



Is it possible to simplify environmental monitoring? Approaches with zooplankton in a hydroelectric reservoir

É possível simplificar o monitoramento ambiental? Abordagens com o zooplâncton em um reservatório hidroelétrico

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Abstract: Aim: In order to contribute to the knowledge about the simplification of biological surveys, this study evaluated the use of substitute groups, numeric and taxonomic resolution for the three main groups of zooplankton (cladocerans, copepods and rotifers) in a Hydropower Plant (UHE). The following issues were addressed: (i) the patterns of spatial and/or temporal ordering generated between each zooplankton group are in concordance? (ii) The concordance is maintained using presence/absence data instead of density data? (iii) The identification of organisms to the species level can be replaced by genus or family level? **Methods:** Samples were taken in seven sample units over five campaigns between 2009 and 2010 in the UHE Serra da Mesa (Goiás, Brazil). To evaluate the correlation between each pair of matrices was used the Mantel test. **Results:** The results demonstrate that the replacements should not be made among the zooplanktonic groups, requiring the monitoring of three groups (copepods, cladocerans and rotifers). Furthermore, the results suggest the use of density data of individuals rather than just presence/absence of species. Finally, the results of this study indicate the possibility to use data at species level instead of data at genus or family level. **Conclusion:** For zooplankton community monitoring purposes only the use of taxonomic resolution showed to be efficient for this area of study, not being recommended the use of surrogate groups or numerical resolution.

Keywords: cladocera; copepoda; rotifera; numerical resolution; taxonomic resolution.

Resumo: Objetivo: A fim de contribuir para o conhecimento a respeito da simplificação de levantamentos biológicos, o presente estudo avaliou o uso de grupos substitutos, resolução taxonômica e numérica para os três principais grupos da comunidade zooplanctônica (cladóceros, copépodes e rotíferos) em uma Usina Hidrelétrica (UHE). As seguintes questões foram abordadas: (i) Os padrões de ordenação espacial e/ou temporal gerados entre cada grupo zooplanctônico são concordantes? (ii) A concordância se mantém utilizando dados de presença e ausência em substituição a dados de densidade? (iii) A identificação dos organismos em nível de espécie pode ser substituída por gênero ou



família? **Métodos:** Foram realizadas coletas em sete unidades amostrais ao longo de cinco campanhas entre os anos de 2009 e 2010 na UHE de Serra da Mesa (Goiás, Brasil). Para avaliar a correlação entre cada par de matrizes foi utilizado o teste de Mantel. **Resultados:** Não se deve realizar substituições entre os grupos zooplancônicos, sendo necessário o monitoramento dos três grupos (copépodos, cladóceros e rotíferos). Além disso, sugerimos a utilização de dados de densidade de indivíduos ao invés de apenas dados de presença/ausência de espécies. Por fim, os resultados deste estudo indicam a possibilidade de dados em nível de espécies serem substituídos por dados em nível de gênero ou família. **Conclusão:** Para fins de monitoramento da comunidade zooplancônica, apenas o uso da resolução taxonômica mostrou-se eficiente para esta área de estudo, não sendo recomendado o uso de substitutos nem resolução numérica entre os grupos.

Palavras-chave: cladocera; copepoda; rotifera; resolução numérica; resolução taxonômica.

1. Introduction

The environmental impacts have been occurring faster than we can monitor and maintain biodiversity (Bini et al., 2007; Landeiro et al., 2012; Martinelli et al., 2010). The increase of impacted areas affects directly and indirectly the functioning of terrestrial and aquatic ecosystems, highly contributing to the extinction of species (Ceballos et al., 2015). In this way, the monitoring of the biological communities becomes an important practice to evaluate the level of environmental degradation, mainly through variations in richness, density, and functional traits (Harmon et al., 2009; Ribeiro et al., 2016).

Monitoring programs are most effective when they evaluate environmental and biological dimensions across space and time (Alahuhta & Aroviita, 2016; Alahuhta et al., 2016). However, the increase in sampling number brings cost growth, while evaluate biological dimension brings the need of specialists in different biological groups. To mitigate this problem is possible to use biological surrogate groups, which is the use of substitution between groups that present congruent patterns over time and space for biomonitoring purposes (Padial et al., 2012) or to work with presence/absence of species (rather than density) at lower taxonomic resolutions (Gomes et al., 2015; Machado et al., 2015).

In aquatic environments, several studies seek to assess existing relations between different assemblies, mainly fish, benthic macroinvertebrates, zooplankton and phytoplankton (Gubiani et al., 2011; Padial et al., 2012). Thus, if the community variation patterns are consistent between at least two groups, is possible to simplify monitoring programs by sampling only one group (Johnson & Hering 2010; Landeiro et al., 2012). Furthermore, higher taxonomic levels can be used, as information on family level or genus replacing species (taxonomic resolution) or species occurrence

data (presence/absence) instead of organisms density (numerical resolution) would be sufficient (Carneiro et al., 2010; Heino, 2014). The use of simplifications in biomonitoring of aquatic environments becomes extremely relevant given the growing need for global supplies that add to the anthropogenic effects on the water quality of many reservoirs, such as: land use, inadequate water management and climate variations (Peters & Meybeck, 2000; Lee & Biggs, 2015).

Among the main groups of aquatic organisms, zooplankton stands out for being able to react quickly to environmental and toxicological changes (Moreira et al., 2014; Vieira et al., 2011). In this sense, the zooplankton can be used as variable for environmental monitoring because, in addition to responding human impacts, it plays an important role in nutrient cycling and energy flow of food webs (Gagneten & Paggi, 2009; Oberhaus et al., 2007; Vieira et al., 2011).

The aim of this study was to investigate the possibility of using only one of three zooplankton component groups: copepods, cladocerans and rotifers. It was also evaluated the use of numerical and taxonomic resolutions in this community. Thus, we sought to answer the following questions: (i) Are the spatial and/or temporal ordering patterns generated between each zooplankton group concordant? (ii) Is the concordance maintained using presence/absence data as a substitute for density data? (iii) Can the identification of organisms to the species level be replaced by genus or family level? Our expectations are: i) copepods and cladocerans might exhibit higher concordance because they are phylogenetically closer (both crustaceans) and they have more similar ecological niches ii) that it is possible to replace density data for presence/absence species data and iii) the substitution of data at species level may be also possible, both for genus and family level.

2. Material and Methods

2.1. Study area

The Serra da Mesa reservoir is located in Brazilian Midwest region (Figure 1) and its main drainage basin is constituted by the Tocantins River (Caramaschi et al., 2012). The dam's Hydropower Plant (UHE) of Serra da Mesa was built in 1996 in the upper Tocantins River and became the largest reservoir of the country in water volume, with 54.4 billion m³ and an area of 1,784 km² (Caramaschi et al., 2012). The climate is tropical rainy with dry periods and average temperature of 20 °C (Sousa, 2003).

2.2. Collection and identification

A total of 28 samples were obtained in the following months: August/2009 (5 samples, points 1, 2, 3, 5 and 6), November/2009 (6 samples, points 1, 2, 3, 4, 5 and 6), March/2010 (7 samples, points 1, 2, 3, 4, 5, 6 and 7), September/2010 (6 samples,

points 1, 2, 3, 4, 5 and 6) and November/2010 (4 samples, points 2, 3, 5 and 6) (Figure 1).

The samples were collected with a motorized pump at a depth of 0.5 m, being filtered 1000 of water per sample through a 68 µm mesh plankton net. The collected material was conditioned in polyethylene flasks and fixed in 4% formaldehyde solution. Samples were concentrated into a volume of 100 mL and the survey of density was conducted with 10 mL of downsampling in Sedgewick-Rafter chambers, taken with the Hensen-Stempel pipette and then analyzed using an optical microscope (Bottrell et al., 1976). After the counts, qualitative analyzes were performed, taking sub-samples until no new species were found. The final density was expressed in individuals * m⁻³.

2.3. Data analysis

Firstly, all data were separated by species, genus, families and zooplanktonic groups (copepods, cladocerans and rotifers) and transformed into

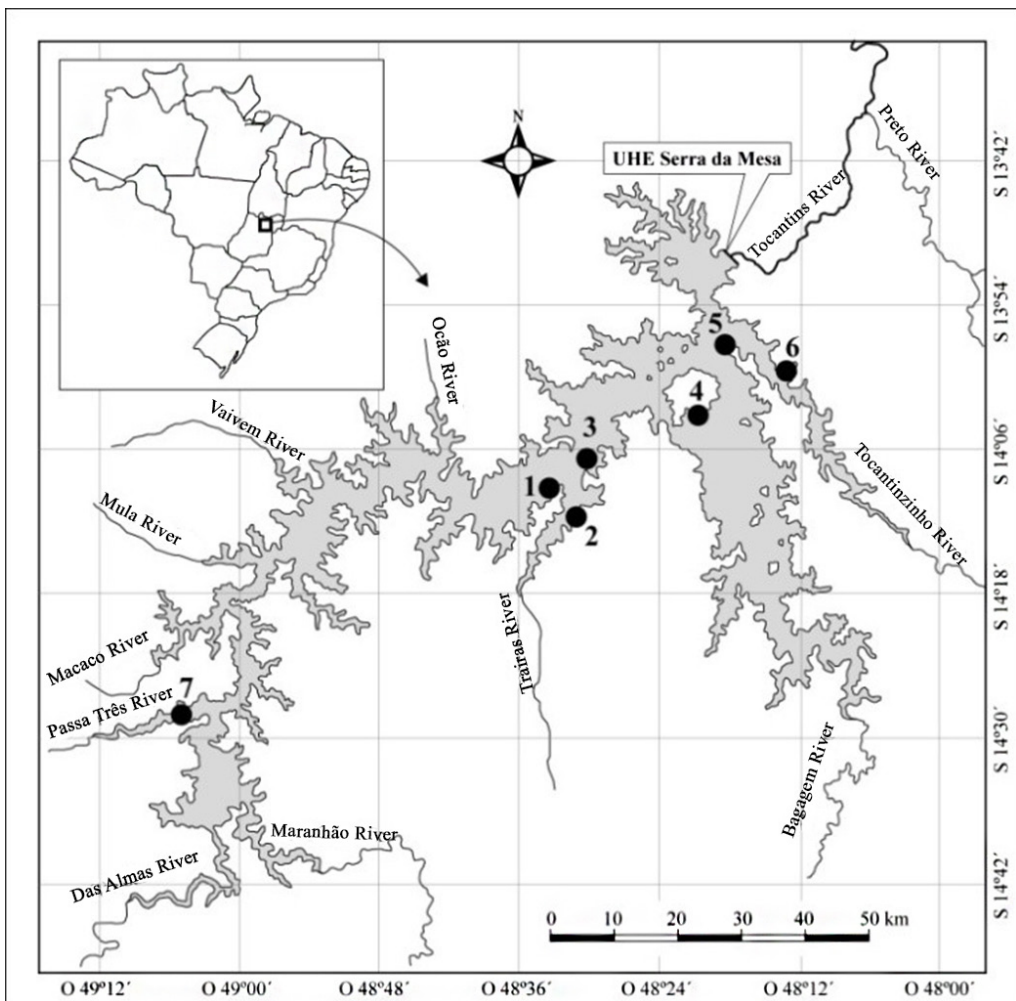


Figure 1. Serra da Mesa Reservoir and sampling points (Brazil).

logarithmic scale ($x + 1$). Subsequently, the data set was converted into distance matrices using Bray-Curtis for density data and Jaccard index for presence/absence species (Legendre & Legendre, 2012).

To evaluate the correlation between each pair of matrices was used the Mantel test (Legendre & Legendre, 2012), which calculates the correlation between two distance matrices. The correlation strength was measured using the value of r (ranging from -1 to +1) and its significance was measured using 999 randomizations.

All analyzes were performed using *vegdist* and *mantel* functions of *vegan* package (Oksanen et al., 2013) in the statistical software R (R Core Team, 2016).

3. Results

A total of 45 taxa were sampled, being distributed as follows: 27 taxa of rotifers, 12 of cladocerans and six of copepods (Table 1). Regarding density, 354,320 individuals were sampled, with 210,359 rotifers, 97,289 copepods and 46,672 cladocerans, comprising respectively: 59.4%, 27.4% and 13.2% of all occurrences. The rotifers had the highest species richness in all campaigns and higher densities in Aug/09 and Nov/09 (Figure 2).

Only copepods and rotifers presented spatial distribution patterns concordant being the high level of concordance in Nov/09 and medium in Aug/09 and Sep/10 (Table 2).

The results of the numerical resolution ranged between the campaigns in a way that significant values were observed for all groups in Nov/09 and only for copepods in March/10 and cladocerans in Sep/10 (Table 3). On the other hand, the taxonomic resolution showed high values and homogeneous

in all campaigns, indicating that the use of data on genus or family level is equivalent to the use of species (Table 3). The copepods were not included in this analysis because it presented a small number of species and genera.

4. Discussion

The results showed that the three zooplanktonic groups (copepods, cladocerans and rotifers) should not be used as substitutes for each other, due to high variability over time with relatively low levels of concordance (<0.7) (Heino, 2010). Therefore, our expectations were not corroborated, since (i) the correlation was higher among copepods and rotifers and (ii) the few significant concordance levels were low.

Even among taxonomically different biological groups, such as macrophytes and macroinvertebrates (Traversetti et al., 2015), vascular plants, bryophytes and birds (Rooney & Azeria, 2015), concordant distribution patterns has been found. However, Our results do not indicate concordance between the zooplanktonic community groups. This absence of concordance was also observed in other studies related to zooplankton community (Bessa et al., 2011; Bini et al., 2008; Vieira et al., 2015). Although the species of each group may respond differently to environmental gradients (Adamczuk et al., 2015) the absence of concordance among copepods, cladocerans and rotifers is interesting, once they are part of the same assembly. This result reinforces the need to incorporate all zooplanktonic groups (copepods, cladoceran e rotifers) in environmental monitoring programs.

The numerical resolution also showed that the use of presence/absence values of species as substitute of density data is not indicated, which is similar to results found by other authors

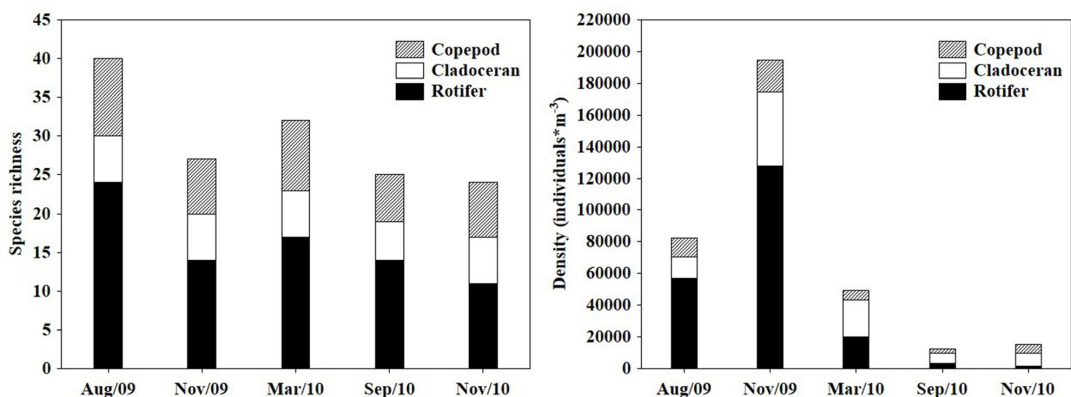


Figure 2. Species richness and density of rotifers, cladocerans and copepods in Serra da Mesa Reservoir (Brazil).

Table 1. Density (Dens), Mean and Standard Deviation (SD) of the zooplankton species density sampled in reservoir Serra da Mesa-GO (Brazil).

Family	Species	Aug/09			Nov/09			Mar/10			Sep/10			Nov/10		
		Dens	Mean	SD	Dens	Mean	SD	Dens	Mean	SD	Dens	Mean	SD	Dens	Mean	SD
Cladoceran																
	<i>Bosmina hagmanni</i>	5031	1006.2	2121.3	4864	810.7	1108.7	1385	197.9	298.2	834	139.1	122.6	1592	397.9	235.4
	<i>Bosmina tubicen</i>	131	26.2	34.4	600	100	221	1120	160	230.3	1150	191.7	277.6	330	82.5	95.3
	<i>Bosminopsis deitersi</i>	6927	1385.3	2915.4	10407	1734.4	3664.9	1258	179.7	192.2	448	74.7	68.4	2318	579.6	455.9
	<i>Alona poppei</i>	1	0.2	0.4	0	0	0	0	0	0	0	0	0	0	0	0
	<i>Alona</i> sp.	0	0	0	400	66.7	163.3	6	0.9	2.3	0	0	0	0	0	0
	<i>Chydoridae</i>	8	1.6	3.6	0	0	0	25	3.6	9.4	0	0	0	0	0	0
	<i>Pleuroxus</i> sp.	2	0.4	0.9	0	0	0	0	0	0	0	0	0	24	6.1	11.5
	<i>Ceriodaphnia cornuta</i>	60	11.9	15.4	1034	172.4	374.9	2105	300.7	695.4	225	37.5	47.7	545	136.2	152.7
	<i>Ceriodaphnia</i> sp.	29	5.8	13	500	83.3	204.1	17	2.4	6.3	0	0	0	362	90.4	151.3
	<i>Simocephalus</i> sp.	123	24.5	54.8	0	0	0	5	0.7	1.9	0	0	0	0	0	0
	<i>Moina minuta</i>	29	5.8	13	0	0	0	0	0	0	33	5.6	13.6	0	0	0
	<i>Diaphanosoma spinulosum</i>	0	0	0	2175	362.5	709.2	214	30.6	55.7	232	38.6	39.2	124	31.1	47.2
Copepod																
	Copepodito	1852	370.3	326.9	17608	2934.7	4241.6	11383	1626.2	2214.6	3467	577.8	544	4413	1103.3	523.6
	Nauplius	10742	2148.3	3616.9	23467	3911.1	4043	10758	1536.9	1786.1	1887	314.4	236	3168	792.1	410.2
	<i>Thermocyclops</i> sp.	4	0.8	1.3	15	2.5	3.5	12	1.7	2.1	7	1.2	1.2	7	1.8	1.7
	Copepodito	663	132.5	262.1	3633	605.6	834.6	578	82.6	67	355	59.2	42.7	265	66.3	73.9
	Nauplius	45	8.9	18.3	1733	288.9	308.3	558	79.8	64.7	613	102.1	140.6	48	12.1	15.8
	<i>Notodiaptomus</i> sp.	1	0.2	0.4	1	0.2	0.4	3	0.4	0.5	0	0	0	2	0.5	1
Rotifer																
	<i>Anuraeopsis coelata</i>	450	90	201.2	0	0	0	0	0	0	0	0	0	0	0	0
	<i>Brachionus dolabratus</i>	150	30	67.1	0	0	0	1	0.1	0.4	0	0	0	0	0	0
	<i>Brachionus falcatus</i>	3	0.6	0.9	842	140.3	323.6	226	32.3	58.9	50	8.3	13.9	93	23.3	44.5
	<i>Keratella americana</i>	4281	856.2	1786.8	2468	411.4	349.9	660	94.3	165.1	263	43.9	47.9	213	53.3	85.9
	<i>Keratella cochlearis</i>	40267	8053.3	13958.3	117550	19591.7	33434.1	16075	2296.4	2144.4	1308	218.1	150.2	1273	318.3	359
	<i>Keratella lenzi</i>	3394	678.7	1382.6	2828	471.3	719.4	694	99.1	183.4	259	43.2	42.8	2	0.5	1
	<i>Keratella tropica</i>	0	0	0	302	50.3	122.3	0	0	0	0	0	0	15	3.8	7.5
	<i>Platonus patulus patulus</i>	36	7.2	11	734	122.4	179.3	394	56.2	50.7	427	71.1	83.6	135	33.8	67.5
	<i>Platylas quadricornis</i>	0	0	0	0	0	0	25	3.6	9.4	0	0	0	0	0	0
	<i>Filinia longiseta</i>	150	30	67.1	1	0.2	0.4	150	21.4	56.7	17	2.8	6.8	33	8.3	16.7

Table 1. Continued...

Family	Species	Aug/09			Nov/09			Mar/10			Sep/10			Nov/10		
		Dens	Mean	SD	Dens	Mean	SD	Dens	Mean	SD	Dens	Mean	SD	Dens	Mean	SD
	<i>Lecane bulla</i>	150	30	67.1	0	0	0	0	0	0	0	0	0	0	0	0
	<i>Lecane cornuta</i>	150	30	67.1	0	0	0	0	0	0	0	0	0	0	0	0
	<i>Lecane halicysta</i>	75	15	22.4	50	8.3	20.4	18	2.5	6.2	0	0	0	0	0	0
	<i>Lecane hornemanni</i>	58	11.7	16.2	0	0	0	0	0	0	0	0	0	0	0	0
Lecanidae	<i>Lecane luna</i>	0	0	0	0	0	0	17	2.4	6.3	83	13.9	26.7	1	0.3	0.5
	<i>Lecane lunares</i>	150	30	67.1	0	0	0	3	0.4	1.1	0	0	0	0	0	0
	<i>Lecane proiecta</i>	14	2.8	3.9	4	0.7	1.6	128	18.3	31.1	150	25	29.3	23	5.8	11.7
	<i>Lecane signifera</i>	243	48.5	76.3	18	2.9	6.7	0	0	0	33	5.6	13.6	0	0	0
	<i>Lecane sp.</i>	27	5.4	11	69	11.4	23.2	281	40.1	83.5	102	17	25.6	108	27	52
Lepadellidae	<i>Lepadella sp.</i>	1	0.2	0.4	0	0	0	0	0	0	0	0	0	0	0	0
Philodinidae	Bdelloidea	5239	1047.8	1625.8	2617	436.1	277.5	1248	178.2	272.3	443	73.8	57.1	3	0.8	1
Synchaetidae	<i>Polyarthra sp.</i>	150	30	67.1	0	0	0	0	0	0	0	0	0	0	0	0
Testudinellidae	<i>Testudinella patina</i>	26	5.2	11.1	0	0	0	25	3.6	9.4	65	10.8	20.1	0	0	0
	<i>Trichocerca bicristata</i>	1287	257.3	446.4	618	102.9	243.6	75	10.7	19.7	113	18.9	33.8	0	0	0
Trichocercidae	<i>Trichocerca cylindrica</i>	600	120	268.3	0	0	0	0	0	0	0	0	0	0	0	0
	<i>Trichocerca iernis</i>	75	15	33.5	8	1.4	3.4	0	0	0	0	0	0	0	0	0
Trichotritidae	<i>Macrochaetus sp.</i>	25	5	11.2	0	0	0	1	0.1	0.4	17	2.8	6.8	0	0	0

Table 2. Correlation coefficients among rotifers, cladocerans and copepods in Serra da Mesa Reservoir (Brazil).

Campaign	Groups	<i>r</i>	<i>P</i>
Aug/09	Cladoceran x Copepod	0.35	0.188
	Cladoceran x Rotifer	0.48	0.143
	Copepod x Rotifer	0.64	0.031
Nov/09	Cladoceran x Copepod	0.17	0.239
	Cladoceran x Rotifer	0.30	0.145
	Copepod x Rotifer	0.88	0.004
Mar/10	Cladoceran x Copepod	-0.29	0.801
	Cladoceran x Rotifer	0.19	0.201
	Copepod x Rotifer	0.20	0.179
Sep/10	Cladoceran x Copepod	0.07	0.331
	Cladoceran x Rotifer	-0.31	0.813
	Copepod x Rotifer	0.55	0.036
Nov/10	Cladoceran x Copepod	-0.83	0.948
	Cladoceran x Rotifer	-0.41	0.787
	Copepod x Rotifer	0.38	0.116

P<0.05.

Table 3. Numerical resolution.

Campaign	Groups	Numeric resolution		Taxonomic resolution			
		Dens x PA		Sp x Gn		Sp x Fa	
		<i>R</i>	<i>P</i>	<i>r</i>	<i>P</i>	<i>R</i>	<i>P</i>
Aug/09	Cladoceran	0.67	0.091	0.99	0.013	0.94	0.034
	Copepod	0.02	0.456	-	-	-	-
	Rotifer	0.33	0.153	0.99	0.015	0.99	0.012
Nov/09	Cladoceran	0.52	0.031	0.97	0.001	0.69	0.001
	Copepod	0.69	0.008	-	-	-	-
	Rotifer	0.47	0.033	0.99	0.001	0.99	0.002
Mar/10	Cladoceran	0.42	0.101	0.95	0.001	0.77	0.001
	Copepod	0.74	0.046	-	-	-	-
	Rotifer	0.13	0.282	0.99	0.001	0.98	0.001
Sep/10	Cladoceran	0.57	0.016	0.99	0.002	0.96	0.004
	Copepod	0.44	0.137	-	-	-	-
	Rotifer	0.26	0.149	0.96	0.003	0.39	0.094
Nov/10	Cladoceran	0.28	0.255	0.89	0.091	0.36	0.288
	Copepod	-0.02	0.583	-	-	-	-
	Rotifer	0.25	0.212	0.94	0.222	0.82	0.211

(Dens = density; PA = presence/absence of species) and taxonomic (Sp = species, Gn = genus, Fa = family); *P*<0.05; Copepods were not included in the second part of the analysis due to their low species richness.

(Bessa et al., 2011; Giehl et al., 2014; Heino, 2008; Valente-Neto et al., 2016). However, some studies indicate the use of numerical resolution for zooplanktonic community (Gomes et al., 2015) and other groups (Carneiro et al., 2010; Ribas & Padiál, 2015).

Our results indicate that the use of genus level for zooplankton groups of Serra da Mesa hydroelectric reservoir would be equivalent to the use of the species. Similar results were found for different groups (Giehl et al., 2014; Souza et al., 2016; Valente-Neto et al., 2016) including zooplankton (Carneiro et al., 2013). The concordance with higher taxonomic levels can be justified by the

low number of species found by genus and family, which creates a higher similarity between the more and less specific data sets (Giehl et al., 2014). This approach is acceptable when there is not a major loss of information between the data sets (high concordance level), thus resulting in lower effort for taxonomic identification of *taxa* (Carneiro et al., 2010; Heino & Soininen, 2007; Khan, 2006). A study using ants, for example, revealed that the reduction of actual costs for the use of taxonomic resolution at genus level could reach 40% (Souza et al., 2016).

Finally, for zooplankton community monitoring purposes, only the use of taxonomic resolution

showed to be efficient for this area of study, not being recommended the use of substitutes or numerical resolution. It is clear that this strategy (identifying organisms only at the genus level) should not be used indiscriminately. Even with the high values found for Mantel r , only in extreme situations, such as the absence of taxonomists, the need for immediate assessments and/or a significant financial shortfall, the taxonomic resolution at the genus level would be an interesting alternative.

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