		Arcella hemisphaerica (Perty, 1852)	0.41	10.26	2.05	5.00
		Arcella hemisphaerica gibba (Deflandre, 1928)	2.36	55.56	11.10	4.71
		Arcella hemisphaerica undulata (Deflandre, 1928)	5.70	100.00	20.34	3.57
		Arcella megastoma (Penard, 1902)	8.24	150.00	30.36	3.68
		Arcella mitrata (Leidy, 1876)	98.85	2400.00	479.49	4.85
		Arcella polypora (Penard, 1890)	3.97	88.89	17.81	4.49
		Arcella rota (Daday, 1905)	0.27	3.33	0.92	3.46
		Arcella rotundata alta (Playfair, 1918)	2.16	16.67	4.59	2.12
		Arcella rotundata aplanata (Deflandre, 1928)	13.07	266.67	53.57	4.10
		Arcella vulgaris (Ehrenberg, 1830)	474.34	9450.00	1879.37	3.96
		Arcella vulgaris crenulata (Deflandre, 1928)	0.40	10.00	2.00	5.00

Table 4. Continued...

Groups	Family	Taxa	Mean	Max	SD	CV (%)
		Arcella vulgaris penardi (Deflandre, 1928)	4.12	66.67	14.92	3.62
		Arcella vulgaris undulata (Deflandre, 1928)	6.99	27.78	10.12	1.45
		Arcella vulgaris wailesi (Deflandre, 1928)	0.41	10.26	2.05	5.00
	Difflugiidae	*Cucurbitella dentata quinquelobata* (Gauthier-Lievre & Thomas, 1960)	0.41	10.26	2.05	5.00
		Cucurbitella mespiliformis (Penard, 1902)	4.89	66.67	17.00	3.48
		Difflugia achlora (Penard, 1902)	3.47	83.33	16.65	4.80
		Difflugia acuminata (Ehrenberg, 1838)	0.48	12.12	2.42	5.00
		Difflugia acutissima (Deflandre, 1931)	1.42	35.56	7.11	5.00
		Difflugia arceolata (Carter, 1864)	1.11	27.78	5.56	5.00
		Difflugia brevicola (Cash & Hopkinson, 1909)	28.04	533.33	109.47	3.90
		Difflugia capreolata (Penard, 1902)	15.21	285.71	57.81	3.80
		Difflugia cf. *glans* (Penard, 1902)	26.04	633.33	126.57	4.86
		Difflugia compressa (Carter, 1864)	11.58	152.38	31.72	2.74
		Difflugia corona (Wallich, 1864)	91.52	1950.00	387.90	4.24
		Difflugia cylindrus (Thomas, 1953)	0.13	3.33	0.67	5.00
		Difflugia distenda (Penard, 1899)	11.40	150.00	36.61	3.21
		Difflugia elegans (Penard, 1890)	4.44	111.11	22.22	5.00
		Difflugia globulosa (Dujardin, 1837)	0.13	3.33	0.67	5.00
		Difflugia gramen (Penard, 1902)	39.08	400.00	91.00	2.33
		Difflugia limnetica (Levander, 1900)	0.71	17.78	3.56	5.00
		Difflugia lithophila (Penard, 1902)	1.66	38.10	7.62	4.60
		Difflugia lobostoma (Leidy, 1879)	20.69	309.52	62.15	3.00
		Difflugia longicollis (Gassowsky, 1936)	0.41	10.26	2.05	5.00
		Difflugia microclaviformis (Kourov, 1925)	6.00	150.00	30.00	5.00
		Difflugia muriformis (Gauthier-Lievre & Thomas, 1958)	50.49	1033.33	207.20	4.10
		Difflugia oblonga (Ehrenberg, 1838)	28.65	304.76	80.40	2.81
		Difflugia penardi (Hopkinson, 1909)	0.76	19.05	3.81	5.00
		Difflugia pseudogramen (Gauthier-Lievre & Thomas, 1960)	1.73	22.22	5.57	3.22
		Difflugia pyriformis (Perty, 1849)	1.33	33.33	6.67	5.00
		Difflugia tuberculata (Wallich, 1864)	8.33	208.33	41.67	5.00
		Difflugia urceolata (Carter, 1864)	0.53	10.00	2.08	3.90
		Difflugia venusta (Penard, 1902)	11.43	285.71	57.14	5.00
		Pontigulasia elisa (Penard, 1893)	21.37	333.33	68.12	3.19
		Protocucurbitella coroniformis (Gauthier-Lievre & Thomas, 1960)	6.27	150.00	29.97	4.78

Table 4. Continued...

Groups	Family	Taxa	Mean	Max	SD	CV (%)
		Protocucurbitella coroniformis ecornis (Gauthier-Lievre & Thomas, 1960)	19.28	450.00	89.83	4.66
	Heleoperidae	*Centropyxis aculeata* (Ehrenberg, 1838)	92.66	609.52	178.85	1.93
		Centropyxis aculeata oblonga (Deflandre, 1929)	111.07	1650.00	347.63	3.13
		Centropyxis aerophila (Deflandre, 1929)	0.71	17.78	3.56	5.00
		Centropyxis cassis (Wallich, 1864)	2.37	35.56	8.39	3.53
		Centropyxis cassis spinifera (Playfair, 1918)	57.54	1366.67	272.94	4.74
		Centropyxis constricta (Ehrenberg, 1841)	32.55	228.57	55.80	1.71
		Centropyxis delicatula (Penard, 1902)	4.41	100.00	20.02	4.54
		Centropyxis discoides (Penard, 1902)	143.46	3400.00	678.69	4.73
		Centropyxis ecornis (Ehrenberg, 1841)	111.08	2076.19	412.03	3.71
		Centropyxis gibba (Deflandre, 1929)	85.31	1350.00	298.36	3.50
		Centropyxis marsupiformis (Wallich, 1864)	68.36	675.56	173.92	2.54
		Centropyxis minuta (Deflandre, 1929)	10.67	266.67	53.33	5.00
		Centropyxis spinosa (Cash, 1905)	15.82	150.00	36.58	2.31
		Heleopera petricola (Leidy, 1879)	8.00	150.00	31.22	3.90
	Hyalospheniidae	*Argynnia dentistoma* (Penard, 1890)	80.80	1866.67	373.26	4.62
	Lesquereusiidae	*Lesquereusia epistomium* (Penard, 1902)	6.82	150.00	29.97	4.39
		Lesquereusia globulosa (Thomas & Gauthier-Lievre, 1959)	6.74	100.00	22.09	3.28
		Lesquereusia modesta (Rhumbler, 1895)	70.64	1500.00	298.56	4.23
		Lesquereusia spiralis (Ehrenberg, 1840)	159.17	3300.00	656.87	4.13
		Lesquereusia spiralis caudata (Playfair, 1917)	37.84	750.00	150.55	3.98
		Lesquereusia spiralis decloitrei (Van Oye,1959)	2.22	55.56	11.11	5.00
		Lesquereusia spiralis hirsuta (Gauthier-Lievre & Thomas, 1959)	94.31	1950.00	389.74	4.13
		Netzelia oviformis (Cash, 1909)	10.06	194.44	38.94	3.87
		Netzelia tuberculata (Wallich, 1864)	24.27	600.00	119.95	4.94
		Netzelia wailesi (Ogden, 1980)	258.90	5850.00	1169.73	4.52
		Quadrulella tropica (Wailes, 1912)	48.57	1200.00	239.90	4.94
	Nebelidae	*Pseudonebela africana* (Gauthier-Lièvre, 1953)	3.22	66.67	13.51	4.19
		Nebela barbata (Leidy, 1874)	30.80	750.00	149.87	4.87
		Nebela dentistoma (Penard, 1890)	1.33	33.33	6.67	5.00
		Nebela tubulata (Brown, 1911)	29.68	450.00	91.58	3.09
	Trigonopyxidae	*Cyclopyxis aplanata* (Deflandre, 1929)	40.00	900.00	180.28	4.51
		Cyclopyxis eurystoma (Deflandre, 1929)	4.00	100.00	20.00	5.00

Table 4. Continued...

Groups	Family	Taxa	Mean	Max	SD	CV (%)
		Cyclopyxis impressa (Daday, 1905)	11.62	133.33	30.97	2.67
		Cyclopyxis kahli (Deflandre, 1929)	5.32	55.56	13.84	2.60
		Cyclopyxis penardi (Deflandre, 1929)	0.13	3.33	0.67	5.00
	Euglyphidae	*Euglypha acanthophora* (Ehrenberg, 1841)	80.53	1800.00	358.49	4.45
		Euglypha denticulata (Brown, 1912)	61.03	1350.00	269.72	4.42
		Euglypha filifera (Penard, 1890)	12.00	300.00	60.00	5.00
		Euglypha tuberculata (Dujardin, 1841)	28.94	600.00	120.06	4.15
	Phryganellidae	*Phryganella hemisphaerica* (Penard, 1902)	0.13	3.33	0.67	5.00
	Rhopalodiaceae	*Pyxidicula cymbalum* (Penard, 1902)	10.13	100.00	25.05	2.47
		Pyxidicula operculata (Agardh, 1827)	0.41	10.26	2.05	5.00

Table 5. Mantel, Partial Mantel and Procrustes's test results for concordance between phytoplankton and zooplankton groups using species density data.

Groups	Tested Matrices	Mantel		Procrustes	
		r	*P*	*r*	*P*
Phytoplankton x Zooplankton		**0.20**	0.015	**0.84**	<0.001
Phytoplankton	Species x FG	**0.47**	0.001	**0.81**	<0.001
	Species x MBFG	**0.41**	0.001	**0.72**	<0.001
	FG x MBFG	**0.50**	0.001	**0.82**	<0.001
	Species x Environmental	**0.27**	0.003	**0.48**	0.004
	FG x Environmental	0.12	0.144	**0.49**	0.003
	MBFG x Environmental	0.03	0.393	0.37	0.067
Zooplankton	Cladocerans x Copepods	**0.24**	0.002	**0.69**	<0.001
	Cladocerans x Rotifers	**0.21**	0.001	0.77	0.722
	Cladocerans x Testate Amoebae	**0.24**	0.001	**0.85**	0.006
	Copepods x Rotifers	**0.28**	0.003	**0.68**	<0.001
	Copepods x Testate Amoebae	0.11	0.132	0.63	0.112
	Rotifers x Testate Amoebae	**0.40**	0.001	**0.82**	0.002
	Zooplankton x Environmental	**0.26**	0.021	**0.43**	0.017
	Cladocerans x Environmental	**0.22**	0.002	0.36	0.067
	Copepods x Environmental	**0.26**	0.021	**0.42**	0.019
	Rotifers x Environmental	**0.17**	0.035	**0.41**	0.029
	Testate Amoebae x Environmental	0.08	0.237	**0.45**	0.012

Table 6. Mantel and Procrustes test results for numerical resolution (density versus presence/absence of species).

Groups	Tested Matrices	Mantel		Procrustes	
		r	*P*	*r*	*P*
Phytoplankton	Species	**0.71**	0.001	**0.93**	<0.001
	FG	**0.93**	0.001	**0.70**	<0.001
	MBFG	**0.86**	0.001	**0.53**	<0.001
Zooplankton	Cladocerans	**0.87**	0.001	**0.86**	<0.001
	Copepods	**0.78**	0.001	**0.63**	<0.001
	Rotifers	**0.84**	0.001	**0.86**	<0.001
	Testate amoebae	**0.93**	0.001	**0.91**	<0.001

Table 7. Mantel and Procrustes test results for concordance between higher taxonomic resolutions (genus and family) and species of phytoplankton and zooplankton using species density data.

Groups	Tested Matrices	Mantel		Procrustes		Mantel		Procrustes	
		Genus x Species		Genus x Species		Family x Species		Family x Species	
		r	*P*	*r*	*P*	*r*	*P*	*r*	*P*
Phytoplankton		**0.59**	<0.001	**0.86**	<0.001	**0.54**	<0.001	**0.85**	<0.001
Zooplankton	Cladocerans	**0.84**	<0.001	**0.95**	<0.001	**0.63**	<0.001	**0.81**	<0.001
	Copepods	**0.97**	<0.001	**0.99**	<0.001	**0.79**	<0.001	**0.96**	<0.001
	Rotifers	**0.74**	<0.001	**0.94**	<0.001	**0.69**	<0.001	**0.93**	<0.001
	Testate Amoebae	**0.73**	<0.001	**0.84**	<0.001	**0.73**	<0.001	**0.83**	<0.001

biological interaction can also generate positive or negative correlation between different organic groups (Paine, 1980). This last possibility is more likely when the biological groups studied have different responses to environmental variables (Grenouillet et al., 2008).

In this study, the matrices of phytoplankton and zooplankton species densities sampled were concordant. Significant levels of concordance between phytoplankton and zooplankton were expected results, as they are directly and intimately connected by trophic interactions (Brett & Goldman, 1996; Havens et al., 2009). However, Heino (2010) warns that it is not enough to find significative concordance between the communities tested for meaningful decision-making in environmental monitoring programs, but the strength of the effect (in this case, the Mantel *r* or the Procrustes *r*) must be equal to or higher than 0.70. Correlations weaker than 0.70 are not advisable to be used in

environmental monitoring programs because an important amount of information may be lost. The value of *r* shown in the comparison between the matrices of phytoplankton and zooplankton was 0.20 for Mantel test and 0.84 for Procrustes test. We choose to work with the most restrictive values given by the two tests analyzed. For this reason we encourage to work with these two communities in an environmental monitoring program in this study area. Significant results, albeit also with *r* values less than 0.70, were found in other studies (Lopes et al., 2011; Padial et al., 2012).

The comparison between phytoplankton species density and its ecological groups (FG and MBFG) suggested significant concordant patterns. However, even though significant, the *r* value was considered low (mean $r = 0.44$ for Mantel test). This result was expected because FG and MBFG approaches are not clearly related to species taxonomical classification, but related to environmental conditions or morphological characteristics, respectively. In order to avoid loss of important information, it is advisable that the FG and MBFG classifications should not be used as substitute for phytoplankton species density in environmental monitoring programs in the study area. Other studies also showed concordant patterns but with low *r* in comparisons between the density of phytoplankton species and their classification in FG and/or MBFG (Gallego et al., 2012; Machado et al., 2015).

It is worth considering that these phytoplankton classifications are not intended to replace the full extent of the information that can be obtained from the species density data. These phytoplankton classifications bring different and complementary information about this community and may be so important as density data, depending on the aim of the study. Knowing which species dominate a functional group, for example, is of prime importance when information about conservation, trophic functions and toxicity, among others, are essential to confront certain ecological or environmental issues (Salmaso et al., 2015).

In relation to zooplankton, higher concordance between cladocerans and copepods and concomitantly lower concordance among the rotifers and microcrustaceans (cladocerans and copepods) were expected results. This can be explained by the fact that these microcrustaceans are phylogenetically closer to each other than to the others, thus presenting a more similar ecological niche. Consequently, it was expected that rotifers and microcrustaceans would respond differently to underlying environmental gradients (Bini et al., 2008). Almost all combinations assessed between zooplankton groups in this study showed significant values (except between copepods and testate amoebae in both Mantel and Procrustes tests and cladocerans and rotifers in Procrustes test). However, as found in the phytoplankton, all the restrictive significant combinations of zooplankton taxonomical groups matrices showed lower *r* values (0.27 mean for Mantel test), suggesting that these taxonomical groups could not replace other in monitoring this region.

For environmental monitoring purposes in the study area, almost all biological analyses can be performed using presence/absence data, except for MBFG classification and copepods (both less than 0.70 in Procrustes test). Similar results regarding to zooplankton community were found in other articles (Xu et al., 2011; Gomes et al., 2015). A probable reason for this result may be the fact that the community patterns in our study system were not boosted by some dominant species, mainly due to the logarithmic transformation, which tends to decrease the weight of the effects of abundant species on patterns of ordination (Carneiro et al., 2010).

The use of genus or family as a replacement for the identification at the species level offers advantages, since the identification of some species depends on the examination of structures that may not always be present, or involves groups with high morphological variability (e.g. phytoplankton species of *Scenedesmus*, *Cladophora* and *Stigeoclonium* genera). Furthermore, the species identification of complex groups based on small physical structures can be extremely difficult (Irfanullah, 2006). Generally, identification at genus and/or family level may be less time consuming, with reduced costs, and can even be more reliable and safer. Species identification is complex and laborious, especially in many tropical and subtropical environments. Previous studies have shown that higher taxonomic resolution is easily understood as a valid strategy to describe the community variation (Sanchez-Moyano et al., 2006; Ribas & Padial, 2015).

The results presented in this study revealed that higher taxonomic levels (genus and family) were concordant with the species data for both phytoplankton and zooplankton communities. However, we found that the *r* values showed a small decrease as the taxonomic level became higher, so that higher *r* values were obtained for the genus data and lower for the family data,

except for testate amoebae, which had the same value for both taxonomic levels. Therefore, in relation to zooplankton, we recommend the use of data at genus or family level for copepods and testate amoebae, and only data at genus level for cladocerans and rotifers in monitoring studies in the study area. This result is in agreement with previous studies for different organisms, such as fungi, plants (Villaseñor et al., 2005), invertebrates (Balmford et al., 2000; Maurer, 2000; Olsgard & Somerfield, 2000; Wunsam et al., 2002; Dauvin et al., 2003; Waite et al., 2004; Guzman-Alvis & Carrasco, 2005; Melo, 2005; Bilton et al., 2006; Khan, 2006; Marshall et al., 2006; Sanchez-Moyano et al., 2006; Heino & Soininen, 2007; Lovell et al., 2007) and phytoplankton (Passy & Legendre, 2006; Carneiro et al., 2010; Gallego et al., 2012). Therefore, related to phytoplankton community, it is not advisable to use data at genus or family levels because the *r* value obtained was smaller than 0.70.

5. Conclusion

As we have seen in this study, it is important to establish a permanent limnological monitoring program to rapidly detect any disturbance in water bodies, especially those associated with anthropic activities such as agriculture. For this reason, it is necessary to optimize the environmental monitoring with easy, fast and low cost analyzes. *But this optimization should not occasion major loss of environmental and biological information.*

In this sense, we do not advise to simplify the environmental monitoring by sampling only the zooplankton or phytoplankton community, because one community is not surrogate of the other one. In the same way, we suggest to use phytoplankton species density and their functional and morphofunctional approaches, depending on the objective of the study, in order to avoid loss of information. Likewise, it is important that all zooplankton groups are sampled (cladocerans, copepods, rotifers and testate amoeba) because no group had effectively replaced other groups, as well as the environmental variables.

However, it is feasible that both phytoplankton and zooplanktonic biological analyzes are performed using presence/absence species data, except for copepod and MBFG classification. With regard to the use of a higher taxonomic resolution, it is also feasible to use genera level data for all zooplankton community and only family level data for copepods and testate amoebae.

Acknowledgements

We thank the Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq) that funded the project Process Number: 477076/2011-4.

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Received: 30 March 2017
Accepted: 09 May 2019