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RESEARCH ARTICLE

Low cross-taxon congruence among aquatic organisms in artificial tropical ponds: implications for biomonitoring

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Abstract – The use of biodiversity surrogates is often suggested to increase the cost-effectiveness of biomonitoring programs, as this demands less time and taxonomic expertise. In addition, the detection of multi-taxon associations is a first step toward a better understanding of how organisms interact with each other. Such a multi-taxon association is termed a congruence, and can be detected through measuring the similarity in the distributional patterns shown by different biological groups. To assess the ability of different taxa to serve as surrogates for others, we carried out a Procrustes analysis on the beta diversity patterns of seven biological groups (aquatic birds, Amphibians, Macrophytes, Coleoptera, Odonata, Heteroptera and phytoplankton) in 35 ponds of the Cerrado biome. We found that: (i) the values of congruence in the studied ponds were weak; (ii) among all the biological groups compared, the highest congruence was found between amphibians and macrophytes; (iii) amphibians were congruent with the Coleoptera, Heteroptera, and macrophytes; (iv) the different taxa studied had different responses to environmental conditions; and (v) although they showed relatively weak congruence with the other taxa in each pond environment, amphibian communities were the most strongly influenced by environment variables. Almost all the communities observed in these systems showed unique pattern and thus should be studied and monitored in their entirety.

Keywords: waterbodies / biomonitoring / aquatic communities / biodiversity surrogates / freshwater biodiversity

1 Introduction

Several studies have highlighted the impacts of anthropogenic and environmental changes on aquatic ecosystems, and the consequent declines in these biodiversity hotspots (Strayer and Dudgeon, 2010). Among freshwater ecosystems, temperate ponds have been reported to have a higher capacity to support rare and threatened species compared to that of other freshwater systems (Oertli *et al.*, 2005; Williams *et al.*, 2004; Ruggiero *et al.*, 2008; Gioria *et al.*, 2010). In addition, natural or artificial ponds are common in rural and urban landscapes (Downing *et al.*, 2006; Oertli, 2018). The International Union for Conservation of Nature (IUCN) has indicated the importance of farmland ponds to maintaining freshwater biodiversity, since many of these ponds contain species on the IUCN Red List. Therefore, ponds are important in maintaining biodiversity not only on a regional scale, but also at the global level (Gioria *et al.*, 2010). However, these environments have been undervalued for a long time (Boix *et al.*, 2012), especially in tropical areas, where the biodiversity in artificial ponds has been overlooked so far.

Since the resources available for biodiversity assessment are limited, studies have proposed strategies to simplify monitoring programs while maintaining their ability to capture biodiversity patterns (Kallimanis *et al.*, 2012). These strategies aims at reducing human (*i.e.* taxonomists) and financial resources, as sampling represents a considerable portion of the costs of bioassessments (Birk *et al.*, 2012). One strategy consists in the use of coarser taxonomic resolution to represent the biodiversity patterns at finer taxonomic resolutions, such as the species level (Carneiro *et al.*, 2010; Souza *et al.*, 2019). Another strategy is to assess the cross-taxon congruence between assemblages or communities, which assesses the

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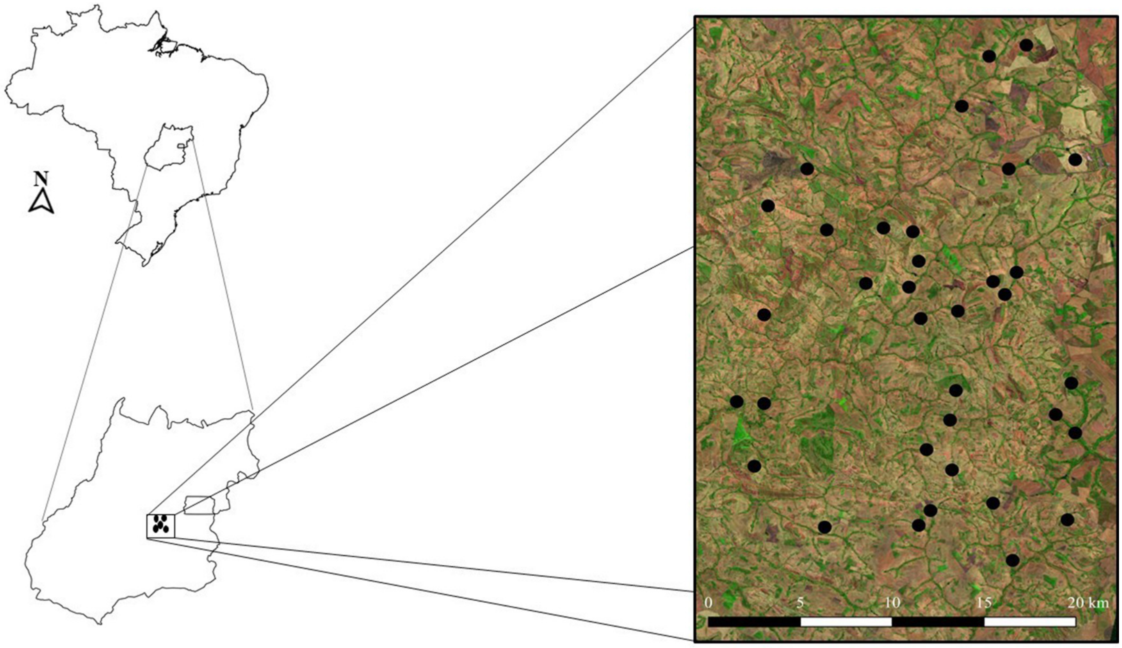

Fig. 1. The study area, including the 35 artificial ponds sampled in Goiás State, Brazil.

ability of a subset of the community or even the whole community to be used as a representation of another subset or community (Lopes *et al.*, 2011).

While environmental predictors of terrestrial biodiversity are well known, those of freshwater biodiversity remain poorly understood (Tisseuil *et al.*, 2012). Several taxa have been used to indicate the ecological status of aquatic ecosystems, such as phytoplankton, benthic invertebrates, macroscopic plants, and fishes (Birk *et al.*, 2012). Logically, the fewer taxonomic groups are considered in a monitoring program, the lower the costs (Padial *et al.*, 2012a). However, we do not know which of the available taxa best represent the biodiversity of a particular environment, or even if one single taxon can be used as an indicator of all others, without actually assessing cross-taxon congruence. Previous studies done in temperate biomes from Europe and the United States of America (USA) suggested that a wide range of taxonomic groups needs to be taken into account in pond biodiversity assessments, rather than just using a few surrogates (Ilg and Oertli, 2016; Kirkman *et al.*, 2012), although similar cross-taxon congruence values were found for marine and terrestrial environments (De Morais *et al.*, 2018). Nevertheless, this hypothesis has not yet been tested for tropical biomes, where the regional species pools are often much larger than those in temperate regions.

There is no standard approach to identifying and using biodiversity surrogates, nor a single congruence limit that is widely considered acceptable (De Morais *et al.*, 2018, but see Lovell *et al.*, 2007; Heino, 2010). Scientists typically identify one taxon with strong ecological links to other taxa, which can be used as a surrogate for the whole system. However, the definition and use of an effective surrogate require thorough communication with land managers and policy makers (Sato *et al.*, 2019).

Two explanations have been previously proposed for the congruence among different taxa: (i) different taxa may have the same responses to environmental gradients (Padial *et al.*, 2012a); or (ii) congruence may occurs because of ecological interactions among different groups, such as the relationships between predators and preys (Larsen *et al.*, 2012). The responses of taxa to environmental gradients include those that took place in the past, associated with historical events and dispersion, or taking place in the present, in response to environmental heterogeneity. In this way, we hypothesized that the communities that depend directly on both water and land are likely more congruent with each other (*e.g.*, amphibians, Odonata (in part), and macrophytes) than those that live in only one of these habitats (*e.g.,* phytoplankton, aquatic insects, and birds). We also expect higher congruence between taxa that live in the same habitat, in this case those that live solely in freshwater (Rodrigues and Brooks, 2007; De Morais *et al.*, 2018). Therefore, we tested whether the distributional patterns of several different aquatic biological groups (phytoplankton, macrophytes, aquatic insects in the orders Odonata, Heteroptera, and Coleoptera, amphibians, and birds) were congruent in 35 artificial tropical ponds.

2 Materials and methods

2.1 Study area

The study area was located 25 km outside the limits of the city of Goiania (the capital of Goiás State, Brazil) to ensure that only landscapes dominated by agriculture were sampled, avoiding urban areas (Fig. 1). Goiania is located at a central position within the Brazilian Cerrado. All water bodies in the core area were identified visually from satellite images in Google Earth. The shapes generated during this process was used to calculate pond size. A total of 2787 ponds were found in the core area, reflecting a dense pond network within a relatively small geographical extent. The ponds were selected for sampling based on their size and isolation (De Marco *et al.*, 2013). For the purpose of this study, we selected 35 ponds (Fig. 1), from which we collected samples of several aquatic communities at the same time.

We sampled all ponds during the dry season, between June and September of 2012. Sampling protocols used for macrophytes, Odonata, water bugs (Heteroptera), and water beetles (Coleoptera) were adapted from the PLOCH standardized method of pond sampling (Oertli *et al.*, 2005a). Thus, sub-samples within each pond were located in different microhabitats, with the number of sub-samples adjusted according to pond size. Thus, the number of sub-samples in each pond is: ***, where n is the number of sub-samples required for a pond with area S. These habitat categories were only identified to ensure that all the important habitats present in each pond were conveniently sampled. More details of the sampling protocols used were described by De Marco *et al.* (2013).

2.2 Phytoplankton

In each pond, a sub-surface water sample was collected with a 100 mL amber bottle and fixed with acetic Lugol solution (Vollenweider, 1974; Bicudo and Menezes, 2006). A net sample was used for species identification, and the bottle sample was used to estimate species density according to Utermöhl (1958). The phytoplankton were identified to species if possible, or, if not, then to the finest taxonomic level.

2.3 Macrophytes

In each pond, macrophytes were examined and all species present were recorded. The number of areas of the pond banks sampled also followed the general rule in relation to pond size noted above. Quantitative samples were taken using 0.50 m × 0.50 m quadrats in transects 2 m inside the pond and parallel to the pond margin, while recording the coverage of each species present using the Dromin-Kajima scale (0 = absent; 1 = 0–20% cover; 2 = 21–40% cover; 3 = 41–60% cover; 4 = 61–80% cover; and 5 = 81–100% cover).

2.4 Heteroptera and Coleoptera

Water bugs and beetles were sampled using a small 14 cm × 10 cm rectangular net with a 0.5-cm mesh, as in Oertli *et al.* (2002, 2005). Each sample was taken within the 2 m littoral margin of the pond for 30 s in each previously selected habitat. The samples were preserved in ethanol and separated in the lab for further identification. Subsequently, the classification of adult water bugs to the family and genus levels was performed according to Nieser and Melo (1997). Adult water beetles were identified to the family and genus levels following Benetti *et al.* (2018) and Segura *et al.* (2011).

2.5 Odonata

Odonate adults were sampled only between 10:00 and 15:00 h, when air temperatures were always higher than 19 °C (De Marco and Resende, 2002). We used a modified scanning method with fixed areas (De Marco, 1998; Silva *et al.*, 2010), using 5 m segments distributed within the previously selected microhabitats. All adults were visually counted by an experienced collector, and all dubious individuals (especially belonging to small species) were captured. Subsequent species identification was then performed by comparison with materials in the odonate collection of Federal University of Goiás and the relevant literature (Lencioni, 2005, 2006).

2.6 Amphibians

Adult amphibians were sampled during the rainy season, from October 2012 to February 2013, always between 20:00 and 00:00 h at night. Over a period of 50 min, we walked around the pond and registered all individual amphibians the we saw or heard, following the standard methods of visual encounter surveys (Crump and Scott, 1994) and audio strip transects (Zimmerman, 1994), respectively. Individuals heard in nearby ponds were not included. Amphibian species identification followed Frost (2013).

2.7 Birds

As the bird species in the studied ponds are well known, a direct estimation of the absolute species richness of birds in each pond was possible. All individuals at the shore or among floating or swamp vegetation were recorded visually (using 10 × 50 binoculars) and by song recognition during a complete walk around the pond at a constant velocity.

2.8 Environmental characteristics

All physical and chemical water parameters were measured *in situ*. Our environmental data comprised information on the water temperature, water transparency, pH, electrical conductivity, levels of chlorophyll-*a*, dissolved oxygen, ammonium, and chloride. For the measurement of pH, water temperature, and chlorophyll-*a*, dissolved oxygen, chloride, and ammonium content, we used a 6820v2-1-C-S Multi-Parameter Water Quality Logger during the dry season (June–September 2012). The water sample used for these analyses was taken from the center of each pond at a depth of 30 cm. Readings from the Multi-Parameter Water Quality Logger were only recorded after the parameters' values stabilized (De Marco *et al.*, 2013).

2.9 Data analysis

For each group (phytoplankton, Coleoptera, Heteroptera, Odonata, amphibians, macrophytes, and birds), we used species abundance data in our analyses. Prior to analyses, the species abundance data were log-transformed ($\log X + 1$) to reduce the influence of outliers. Procrustes analysis was then applied, which is a method commonly used to identify the association between two biological distance matrices (Jackson, 1995). Procrustes analysis is more powerful and has lower type I error rates than other tests (*e.g.*, Mantel) used to detect matrix association (Peres-Neto and Jackson, 2001). Prior to the Procrustes analysis, we performed a two-dimensional non-metric multidimensional scaling (nMDS) to ordinate the communities in the ponds (Legendre and Legendre, 1998) based on their pairwise Bray-Curtis dissimilarities. In Procrustes analysis, a pair of data matrices (in this study, the scores generated from two of the nMDS ordinations, for example, those generated for phytoplankton and Odonata) is compared using a rotational-fit algorithm that minimizes the residual sum of squares between the two matrices, resulting in a goodness-of-fit statistic called the m^2-value. The m^2 statistic reflects the lack of overlap between two ordinations, and varies from 0 to 1. We used a transformation of the m^2 statistic value ($r = \sqrt{1 - m^2}$), so herein values closer to 1 indicated total overlap between the two compared matrices (*i.e.* the results of the two ordinations were the same) and values closer to 0 indicated great differences between the ordination patterns. The significance of the Procrustes statistics was evaluated after 1,000 random permutations. Cross-taxon species richness correlations were then investigated with Spearman rank correlation tests.

We used partial redundancy analysis (pRDA) to evaluate the effects of spatial and environmental patterns on the biological groups studied. All the species matrices were Hellinger-transformed prior to analysis (Legendre and Gallagher, 2001). Peres-Neto *et al.* (2006) have shown that this transformation provides more accurate estimates in variation partitioning techniques. In the pRDA, we used the environmental variables listed above, and the spatial pattern was represented by spatial filters extracted using principal coordinates of neighbor matrices (PCNM) from a geographic matrix (Borcard and Legendre, 2002). The following sets of predictors were generated to explain patterns in each biological group: [a] variation explained by local variables (environmental variables) only; [b] variation explained by the environmental variables and spatial distance combined; [c] variation explained by spatial distance only; and residual variation (the variation not explained by either of the tested predictors). We also used a forward selection procedure to retain the most important environmental and spatial variables for the pRDA. All analyses were performed in the R program (R Development Core Team, 2011). The Procrustes, redundancy, and variation partitioning analyses were all ran using the functions protest, rda, varpart, and forward.sel, respectively, available in the vegan, permute and packfor package in R (Oksanen *et al.*, 2013). In the forwarded selection function, the model starts with no predictors, the most contributive predictors are add iteratively, and stops when the improvement is no longer statistically significant (Oksanen *et al.*, 2013).

3 Results

In the 35 artificial ponds sampled in this study, a total of 479 species were recorded, comprising 199 species of phytoplankton, 34 species of Coleoptera, 23 species of Heteroptera, 50 species of Odonata, 38 species of macrophytes, 28 species of amphibians, and 107 species of birds. Species richness and density differed significantly among the different biological groups (Kruskal–Wallis test, $P < 0.005$; Fig. 2).

Pairwise cross-taxon correlations showed different levels of overall congruence among the 7 biological groups in all of the studied ponds (Tab. 1). Phytoplankton showed negative cross-taxon congruence in species richness with all other biological groups, except for Heteroptera, but congruence was only significant with Coleoptera. In terms of species richness, the highest congruence values were found between Coleoptera and macrophytes (0.57). Macrophyte species richness was significantly congruent with that of Coleoptera, Odonata, and birds. Birds species richness also was significantly congruent with Odonata (Tab. 1).

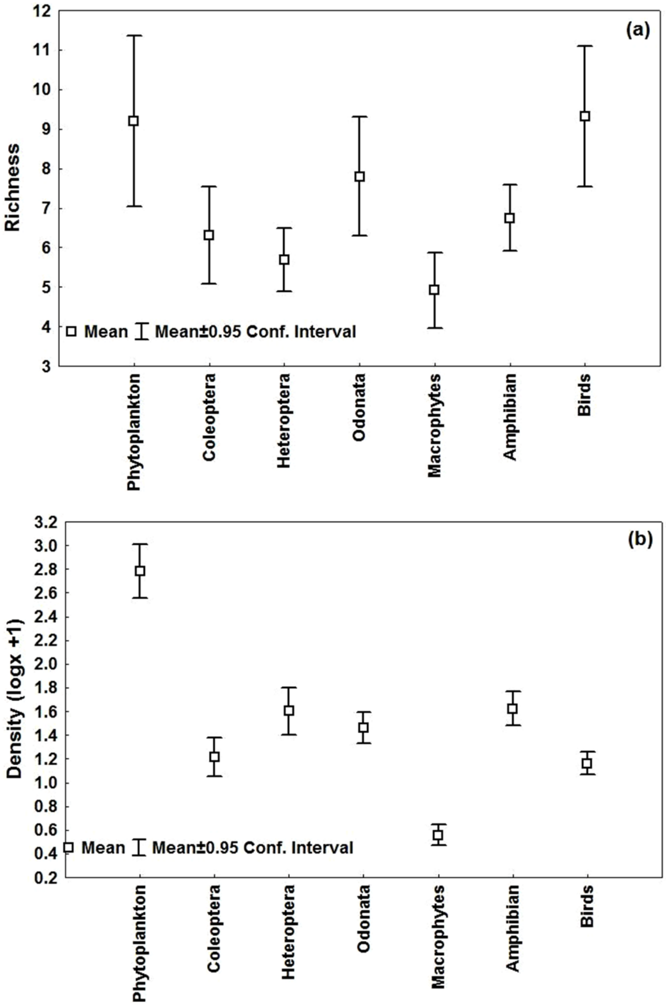

Fig. 2. The (a) species richness and (b) abundance of the 7 biological groups found in each of the 35 tropical ponds sampled. Values are means and confidence intervals, and differed among biological groups (Kruskal–Wallis test, $P < 0.005$).

When the cross-taxon similarity of species composition was tested, the groups with the highest congruence with each other were different from those found for species richness (Tab. 2). All biological groups in the artificial ponds showed low levels of congruence in this metric, as even the significant correlation values were weak (*i.e.* $r < 0.5$). An amphibian was the best surrogate group in terms of abundance, since it was congruent with macrophytes, as well as with Coleoptera and Heteroptera. The Coleoptera and Odonata groups were also congruent with one another (Tab. 2). Overall, birds showed the lowest congruence with the other biological groups, especially with phytoplankton and Coleoptera.

Table 1. Correlations (Spearman rank coefficients) among the species richness values of 7 biological groups surveyed in 35 tropical ponds. Significant values: $^*P < 0.05$, $^{**}P < 0.001$.

	Phytoplankton	Coleoptera	Heteroptera	Odonata	Macrophytes	Amphibian	Mean
Phytoplankton	1.00						–0.13
Coleoptera	–0.35*	1.00					0.15
Heteroptera	0.04	0.12	1.00				0.10
Odonata	–0.01	0.25	0.23	1.00			0.24
Macrophytes	–0.19	0.57^{**}	0.19	0.42^{*}	1.00		0.22
Amphibian	–0.04	0.02	0.02	0.19	–0.08	1.00	0.01
Birds	–0.22	0.28	–0.03	0.35^{*}	0.38^{*}	–0.05	0.13

Table 2. Strength of the congruence between each pair of biological groups based on species composition and determined by Procrustes analysis. Significant values: $^*P < 0.05$.

	Phytoplankton	Coleoptera	Heteroptera	Odonata	Macrophytes	Amphibian	Mean
Phytoplankton	1.00						0.19
Coleoptera	0.25	1.00					0.24
Heteroptera	0.30	0.23	1.00				0.24
Odonata	0.10	0.34^{*}	0.14	1.00			0.20
Macrophytes	0.16	0.19	0.14	0.18	1.00		0.22
Amphibian	0.24	0.34^{*}	0.37^{*}	0.22	0.42^{*}	1.00	0.30
Bird	0.06	0.06	0.28	0.23	0.22	0.22	0.18

Table 3. Environmental variables and spatial filters (PCNM) tested in the variance partition analysis. Environmental variables, including chlorophyll-*a* (Chl-*a*), dissolved oxygen (DO), pH, ammonium (NH_4^+), chloride (Cl) content, and pond size (Size), are listed in the order of importance in which they were retained in the forward selection procedure as follows: [a] environmental fraction, [b] shared fraction, and [c] spatial fraction. The bold values are the r adjusted ($p < 0.05$).

Group	Environment	PCNM	[a]	[b]	[c]
Phytoplankton	–	–	–	–	–
Coleoptera	Size	–	**0.15**	–	–
Heteroptera	Chloride, DO	–	**0.15**	–	–
Odonata	–	–	–	–	–
Macrophytes	–	–	–	–	–
Amphibian	Size, Chloride, DO, Temp., NH_4^+	–	**0.14**	–	–
Bird	pH, DO, Chloride	–	**0.03**	–	–

Pond size, temperature, and chloride, dissolved oxygen, and ammonium content were the most important environmental variables retained in the forward selection analysis (Tab. 3). Coleoptera ($r_{adj} = 0.15$), Heteroptera ($r_{adj} = 0.15$), and amphibians ($r_{adj} = 0.14$) were the groups whose distributions were best explained by the environmental gradients among ponds (Tab. 3). Pond size also had a significant relationship with the distribution of Coleoptera and amphibians. Between Heteroptera and amphibians, the common variables explaining their distributions were chloride and dissolved oxygen content. However, between Coleoptera and Odonata, and between amphibians and macrophytes, no explanatory environmental or spatial variables were shared. Spatial gradients were not significantly able to predict the distribution of any of the examined groups (Tab. 3).

4 Discussion

Our results suggest caution to use a surrogate as a proxy for overall species richness and community composition in artificial tropical ponds. The level of concordance between different ponds was highly dependent on which metric was used; this was true for both different and equal taxonomic group. In a review of 297 different water-surface evaluation methods, species composition was better than richness as a proxy for conditions (Birk *et al.*, 2012). A previous meta-analysis highlighted several sources of bias when measuring congruence between taxa, including spatial scale, latitude, and sample size (Westgate *et al.*, 2014). As we hypothesized, communities that directly depend on both water and land were more congruent with each other (*e.g.*, amphibians and macrophytes) than those which live only in one of these environments (*e.g.*, phytoplankton, aquatic insects, and birds). Our results did not corroborated wit studies which found increased congruence between taxa living in the same single environment (*i.e.* water or land), then between those living in different single environments (*i.e.* water and land) (Rodrigues and Brooks, 2007; De Morais *et al.*, 2018).

Amphibians showed relatively good congruence between measures of their species composition and that of other taxa, although macrophytes were the most representative of species richness. Indeed, aquatic macrophytes are known to enhance the habitat heterogeneity of aquatic ecosystems, influencing the richness of other taxonomic groups within aquatic communities (Dibble *et al.*, 1996; Pelicice *et al.*, 2005; Thomaz and Cunha, 2010). For instance, habitats with increased aquatic plant richness and diversity provide a greater range of foraging and breeding sites for water bird species (Hassen-Aboushiba, 2017). In general, the beta-diversity patterns depicted in each of the groups analyzed herein cannot serve as biodiversity surrogates by themselves.

Cross-taxon congruence in species composition and richness was weak ($r < 0.57$) and highly variable (0–0.57), a similar result to that of de Morais *et al.* (2018). A previous study considered optimal values of congruence to be those above 0.75 because they mean that the surrogate represents more than 75% of the patterns in the target group(s) (Lovell *et al.*, 2007). Heino (2010) suggested that surrogates with congruence values above 0.70 should be considered reliable for use in conservation planning. De Morais *et al.* (2018) highlight the problems inherent in defining a threshold for cross-taxon correlation, past which a taxon is considered a reliable surrogate. However, if a single community is found to predict the patterns in several others, even with low congruence values, it could still be considered to serve as a fair surrogate group (Padial *et al.*, 2012b).

Previous research shows that amphibians exhibit high congruence with other taxa in key diversity measures such as species richness or degree of endemicity, and are therefore good surrogate candidates to be used in global freshwater conservation planning (Tisseuil *et al.*, 2012). Another study also highlighted the greater suitability of the species composition of anurans (frogs) as a surrogate comparing to other animal and plant groups (Landeiro *et al.*, 2012), but in temperate ponds amphibian composition was only weakly congruent with other groups (Ilg and Oertli, 2016). In the studied ponds, species richness patterns in amphibians and Heteroptera, and species composition patterns in plants and birds were not satisfactorily represented by any aquatic taxon. This is unfortunate because a review of the metrics used to evaluate water quality showed that phytoplankton were the main component of aquatic communities typically used to indicate the severity of eutrophication and organic pollution in aquatic ecosystems (Birk *et al.*, 2012).

A study that tested the congruence of species distributional patterns in wetlands between waterbirds and macroinvertebrates, as well as between Hemiptera and Coleoptera, found a weak but significant congruence among all these groups (Guareschi *et al.*, 2015). That study explained the weak congruence found as being due to the different responses of these different groups to environmental gradients (Guareschi *et al.*, 2015). Although plants were suggested as surrogate taxa for conservation-priority ponds (Gioria *et al.*, 2010), the species composition of macrophytes was only congruent with that of amphibians in the ponds examined in the present study. This result likely reflects the use of aquatic macrophytes as breeding sites and shelter by amphibians (Cuello *et al.*, 2017; Schiesari *et al.*, 2003).

Spatial variables were not important for the patterns found in any of the groups studied, and only few groups were influenced by environmental variables. Species having similar responses to the same environmental variables has been reported as one of the main causes of congruence in previous studies (Gioria *et al.*, 2010; Guil and Cabrero-Sañudo, 2006; Landeiro *et al.*, 2012; Padial *et al.*, 2012b). Therefore, groups with distinct responses to environmental conditions, as reported herein, were not congruent with each other (Landeiro *et al.*, 2012; Larsen *et al.*, 2012). Environmental conditions are the common ecological mechanisms underlying cross-taxon congruence patterns. Amphibian composition was influenced by the most the environmental variables examined in this study, and was also the best surrogate group we found. Variables directly associated with water quality, such as the ammonium and dissolved oxygen content, were significantly associated with the patterns in amphibians and their congruent groups, which may be explained by the permeability (and therefore sensitivity) of amphibian skin, and the complex life cycle of amphibians, which requires suitable conditions across both aquatic and terrestrial environments (Boyer and Grue, 1995; Calderon *et al.*, 2019). We also found high congruence between the species richness of water birds and Odonata, and water birds and macrophytes. Water birds are at the top of the aquatic food web, and can provide information about lower trophic levels (Sulai *et al.*, 2015). Water quality variables such as pH, dissolved oxygen, and chloride influence the aquatic food web, and are therefore expected to have indirect effects on water birds (Yardi *et al.*, 2019). Pond size was also an explanatory variable shared between congruent groups, such as Coleoptera and Odonata. In French ponds, Odonata species richness was previous shown to be correlated to pond size (Ruggiero *et al.*, 2008).

Some groups, such as amphibians and macrophytes, as well as Coleoptera and Odonata, were significantly congruent, but they were not influenced by any shared environmental variables. The occurrence of a weak but significant congruence without a shared environmental or spatial gradient between taxa can indicate the effects of ecological interactions (Curry *et al.*, 2012; Larsen *et al.*, 2012; Padial *et al.*, 2012b). Coleoptera have a broad trophic spectrum, with different species having preferences for phytophagous, saprophagous, and predatory life habits. Coleoptera and Odonata also have predator-prey relationships with each other (Pakulnicka *et al.*, 2015), and these were the only taxa that showed a consistent pattern of congruence in terms of their richness and composition in the tropical ponds sampled. A possible explanation to this consistent congruence independent on the metric (richness and composition) between Coleoptera and Odonata is the similar level of taxonomic classification in these groups. Aquatic insects are often identified in a lower resolution than other groups here studied. However, previous studies also combine groups with different taxonomic resolution and found similar results (Negi and Gadgil, 2002; Ruhí *et al.*, 2014; Ilg and Oertli, 2016).

5 Conclusion

Our study showed a weak and highly variable congruence between biological groups in tropical artificial ponds. Although the congruency found for them was weak, amphibians were able to partially represent patterns in the abundance of Coleoptera, Heteroptera, and macrophytes. In terms of richness, macrophytes were able to partially represent patterns in Odonata, Coleoptera and birds. In this way, at least for abundance, our results partially supported the hypothesis that the biotic communities that depend directly on both water and land (*e.g.,* amphibians and macrophytes) are more congruent with each other than those living only in one of these environments. Ultimately, we do not recommend the use of a single surrogate taxon to measure biodiversity: weak overall congruence between taxa; limited biological knowledge about tropical artificial ponds; and numerous taxa whose diversity patterns could not be represented by any surrogate group (phytoplankton, Heteroptera, and birds) illustrate the unsuitability of this approach.

The weak influence of the environmental gradients examined on the tested groups and the weak congruence among them indicates that a complex diversity of factors controls the biodiversity in the studied ponds. Therefore, the monitoring of several biological groups is necessary to understand patterns in the biodiversity in such artificial tropical ponds. Our study confirmed that environmental conditions strongly influence biodiversity patterns, but suggests that other important mechanisms, which have not been properly evaluated so far, are also involved in the observed cross-taxon congruence. This indicates the need to incorporate additional processes (*e.g.*, biogeographic and evolutionary history or trophic interactions) to better understand cross-taxon congruence and/or the existence of shared detection biases among taxa and regions.

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