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Composition and species richness of flagellate protozoa from environments associated to the Baía river (Mato Grosso do Sul State, Brazil): influence of the hydrological period and the connectivity

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ABSTRACT. Despite flagellate protozoa are important for the metabolism of aquatic ecosystems, researches about the ecology of this community is scarce. Therefore, this study investigated the influence of flood regime and hydrological connectivity on the patterns of composition and species richness of protozoan flagellates from aquatic environments in the upper Paraná river floodplain. To this end, samplings were undertaken in two periods of the hydrological cycle (March 2008 and September 2008), at six lentic environments associated with the Baía river (three are connected to the river, and three are isolated). 120 taxa were identified in the studied area, distributed in 10 orders and one residual group. This high species richness was sustained by the order Euglenida, which contributed with 70% of total species. The species composition was significantly different between periods and environments, as well as species richness, which was higher in connected environments during the high water period. The results evidenced that the flood pulse and hydrological connectivity are relevant factors driving the structure and dynamic of plankton flagellate protozoa community in the upper Paraná river floodplain.

Key words: Protozooplankton, faunistic inventory, floodplain.

RESUMO. Composição e riqueza de espécies de protozoários flagelados de ambientes associados ao rio Baía (Mato Grosso do Sul, Brasil): influência do período hidrológico e da conectividade. Apesar dos protozoários flagelados serem importantes para o metabolismo dos ecossistemas aquáticos, os estudos sobre a ecologia desta comunidade são escassos. Nesse contexto, este estudo tem por objetivos investigar a influência do regime de inundação e da conectividade hidrológica sobre os padrões de composição e riqueza de espécies de protozoários flagelados da planície de inundação do alto rio Paraná. Para tal, foram realizadas coletas em dois períodos do ciclo hidrológico (março/2008 e setembro/2008), em seis ambientes lênticos associados ao rio Baia (sendo três conectados ao rio e três desconectados). Foram identificados 120 táxons na área de estudo, distribuídos em 10 ordens e um grupo residual. Essa elevada riqueza de espécies foi sustentada pela ordem Euglenida, que contribuiu com 70% do total das espécies registradas. A composição de espécies foi significativamente diferente entre os períodos e entre os ambientes, assim como a riqueza de espécies, que foi maior nos ambientes conectados e durante o período de águas altas. Esses resultados demonstraram que o regime de inundação e a conectividade hidrológica são fatores relevantes na estruturação e na dinâmica da comunidade de protozoários flagelados planctônicos, na planície de inundação do alto rio Paraná.

Palavras-chave: Protozooplâncton, inventário faunístico, planície de inundação.

Introduction

The hydrological regime is considered the driving force both for the ecological functioning and for the maintenance of biodiversity patterns in floodplains, since the periodical oscillations of the water flow induce deep changes in the structure and dynamic of the biota (NEIFF, 1990; JUNK et al., 1989).

Among the aquatic communities in floodplains, flagellate protozoa play important role in the energy flow and nutrient cycling (AZAM et al., 1983), because they transfer to the upper trophic levels the energy obtained through the consumption of bacteria, organic detritus, viruses and pico and nanoplanktonic algae (XU et al., 2005) and, contribute significantly for the primary production in the ecosystems (SAFI; HALL, 1997).

Although it is unquestionable the importance of this community to aquatic ecosystems, studies about are still scarce. Only the autotrophic and mixotrophic fractions have received a little more attention in studies on phytoplankton. Thus, holistic studies incorporating all the fractions are almost nonexistent, especially in floodplains. Consequently, the effect of the flood regime and the hydrological connectivity on the composition and species richness of flagellate protozoa is not known.

Furthermore, few studies have investigated the species composition of flagellate protozoa and most of them did not examine all the fractions of this community (AUER; ARNDT, 2001; COMTE et al., 2006; DOMAIZON et al., 2003; KISS et al., 2009; LAVRENTYEV et al., 2004; TIKHONENKOV, 2007; TIKHONENKOV; MAZEI, 2006, 2008; WEITERE; ARNDT, 2003). In the same way, there are no records of studies specifically approaching the species richness patterns of these organisms. In Brazil, the studies on this community are still scarce (ARAÚJO; COSTA, 2007; ARAÚJO; GODINHO, 2008; PEREIRA et al., 2005) and most of them does not present taxonomical focus and includes the other components of the protozooplankton.

In this way, the present study aimed to accomplish a species faunistic inventory and investigate the influence of the flood regime and hydrological connectivity on the patterns of composition and species richness of flagellate protozoa from six lentic environments associated to the Baía river in the upper Paraná river floodplain.

To this end, we predict that the patterns of composition and species richness are different between the environments (with and without connection) and between the periods of the hydrological cycle (high and low water), and we expect that: i) the species composition is more similar between the environments with and without connection during the high water period due to the homogenizing effect of the floods (THOMAZ et al., 2007) and ii) the higher species richness occur in the environments connected to the Baía river during the high water period due to the lotic influence.

Material and methods

The present study was developed in the upper Paraná river floodplain that presents high environmental heterogeneity, due to presence of lakes, backwaters, channels and rivers. Among these environments, Baía river (22°43'23.16"S; 53°17' 25.5"W) is situated in the right bank of Paraná river, in the Mato Grosso do Sul State. It is a meandering river that presents a great number of concatenated lakes along its course. Moreover, due to the low current flow and small slope of its bed, this river is characterized as semilotic (SOUZA FILHO; STEVAUX, 1997).

We accomplished two semestrial samplings in six lakes associated to the Baía system (Figure 1), three without connection to the river (Aurélio, Fechada and Pousada das Garças) and other three connected to it (Guaraná, Maria Luiza and Porcos). The first sampling was performed in March 2008, during the high water period, and the second in September 2008, during the low water period. All the samplings, in replica, were performed in the littoral and pelagic region from each (n = 48), using a plankton net (20 μm) and also through passage of a flask at subsurface.

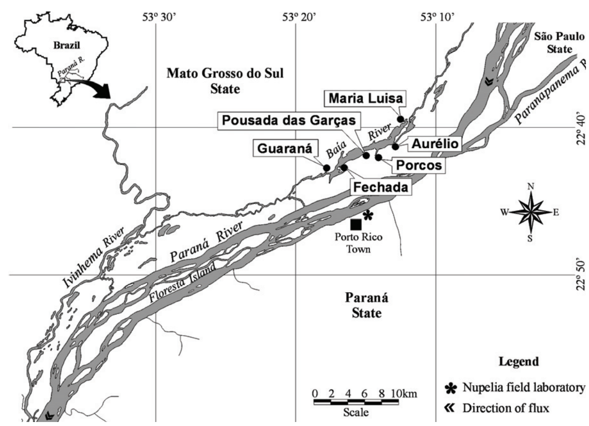

Figure 1. Location of the environments associated to the Baía river in the upper Paraná river floodplain.

The individuals were analyzed *in vivo*, under optical microscope, to avoid alterations in the cell shape and dimension arisen from the preservation process. The aliquots were obtained using a monochannel micropipette and placed on glass slides, which were examined until no new species arose during this analysis. The individuals were identified, whenever possible, at species level, based on morphological traits and specialized literature. The results were presented according to the classification system developed by Lee et al. (2000).

In order to test the differences in the species richness between the environments (with and without connection with the river) and between the periods (high and low water) we employed a factorial analysis of variance (Two-way ANOVA). The spatial and temporal patterns in the species composition were evaluated using a detrended correspondence analysis (DCA), since according to Gauch (1982), this analysis is the most indicated for group of ecological data because it describes well the distribution of the sampled population. Afterwards, we applied further analyses of variance (Two-way ANOVA) to the scores from each axis to test differences in the species composition between the environments (with and without connection with the river) and periods (high and low water). The assumptions of normality and homoscedasticity were previously tested and the significance level adopted was of $p < 0.05$.

Results

The community of flagellate protozoa was represented by 120 taxa (Table 1 and Figure 2), belonging to 10 orders and one residual group: Choanoflagellida (1 taxa), Chromulinales (6 taxa), Cryptomonadida (8 taxa), Euglenida (81 taxa), Gymnodiniales (3 taxa), Kinetoplastea (4 taxa), Peridiniales (5 taxa), Synurales (3 taxa), Volvocida (6 taxa) and three residual taxa. Euglenida was the most species-rich order, due to the great contribution of *Trachelomonas* (32 taxa), *Euglena* (14 taxa) and *Phacus* (12 taxa), respectively. Moreover, other genera from other orders also contributed with high species richness in the studied environments (Table 1).

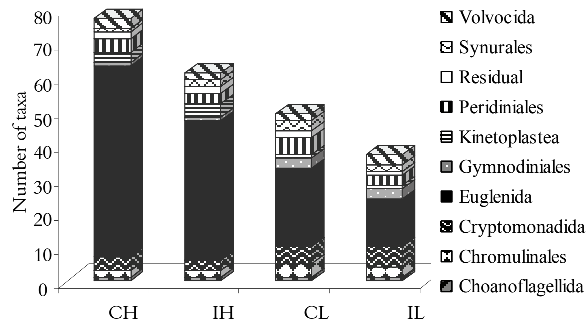

Figure 2. Species composition in the studied environments (CH: Connected, high water; IH: Isolated, high water; CL: Connected, low water; IL: Isolated, low water).

Table 1. Faunistic inventory of flagellate protozoa community recorded in six environments (Where: Guar: Guaraná; M-Lui: Maria Luiza; Por: Porcos; Auré: Aurélio; Fech: Fechada; P-Gar: Pousada das Garças) associated to Baía river, during the periods of high water (H) and low water (L), in the upper Paraná river floodplain.

Connectivity	Connected						Isolated					
Environments	Guar		M-Lui		Porc		Auré		Fech		P-Gar	
Period	H	L	H	L	H	L	H	L	H	L	H	L
Choanoflagellida												
Monosiga cf. *ovata* Kent.	X	X	-	X	X	-	X	-	-	X	-	-
Chromulinales												
Anthophysa vegetans (O. F. Müller) Stein.	X	X	-	-	X	-	-	-	-	X	-	-
Ochromonas sp.	-	-	-	-	-	-	X	X	-	-	-	-
Oicomonas cf. *socialis* Moroff.	X	-	X	-	-	-	X	-	X	X	-	-
Spumella sp.	-	-	-	X	-	-	-	-	-	-	-	-
Uroglena sp.	-	X	-	-	-	-	-	-	-	-	-	-
Unidentified Chromulinales.	-	X	-	-	-	X	-	-	-	-	-	-
Cryptomonadida												
Cyatomonas sp?	-	-	-	-	-	-	-	X	-	-	-	-
Chilomonas sp.	-	-	-	-	-	-	-	-	-	-	X	-
Chroomonas cf. *acuta* Uterm.	X	X	X	X	X	X	-	X	-	X	X	X
Cryptomonas cf. *curvata* Ehr. emend. Pen.	X	-	X	-	X	-	-	-	-	-	-	-
Cryptomonas cf. *marssonii* Skuja	X	X	X	X	X	X	-	X	-	X	-	-
Cryptomonas sp.	X	X	-	X	X	X	X	X	-	-	X	X
Protochrysis sp?	-	-	-	-	-	X	-	X	-	-	-	-
Colorless unidentified Cryptomonadida.	-	-	-	X	-	-	-	X	-	X	-	-
Euglenida												
Anisonema acinus Duj.	-	X	-	-	-	-	-	-	-	-	-	-
Anisonema sp.	X	-	-	-	-	-	-	-	-	-	X	-
Astasia sp.	-	-	-	-	-	X	-	-	-	-	-	-
Colacium vesiculosum f. *arbuscula* (Stein) Hub. Pest.	-	-	-	-	-	-	-	-	-	-	X	-
Cryptoglena sp.	-	-	-	-	X	-	-	-	-	-	-	-
Entosiphon sulcatum (Duj.) Stein	X	-	-	-	-	-	-	-	X	-	-	-
Euglena acus var. *acus* Ehr.	X	X	-	-	-	-	-	-	-	-	-	-
E. caudata Hübn.	X	-	-	-	X	-	-	-	-	-	-	-
E. clavata Skuja	X	-	-	-	X	-	-	-	-	-	-	-
E. ehrenbergii Kleb.	-	-	-	-	-	-	-	-	X	-	-	-
E. limnophila Lemm. var. *limnophila* (Sec. Seckt)	-	-	-	-	-	-	X	-	X	-	-	-
E. minuta Prescott	-	-	-	X	X	-	-	-	X	-	X	-
E. oxyuris Schm.	X	X	X	-	X	-	X	-	-	-	X	-
E. polimorpha Dang.	X	-	-	-	-	-	-	-	-	-	-	-
E. proxima Dang.	X	X	X	-	X	X	X	X	-	X	-	-
E. splends Dang.	X	-	-	-	-	-	-	-	-	-	-	X
E. spirogyra Ehr.	-	X	-	-	X	-	-	-	-	-	-	-
E. viridis Ehr.	-	-	X	-	X	-	-	-	X	-	-	-
Euglena sp1.	X	-	-	-	-	-	-	-	-	X	-	X
Euglena sp2.	-	-	-	X	-	-	-	-	-	-	-	-
Lepocinclis fusiformes (Car.) Lemm. Conr.	X	-	-	-	X	-	-	-	-	-	-	-
L. ovum (Ehr.) Lemm.	X	X	-	X	X	X	X	X	-	-	X	-
L. texta (Duj.) Lemm.	X	-	X	-	X	-	X	-	X	-	X	-
Menoidium sp.	X	-	-	-	-	-	-	-	-	-	-	-

Continue...

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Notosolenus cf. *canellatus* Skuja	X	-	X	-	X	-	-	-	-	-	X	-
Peranema trichophorum (Ehr.) Stein.	X	-	-	-	X	-	-	-	-	-	-	-
Petalomonas sp.	-	-	-	-	-	-	-	-	X	X	-	-
Phacus contortus Bourr.	X	-	-	-	-	-	-	-	-	-	-	-
P. curvicauda Swirenko	-	X	-	X	-	X	-	X	-	X	-	-
P. horridus Pochm.	X	-	-	-	X	-	X	-	X	-	X	-
P. longicauda (Ehr.) Duj.	X	X	-	-	X	-	-	-	-	-	X	-
P. melagopsis Pochm.	-	X	-	-	-	-	-	-	-	-	-	-
P. orbicularis Hübn.	X	X	X	X	X	-	X	X	-	X	-	-
P. pleuronectes (Müll.) Duj.	X	-	X	-	X	-	X	-	X	-	X	-
P. pseudonordstedtii Pochm.	X	-	-	-	-	-	-	-	-	-	-	-
P. pusillus Lemm.	-	-	-	-	-	-	-	-	X	-	X	-
P. similis Christen	-	X	-	-	-	-	-	-	-	-	-	-
P. tortus (Lemm.) Skv.	-	-	-	-	-	-	X	-	X	-	-	-
Phacus sp.	X	-	-	-	X	-	-	-	-	-	-	-
Ploetia sp.	X	-	X	-	-	-	X	-	-	-	-	-
Sphenomonas sp.	X	-	-	-	-	-	-	-	-	X	-	-
Strombomonas acuminata (Schm.) Deft.	-	-	-	-	X	-	-	-	-	-	-	-
S. gibberosa (Playf.) Defl.	X	-	X	-	X	-	-	X	X	-	X	-
S. fluviatilis (Lemm.) Defl.	X	-	-	-	-	-	-	-	-	-	-	-
S. schawinslandii (Lemm.) Defl.	-	-	X	-	-	-	-	-	-	-	-	-
S. tetraptera Balech. et Dast	X	-	-	-	-	-	-	-	-	-	-	-
Strombomonas sp.	-	X	X	-	-	-	-	-	-	-	-	-
Trachelomonas acanthophora Stokes var. *acanthophora*	X	-	-	-	-	-	X	-	-	-	-	-
T. acanthophora Stokes var. *speciosa* (Defl.) Balech.	-	-	-	-	-	-	X	-	-	-	-	-
T. armata var. *armata* (Ehr.) Stein	X	-	X	-	X	-	X	-	X	-	X	-
T. armata var. *litoralensis* Tell et Zaloc.	-	-	-	-	X	-	-	-	-	-	-	-
T. armata (Ehr.) Stein *var. longispina* (Playf.) Defl.	-	-	-	-	-	-	-	-	-	-	X	-
T. bacillifera Playf.	-	X	-	-	-	-	-	-	-	-	-	-
T. bernardii Wol.	X	-	X	-	-	-	X	-	X	-	-	-
T. caudata (Ehr.) Stein	X	-	-	-	-	-	-	-	-	-	-	-
T. cylindrica Playf.	X	-	X	-	X	-	-	-	-	-	-	-
T. gracillima Balech. et Dast.	-	-	-	-	-	-	X	-	-	-	-	-
T. hispida (Perty) Stein emend. Defl. var. *hispida*	X	X	X	-	X	-	X	X	X	X	X	-
T.hispida var. *coronata* Lemm.	X	-	-	-	-	-	-	-	-	-	-	-
T. hispida var. *crenulatocollis* (Defl.)Tell et Conf.	X	-	-	-	-	-	-	-	-	-	-	-
T. hispida var. *multispinosa* (Tracanna) Tell et Conf.	-	-	X	-	-	-	X	-	X	-	X	-
T. lacustris Drez.	X	-	-	-	-	-	-	-	-	-	X	-
T. lemmermannii Wolosz. emend Defl.	-	-	-	-	-	-	X	-	-	-	-	-
T. magdaleniana Defl.	X	-	-	-	-	-	-	-	-	-	-	-
T. megalacantha var. *heterocantha* Tell et Zaloc.	-	-	-	-	-	-	X	-	-	-	-	-
T. oblonga Lemm.	-	X	-	X	-	X	X	X	-	X	-	X
T. pseudobulla Swir.	X	-	X	-	X	-	X	-	X	-	X	-
T. pulchra Swir.	X	X	-	-	-	-	X	-	-	-	-	-
T. raciborskii Wolosz.	X	-	X	-	-	-	-	-	-	-	-	-
T. rugulosa Stein emend. Defl.	-	-	X	-	X	-	X	-	-	-	-	-
T. sculpta Balech.	-	-	-	-	-	-	X	-	-	-	-	-
T. sydneyensis Playf.	-	-	-	-	-	-	X	-	-	-	X	-
T. similis var. *spinosa* Hub. Pest.	-	-	X	-	X	X	X	-	X	-	X	-
T. superba Tell	X	-	X	-	X	-	-	-	-	-	-	-
T. verrucosa Defl.	-	-	-	-	-	-	-	-	X	-	-	-
T. volvocina Ehr.	X	X	X	-	X	-	-	-	-	X	-	-
T. volvocinopsis Swir.	X	X	X	X	X	X	X	X	-	X	X	-
T. woycickii Koczw.	X	-	-	-	-	-	-	-	-	-	-	-
Trachelomonas sp.	-	-	X	-	-	-	-	-	-	-	-	-
Unidentified Euglenida 1.	-	-	X	X	X	-	-	-	-	-	-	X
Unidentified Euglenida 2.	-	-	X	-	-	-	-	-	-	-	-	-
Gymnodiniales												
Gymnodinium cf. *caudatum* Prescott	-	-	-	-	-	X	-	X	-	X	-	-
Gymnodinium cf. *fuscum* (Ehr.) Stein	X	X	-	X	-	X	-	-	-	X	X	X
Katodinium sp?	-	-	-	-	-	X	-	-	-	X	-	X
Kinetoplastea												
Bodo caudatus (Duj.) Stein	X	-	X	-	-	-	X	-	X	-	X	-
B. globosus Stein	X	-	-	-	-	-	-	-	-	-	X	-
Bodo sp.	-	X	-	X	-	X	X	-	-	X	-	-
Rhynchomonas sp.	-	-	X	-	-	-	X	-	-	-	-	-
Peridiniales												
Peridinium cf. *cinctum* (Muell.) Ehr.	X	X	X	-	X	-	X	-	-	X	X	-
P. cf. *wisconsinense* Eddy	X	X	-	X	X	X	-	X	-	X	-	-
Peridinium sp1.	X	X	-	-	-	X	-	-	-	-	X	-
Peridinium sp2.	-	-	X	X	-	-	-	-	X	-	-	X
Unidentified Dinoflagellata.	-	-	-	X	-	X	-	-	-	-	-	-
Residual												
Cladonema cf. *pauperum* Pasch.	X	-	X	-	X	-	X	-	-	-	-	-
Polytomella sp.	-	X	-	X	-	-	-	-	-	-	-	-
Rhipidodendron splendidum Stein	-	X	-	-	X	X	X	X	X	X	-	-
Synurales												

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Mallomonas sp1.	-	X	X	X	X	X	X	X	X	X	-	X
Mallomonas sp2.	-	X	-	-	-	X	-	-	-	-	-	-
Synura sp.	-	X	-	-	-	-	X	X	X	-	-	-
Volvocida												
Chlamydomonas sp.	X	-	-	-	-	-	-	-	-	-	-	-
Eudorina elegans Ehr.	-	X	-	X	X	X	X	X	-	-	-	X
Pandorina morum (O. F. Müller) Bory	-	-	-	-	-	-	-	X	-	-	-	-
Sphaerocystis sp.	-	-	-	-	-	-	-	X	-	-	-	-
Volvox aureus Ehr.	-	-	X	-	-	-	X	-	-	-	-	-
Unidentified Chlamydomonadidae.	-	X	-	X	-	-	-	-	-	-	-	-
Total	60	37	38	23	43	23	42	23	25	24	29	11

The detrended correspondence analysis indicated a clear distinction among the environments and mainly between the periods (Figure 3). This pattern was corroborated by the analysis of variance applied to the DCA scores, which evidenced a significant interaction between the factors for the DCA 1 and significant difference between the connected and isolated environments for the DCA 2 (Table 2).

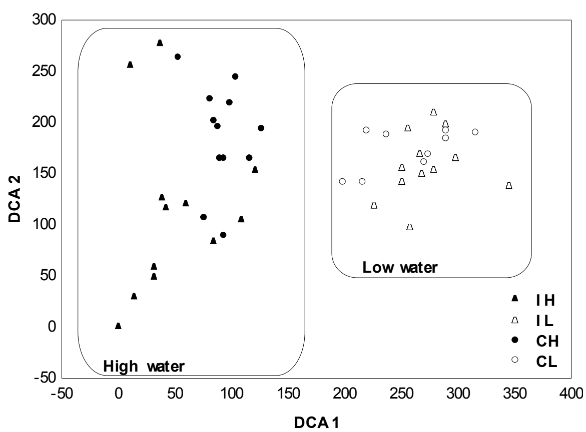

Figure 3. Distribution of the scores along the first two DCA axes, based on presence and absence data of flagellate protozoa species from six environments associated to Baía river, during the high and low water periods (FA: Isolated, high water; FB: Isolated, low water; AA: Connected, high water; AB: Connected, low water).

Table 2. Eigenvalue of the axis 1 and 2 from DCA and results from the analyses of variance (Two-way Anova) applied to the scores from each axis. *Significant values ($p < 0.05$).

Effect/Eigenvalues	DCA 1			DCA 2		
	D.F.	F	p	D.F.	F	p
Connectivity (Connected x Isolated)	1	1.91	0.174	1	8.82	0.005*
Period (High water x Low water)	1	430.74	0.000*	1	1.21	0.277
Connectivity * Period	1	10.69	0.002*	1	2.86	0.098
Eigenvalue		0.48			0.24	

The highest species richness were verified in the environments connected to Baía river during the high water period (Figures 4a and b) and these differences were validated by the analysis of variance that evidenced significant differences between the connected and isolated environments ($F = 26.915$; $p < 0.01$) and between the hydrological periods ($F = 15.561$; $p < 0.01$).

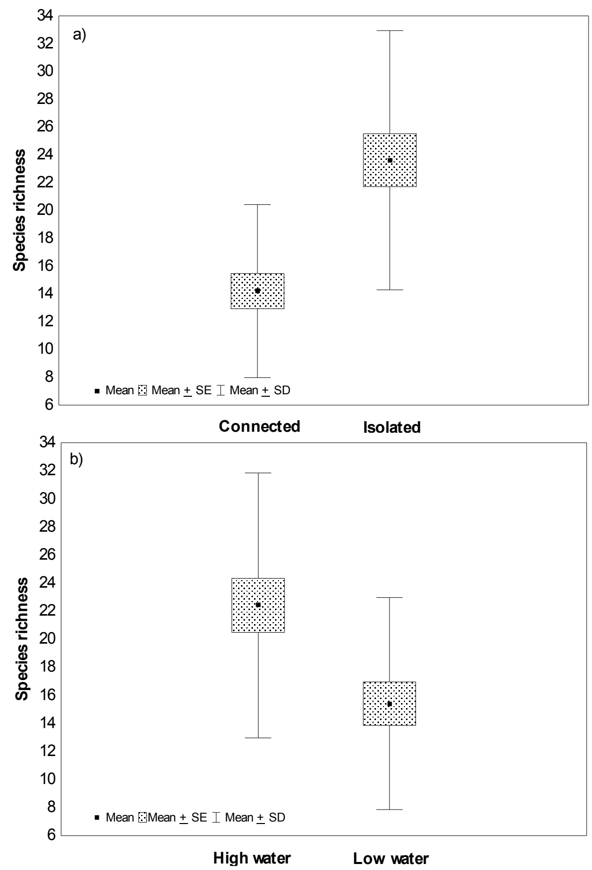

Figure 4. Mean number of registered taxa: a) in the environments (connected and isolated) associated to Baía river; b) during the high and low water periods.

Discussion

The faunistic inventory revealed that the community of flagellate protozoa in the studied environments is quite rich, probably due to the relevant contribution of Euglenida order, which contributed with 67% from the total of identified species. The individuals from this order, specially the genera *Euglena*, *Phacus* and *Trachelomonas*, which were the most species-rich in the present study, are commonly found in aquatic environments with high biochemical demand of oxygen, rich in organic matter and ammonia (REYNOLDS et al., 2002). These preferences might have favored the success of these organisms during the high water period due to the great accumulation of allochthonous organic matter (JUNK et al., 1989; LEWIS JR. et al., 2000; NEIFF, 1990).

The second most important order, especially during the low water period, was Cryptomonadida that contributed with 6% from the total of identified species. The success of these organisms in this period may be associated to the opportunistic traits that provide them competitive advantage to tolerate adverse conditions in the low water period (BOVO-SCOMPARIN; TRAIN, 2008; JONES, 2000). The other orders contributed far less expressive, i.e. all together contributed with 27% from the total of identified species. These orders were only a little more representative during the low water period, probably because many of these organisms (especially the orders Peridiniales, Gymnodiniales and Chromulinales) present adaptations that permit them to tolerate the unfavorable conditions (JONES, 2000; REYNOLDS et al., 2002).

The pattern of species composition recorded in the present study is quite different from those found by other authors in several temperate rivers and lakes (AUER; ARNDT, 2001; COMTE et al., 2006; DOMAIZON et al., 2003; KISS et al., 2009; LAVRENTYEV et al., 2004; TIKHONENKOV, 2007; TIKHONENKOV; MAZEI, 2006, 2008; WEITERE; ARNDT, 2003). The predominance of Chrysomonadida is frequently observed in these environments and in general *Spumella* spp. is the most common species. Similar result to the registered in the present study was verified by Araújo and Costa (2007) that observed a great contribution of Euglenida order for the species richness in reservoirs from Brazilian semiarid region due to the enrichment of the environments by organic matter.

The species composition may be a useful tool to understand the functional processes from an ecosystem since it reflects the environmental characteristics, as observed in the present study. Nevertheless, the first hypothesis of this study cannot be totally accepted, since despite the influence of the flood regime and hydrological connectivity, the species composition from the environments associated and isolated from the Baía river was not similar during the high water period, as previously predicted. This probably occurred because the local factors (such as morphometry, wind action, rainfall etc) were more important than the regional ones.

On the other hand, the patterns of species richness corresponded to the expected, with higher values in the environments connected to the Baía river during the high water period, thus, corroborating our second hypothesis. The greater values of species richness during the high water period may be related to the increase in the connectivity that promotes the exchange of water, sediment, nutrients and organisms between the different habitats (BONECKER et al., 2005; NEIFF et al., 2001; WARD; STANFORD, 1995). Also, to the contribution of periphytic community, since in shallow environments, as wetlands, the increase in the water flow may cause the detachment of periphytic organisms, and then preventing the establishment of limits among the populations from the different compartments of the aquatic ecosystem.

Otherwise, the lower values of richness in the low water period are associated to the absence of lotic activity and to the action of local factors that may limit the flagellate development during this period, such as reduced depth, high turbidity, resuspension of sediment, which cause changes in the biotic interactions (CARVALHO et al., 2001; LEWIS JR. et al., 2000).

In summary, the flood regime and the hydrological connectivity influenced the patterns of composition and species richness of flagellate protozoa as already observed in other planktonic communities from the upper Paraná river floodplain (ALVES et al., 2005; AOYAGUI; BONECKER, 2004; BINI et al., 2003; DOMITROVIC, 2002). However the non corroboration of the homogenizing effect of the floods on the species composition during the high water period may be associated to the temporal scale of the sampling, which was quite limited, since this theory is widely proved with other communities. Therefore it is necessary to accomplish further studies with a longer temporal scale for a better understanding of the processes that regulate the structure and dynamic of this community. In the same way, it is necessary to perform holistic researches evaluating integrally the composition, species richness, abundance and biomass of this community in these systems.

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