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Higher taxa are sufficient to represent biodiversity patterns

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ABSTRACT

The scarcity of knowledge about both biodiversity (Linnean shortfall) and the geographic distributions of species (Wallacean shortfall) makes it hard to conduct biomonitoring programs and studies that seek to explain biodiversity patterns. One way to overcome this difficulty consists in the utilization of data with a lower taxonomic resolution, an approach called taxonomic sufficiency or Higher Taxon Approach (HTA). The main aim of this study was to evaluate, through a systematic review and meta-analysis, whether the HTA is reliable. We also evaluated whether the strength of the HTA (i.e., the relationship between datasets at high and low taxonomic resolutions) depended on different factors such as taxonomic level (genus, family, order and class), ecosystem type (aquatic and terrestrial), biological group (e.g., invertebrates, vertebrates and plants), spatial extent and higher taxa to species richness ratio (φ). We found that the HTA was a reliable approach in revealing species richness and compositional patterns independently of biological groups and ecosystem types. As expected, the strength of the HTA in describing biodiversity patterns decreased as the taxonomic resolution decreased. The strength of the HTA increased with the spatial scale of the studies. The φ was the main predictor of the HTA. Therefore, the use of higher taxonomic level (e.g., genera) is a reliable approach to save time and resources in biomonitoring programs and differs in this regard from other approaches that have already been tested in other studies (e.g., biological surrogacy). While the high HTA efficacy do not replace refined species level information which is crucial for basic and applied ecological studies, we advocate the use of the HTA especially for biological groups with high φ and for biomonitoring programs targeting large spatial extents.

1. Introduction

Natural systems are facing severe threats due to anthropogenic impacts (Early et al., 2016; Halpern et al., 2015; Huang et al., 2017; McGill et al., 2015). In addition to changing the physical and chemical characteristics of ecosystems, these impacts are causing losses of biodiversity and ecosystems services (Bellard et al., 2012; Strassburg et al., 2017; Vörösmarty et al., 2010). In this context, studies seeking to evaluate the effects of anthropogenic activities and the effectiveness of mitigation measures need to be executed as fast as possible. However, most studies are hampered by the paucity of knowledge about the biodiversity in our planet (e.g., the Linnean and Wallacean shortfalls; Brown and Lomolino, 1998; Hortal et al., 2015; Lomolino, 2004). Moreover, there are problems in obtaining data with high taxonomic resolution (e.g., species-level identification) due to the long time needed for processing the samples, lack of investments in biological assessments, and the small number of specialized taxonomists (Lawton et al., 1998; Magurran and Queiroz, 2010). To overcome this problem, it has been suggested that applied studies aiming to identify biodiversity patterns may be performed with data obtained with low taxonomic resolution (Balmford et al., 1996a,b; Gaston, 2000; Gaston and Williams, 1993; Mellin et al., 2011).

The validity of using the Higher Taxon Approach (HTA; i.e., the use of data with low taxonomic resolution as, for example, genus, family, order or class instead of species; also known as taxonomic sufficiency; Ellis, 1985) to describe diversity patterns has been confirmed in several studies (e.g., Alves et al., 2016; Landeiro et al., 2012; Villaseñor et al., 2005). The HTA can be considered effective when diversity patterns observed with high taxonomic resolution data (e.g., species) are well represented by data with low taxonomic resolution (e.g., genera; Bates et al., 2007; Bennett et al., 2014). For example, it has already been shown that genera richness and composition of bacteria, diatoms, and

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macroinvertebrates (and even family richness and composition in the case of macroinvertebrates) are highly correlated with species richness and composition (Vilmi et al., 2016). Therefore, one could conclude that the HTA is effective in representing species richness and composition for these groups. Assuming strong niche conservatism, where higher taxa maintain the ecological characteristics of the constituent species (Rosser, 2017), phylogenetically related species would respond similarly to environmental gradients (Wiens and Graham, 2005). Thus, biodiversity patterns obtained with higher taxa would be similar to those obtained with species data (Rosser, 2017). However, the use of higher taxa has been criticized in the literature (Bertrand et al., 2006; Lenat and Resh, 2001; Rosser and Eggleton, 2012). Some studies, for example, concluded that the HTA is not effective in revealing subtle patterns, especially when the taxonomic resolution is very reduced (e.g., Grimbacher et al., 2008; Lenat and Resh, 2001). Also, previous studies have shown that the greater the reduction of the taxonomic resolution, the lower the effectiveness of the HTA (Kallimanis et al., 2012; Rosser and Eggleton, 2012) and that, depending on the taxonomic level, HTA is more effective for some biological groups than for others (Rosser, 2017; Rosser and Eggleton, 2012; Vilmi et al., 2016). The effectiveness of HTA can also be affected by the ratio between the richness of different taxonomic levels (φ) – e.g., genus richness (G)/ species richness (S) (Andersen, 1995; Bevilacqua et al., 2012; Rosser, 2017; Van Rijn et al., 2015). An increase in this ratio is expected to cause an increase in HTA effectiveness (Andersen, 1995; Gaston and Williams, 1993; Gaston, 2000; Rosser, 2017). For example, if a given dataset has equal numbers of species and genera (i.e., $\varphi = 1$), then genus richness will represent reliably (and inevitably) the species richness.

It is not clear yet to what extent the taxonomic resolution can be reduced without significant loss of biological information (Heino and Soininen, 2007; Villaseñor et al., 2005), and if the HTA is equally effective in different spatial scales (Anderson et al., 2005; La Ferla et al., 2002), biological groups, and types of ecosystems. For example, Rosser and Eggleton (2012) showed that there was a strong correlation between genus and species richness of Coleoptera. However, this correlation was weak for Formicidae. They also found that there was no correlation between family and species richness for both Coleoptera and Formicidae. On the other hand, Timms et al. (2013) showed that there was a strong correlation between higher taxa and species composition of Araneae, Coleoptera, and Lepidoptera. They concluded that higher taxon data would be sufficient to detect impacts of forest disturbances on terrestrial arthropods with higher levels of phylogenetic constraint.

Considering the debates about the effectiveness of the HTA, the objective of this study was to summarize systematically and quantitatively the information about this approach with a meta-analysis. For this, (i) we quantified the decrease in the effectiveness of the HTA due to the reduction of the taxonomic resolution. We also tested whether this effectiveness varied (ii) among biological groups and (iii) types of ecosystems, as well as with (iv) the spatial scale of the study. Finally, (v) we tested the effect of the ratio between the richness of taxonomic levels (φ) on the effectiveness of the HTA.

2. Material and methods

2.1. Search and studies selection

We followed the "Preferred Reporting Items for Systematic Reviews and Meta-Analysis" (PRISMA; Moher et al., 2009) guidelines to conduct this study. We used the Clarivate Analytics Web of Science database (WoS) to search the literature for studies on HTA published between 1985 and 2017 (August 1st, 2017). The following terms and Boolean operators were used in our search: ("taxonomic* resolution" OR "taxonomic sufficiency*" OR "taxonomic* surroga*" OR "surroga* species" OR "high* tax*" OR "coarse tax*") AND ("richness" OR "diversity" OR "community structure" OR "beta diversity" OR "*similarity" OR "assemblage structure" OR "*assessment" OR "*monitoring").

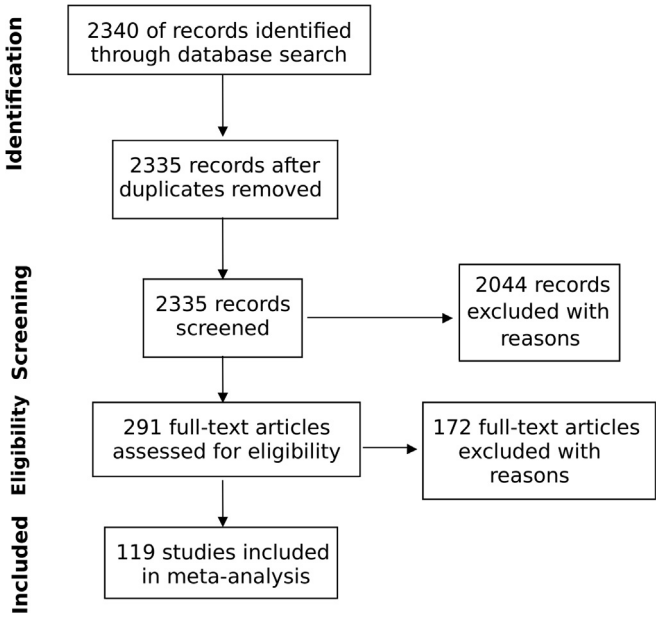

Fig. 1. Flowchart showing the steps involved in this study.

We evaluated the titles and abstracts of 2,340 studies resulting from the aforementioned search string. We excluded the studies that clearly did not evaluate the effectiveness of the HTA (Fig. 1). After, we included in our meta-analysis studies that (1) evaluated the applicability of the HTA, (2) tested a correlation between patterns of richness (or composition) of higher and lower taxonomic levels, and (3) contained standard measures of effect size. Studies that did not follow these criteria were not used in our meta-analysis (see Appendix A for a list of included and excluded articles).

In order to evaluate the consistency of the articles selected in the screening of titles and abstracts, two authors (Jean Ortega and Luiz G. dos Santos Ribas) also performed a selection independently of the first author and of each other. This was done using a random sample of 10% of the studies returned by the WoS search. The concordance between the authors' choices was assessed using the Kappa statistic (Côté et al., 2013). The value of the Kappa statistics was 0.93 and 0.69, respectively, for each author. Considering the values of Kappa greater than 0.6 as substantial (as indicated by Côté et al., 2013), we found a high concordance between the different authors about which papers should be included in the meta-analysis.

2.2. Data extraction

We recorded the sample sizes and correlation coefficients of each study selected for the meta-analysis. Generally, studies evaluating the effectiveness of the HTA use different statistical approaches. For example, different types of correlation coefficients were used to estimate the relationship between the richness of higher and lower taxonomic levels (usually Pearson, Spearman, or Kendall; e.g., Mazón, 2016). On the other hand, studies investigating patterns of community composition generally compare scores derived from ordination analyses or biological distance matrices generated from data with different taxonomic resolutions (e.g., correlation between distance matrices calculated with species and family abundance data; Rosser, 2017; Heino and Soininen, 2007). The data are then compared using the Procrustes correlation (r_p) or the Mantel correlation (r_m).

In addition to the correlation coefficients and sample sizes, we also recorded a set of predictor variables (or moderators in the meta-analysis

jargon) that could explain the variation in the effectiveness of the HTA. We recorded the coarse taxonomic levels (class, order, family, or genus) in each study to explore the extent to which the taxonomic resolution could be reduced without loss of substantial information (as indicate by a high correlation between datasets with different taxonomic resolutions). We categorized the taxa used in the studies into the following groups: microorganisms (e.g., bacteria, ciliate, microcrustaceans and microalgae; Jiang et al., 2016; Ribas and Padial, 2015; Vilmi et al., 2016), macroscopic plants (e.g., bryophytes, vascular plants and macroalgae; Alves et al., 2016; Díez et al., 2010; Jantz et al., 2014; Ribas and Padial, 2015), invertebrates (e.g., aquatic macroinvertebrates, arthropods and insects; Pérez-Fuertes et al., 2016; Rosser, 2017; Vilmi et al., 2016) and vertebrates (e.g., fish, amphibians, reptiles, mammals and birds; Kallimanis et al., 2012; Mazaris et al., 2008; Ribas and Padial, 2015). We also categorized two studies as fungi (Balmford et al., 2000; Sebek et al., 2012), one as macrolichen (Negi and Gadgil, 2002) and two as benthos (Dethier and Schoch, 2006; Gesteira et al., 2003). Also, we recorded whether the study was conducted in aquatic or terrestrial ecosystems. When available, we obtained the spatial scale (extent) of each study. In cases where the spatial extents were not provided in the text, we used the maps of the primary research studies to measure the distance (km) between the farthest apart sites. Finally, the value of φ was obtained using the higher taxa to species ratio (e.g., Bevilacqua et al., 2012). The maximum value of φ is 1.0 (when each species, for example, belongs to a different genus). It is noteworthy that species was the lowest taxonomic level in most studies and, in few cases, some taxa were identified to genus or family only (e.g., Vilmi et al., 2016).

2.3. Data analysis

Initially, we transformed the different correlation coefficients to the Pearson product-moment correlation coefficient (r). The Kendall correlation coefficient (τ) was transformed with the following equation (Lajeunesse, 2013):

$$r = \sin\left(\frac{\pi \times \tau}{2}\right)$$

The Spearman correlation coefficient (ρ) was transformed by the following equation (Lajeunesse, 2013):

$$r = 2 \times \sin\left(\frac{\pi \times \rho}{6}\right), \text{ if } n < 90 \text{ or } r = \rho, \text{ if } n \geqslant 90$$

where n represents the sample size. Next, all the r values were transformed to Fisher's z scores using the following equation (Borenstein et al., 2009):

$$z = 0.5 \times \left(\frac{1 + r}{1 - r}\right)$$

We estimated a cumulative effect size (weighted mean effect size), using a random effects model, and the T^2 statistic as a measure of heterogeneity (variance between studies) for the studies that used simple correlation coefficients (Borenstein et al., 2009). We weighted the effect sizes by the inverse of their variances ($+T^2$) for the simple correlation studies. For Mantel or Procrustes correlation, we weighted the effect sizes by the sample sizes of the studies.

We divided our data into two datasets before modeling the variation in effect sizes. The first dataset was used to separately test the effect of the different moderators. Thus, we maximized our sample size (number of primary studies, k) by using this dataset, while not testing the effects of all moderators simultaneously. This was done to avoid losing information through the test of a single model (i.e., including all moderators with missing data). The second dataset was used to simultaneously model the effects of all moderators. However, to test this model, we were not able to use data from all primary studies due to missing values.

2.3.1. Dataset 1

We used subgroup analysis (Borenstein et al., 2009) to test whether the effect sizes varied significantly as a function of the different taxonomic levels. Thus, it was possible to test whether the reduction of the taxonomic resolution decreases the effectiveness of the HTA. The effects of the types of ecosystems and biological groups were also explored by subgroup analyses. Because of the small number of studies, we did not include the groups benthos, fungi (both with two studies only), and macrolichens (one study). Due to the same reason, we excluded two studies focusing on benthos and that used the Mantel correlation and one study focusing on vertebrates that used the Procrustes correlation. We presented the results of the subgroup analyses in the form of forest plots, where the weighted mean effect size (± 95% confidence intervals (95% CI)) for each level of a moderator are depicted vertically, as well as the weighted mean effect size across all studies (in the form a filled diamond, at the bottom of the forest plot). At the right side of each forest plot, we used different lowercase letters to indicate statistically significant differences between the levels of a given moderator. The effects of the quantitative moderators (spatial extent and φ) were evaluated by a meta-regression (Borenstein et al., 2009). The spatial extent was log-transformed to improve linearity.

2.3.2. Dataset 2

We conducted a meta-regression to explore the simultaneous effects of all moderators (taxonomic levels, biological group, type of ecosystem, spatial extent and φ) on Fisher's z. For this, we used a reduced dataset containing information for all moderators ($k = 34$). We estimated a Pseudo-R^2 for this meta-regression model following Borenstein et al. (2009). Due to the small number of studies, we did not test this model using the Mantel and the Procrustes statistics.

2.3.3. Methods to address multiple outcomes per study, publication bias and temporal variation in effect sizes

A single study can report more than one effect size by, for example, testing the effectiveness of HTA for ants and beetles sampled in the same sampling units (e.g., Rosser and Eggleton, 2012). Thus, this study would contribute with two effect sizes in a meta-analysis. Another common situation, resulting in more than one effect size per study, occurs when a study evaluated the HTA effectiveness for different taxonomic resolutions (e.g., testing the correlation between species and genus richness and between species and family richness; Rosser, 2017; Jiang et al., 2017). In these cases, the effect sizes are not independent (Hedges et al., 2010). Thus, to control for the lack of independence among effect sizes, all analyses described above were conducted using multilevel random-effects meta-analyses (Nakagawa and Santos, 2012).

The impact of publication bias for the studies that used simple correlations was evaluated by the calculation of the Orwin's (1983) *fail-safe number* (*fsn*). We defined a target effect size of 0.65 because there is a consensus in the literature that only correlations greater than 0.7 could indicate the validity of strategies aimed at simplifying and reducing the costs of monitoring programs (e.g., de Morais et al., 2018; Heino, 2010). Thus, if the *fsn* analysis indicates that many studies (not included in the meta-analysis, for example, due to publication bias) are needed to make the observed effect size equal to 0.65, then the results of the meta-analysis can be considered robust. Before the *fsn* analysis, we averaged the effect sizes and variances per study to not use dependent data. We did not evaluate publication bias for the studies that used Mantel and Procrustes tests because it was not possible to estimate the variance of these statistics.

Finally, we conducted a cumulative meta-analysis (Leimu and Koricheva, 2004) to assess the temporal variation in the weighted mean effect sizes. A cumulative meta-analysis begins with a weighted effect size estimated with the oldest study only. Next, a weighted mean effect size is estimated with the two oldest studies, and so on until the weighted mean effect size is estimated with all available studies ($k = 68$ in our case for Fisher's z; $k = 71$ for Mantel r; $k = 12$ for

Procrustes' r).

All analyses were carried out using the "metafor" package (Viechtbauer, 2010) in the R program environment (R Development Core Team, 2017). We considered a significance level of 5% for all analyses.

3. Results

We found 2340 studies in the WoS database. After reading their titles and abstracts, we selected 296 studies. From these, we selected 119 independent studies for the meta-analysis (Fig. 1). Among the primary studies included in this meta-analysis, 68, 71 and 12 were based on simple, Mantel, and Procrustes correlations, respectively. The total number of outcomes exceeds the total number of studies because some studies conducted more than one type of analysis. The maximum values of φ for each study ranged from 0.10 to 1.0 (median = 0.57) and 75% of the studies exhibited a φ up to 0.78 (Fig. S1a). The spatial extent ranged from 1.5 to 7,440 km (median = 97.17 km) and 75% of the studies have a spatial extent up to 810.46 km (Fig. S1b).

3.1. Dataset 1

Fisher's z ranged from 0.01 ($r \approx 0.01$) to 4.95 ($r \approx 1.0$), and the weighted mean effect size was equal to 1.57 (95% CI ± 0.13, $k = 68$, $t = 24.65$, $P < 0.001$; which is equivalent to an r of approximately 0.92, Fig. 2). The heterogeneity between the studies (T^2) was equal to 0.3 and statistically significant ($Q = 14564.60$, $k = 68$, $d.f. = 296$, $P < 0.001$). The effectiveness of the HTA decreased consistently with the reduction of the taxonomic resolution ($Q = 177.90$, $k = 66$, $d.f. = 3$, $P < 0.001$, Fig. 2). In addition, we did not detect significant differences among biological groups ($Q = 2.69$, $k = 66$, $d.f. = 3$, $P = 0.443$) or between terrestrial and aquatic ecosystems ($Q = 0.25$, $k = 68$, $d.f. = 1$, $P = 0.618$; Fig. 2). We found a positive relationship between φ and Fisher's z ($Q = 234.34$, $k = 45$, $d.f. = 1$, $P < 0.001$). Thus, the higher φ, the higher the effectiveness of the HTA (Fig. 3a). Studies conducted at different spatial scales tended to have similar Fisher's z scores ($Q = 1.30$, $k = 46$, $d.f. = 1$, $P = 0.254$, Fig. 3b).

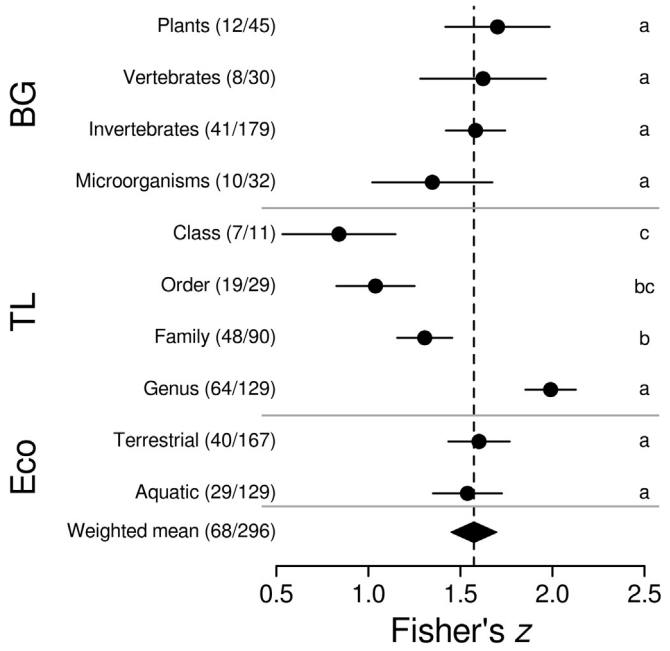

Fig. 2. Variation in the effectiveness of the Higher Taxon Approach (HTA) in relation to ecosystems type, taxonomic level and biological groups for studies that conducted simple correlation analyses. Eco: Types of Ecosystems; TL: Taxonomic levels; BG: Biological groups. Circles and horizontal bars represent, respectively, the mean effect sizes and the 95% confidence intervals (95% CI). The vertical dashed line represents the cumulative effect size for all studies (Fisher's $z = 1.57$, 95% CI ± 0.13). Numbers in parentheses represent, respectively, the number of studies and the number of effect sizes. All effect sizes are significantly different from zero ($P < 0.01$). Levels from a given moderator that did not share the same letter (at the right of the figure) were significantly different in terms of weighted mean effect size. For instance, the results indicate a significant increase in weighted mean effect size from Class (c) to Genus (a), but the effect sizes of Family (b) and Class (c) did not differ from Order (bc).

The Mantel correlations (r_m), evaluating the relationships between compositional distances calculated with different taxonomic resolutions, ranged from 0.02 to 1.00. The weighted mean effect size was equal to 0.77 (95% CI ± 0.16, $k = 71$, $t = 9.34$, $P < 0.001$, Fig. 4). However, subgroup analyses did not detect differences between biological groups ($Q = 0.23$, $k = 69$, $d.f. = 3$, $P = 0.973$), taxonomic resolutions ($Q = 0.86$, $k = 69$, $d.f. = 3$, $P = 0.834$) and types of ecosystems ($Q = 0.07$, $k = 71$, $d.f. = 1$, $P = 0.788$, Fig. 4). Also, effect sizes were not significantly correlated with φ ($Q = 0.99$, $k = 53$, $d.f. = 1$, $P = 0.320$, Fig. 5a) and spatial extent ($Q = 0.03$, $k = 48$, $d.f. = 1$, $P = 0.856$, Fig. 5b). However, it is possible to observe that with increasing φ the variability in r_m decreases specially after a φ value of 0.8 (Fig. 5a).

The Procrustes correlations (r_p) ranged from 0.22 to 1.00, and the weighted mean effect size was 0.69 (95% CI ± 0.26, $k = 12$, $t = 5.24$, $P < 0.001$, Fig. 6). This measure of effect size did not vary between biological groups ($Q = 0.10$, $k = 12$, $d.f. = 1$, $P = 0.756$), taxonomic levels ($Q = 0.53$, $k = 11$, $d.f. = 3$, $P = 0.912$) and types of ecosystems ($Q = 0.50$, $k = 12$, $d.f. = 1$, $P = 0.480$, Fig. 6). The values of r_p were also not correlated with φ ($Q = 1.16$, $k = 10$, $d.f. = 1$, $P = 0.281$; Fig. 7a) or with the spatial extent ($Q = 0.13$, $k = 10$, $d.f. = 1$, $P = 0.723$, Fig. 7b). The Procrustes statistics were, nevertheless, less variable after a ratio (φ) of 0.8 (Fig. 7a).

3.2. Dataset 2

Our meta-regression model allowing for all moderators explained about 71% of the between-study heterogeneity in Fisher's z scores ($Q = 180.29$, $k = 34$, $d.f. = 9$, Pseudo-$R^2 = 0.71$). Studies that were conducted at a larger spatial extent, with a higher φ and at genus level tended to show higher Fisher's z scores, after controlling for the effects of other moderators (Table 1).

3.3. Publication bias and cumulative meta-analysis

Orwin's *fsn* indicates that our results are robust to publication bias (*fsn* = 101 studies). The cumulative meta-analysis indicated that the effect sizes decreased over the years (Fig. 8). However, from 2003 on, all 95% CI from the weighted mean effect sizes estimated with Fisher's z overlapped the estimate obtained with all studies (Fisher's $z = 1.57$). From 2007 on, the weighted mean effect sizes (Fisher's z) stabilized around the global estimate, obtained with all 68 studies (Fig. 8a). Similarly, from 1996 on, the 95% CI from the weighted mean effect sizes estimated with r_m overlapped the estimate obtained with all studies ($r_m = 0.77$). The weighted mean effect sizes (r_m) stabilized around the global estimate from 2008 on (Fig. 8b). The weighted mean effect sizes estimated with r_p varied around the estimate obtained with all studies ($r_p = 0.69$). The weighted mean effect sizes estimated with studies published from 1996 to 2014 were not significantly different from zero. From 2015 on, all weighted mean effect sizes were higher than zero and their 95% CI included the estimate obtained with all studies (Fig. 8c).

4. Discussion

We provide evidence that biomonitoring programs focused on taxonomic diversity can be performed using the HTA, particularly with genera, as indicated by the high effect sizes. As for the Mantel and Procrustes results, effect sizes were high even when the data were

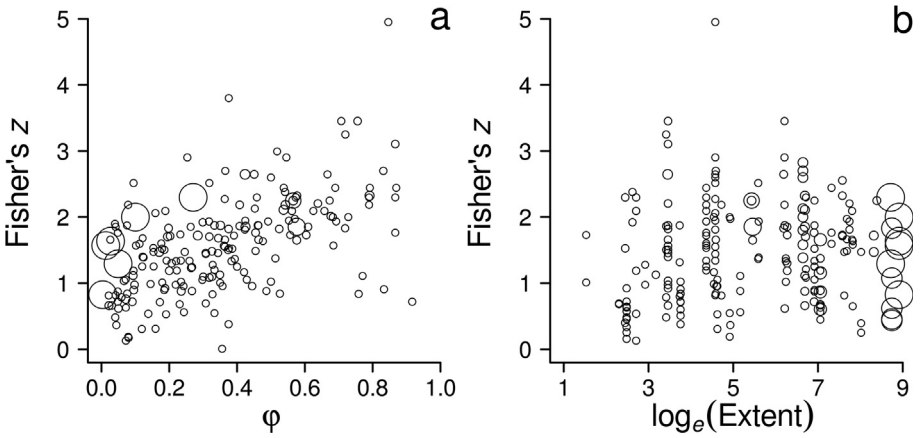

Fig. 3. Relationships between the effectiveness of the Higher Taxon Approach (as measured by Fisher's *z*) and (a) the ratio between higher and lower taxonomic levels (φ) and (b) the spatial extent of the studies (km) for studies that used simple correlation analyses. The size of the circles is proportional to the weight of each effect size.

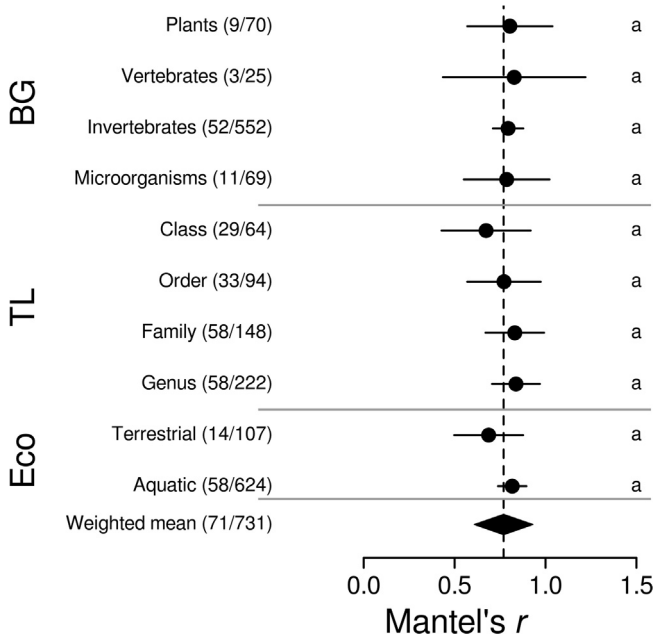

Fig. 4. Variation of the effectiveness of the Higher Taxon Approach in relation to ecosystems type, taxonomic level and biological groups for studies that used Mantel correlation (Mantel's r_m). Eco: Ecosystems; TL: Taxonomic level; BG: Biological groups. The dashed line represents the cumulative effect size considering all studies (r_m = 0.77). All effect sizes are significantly different from zero (P = 0.001). See the description in Fig. 2 for other definitions.

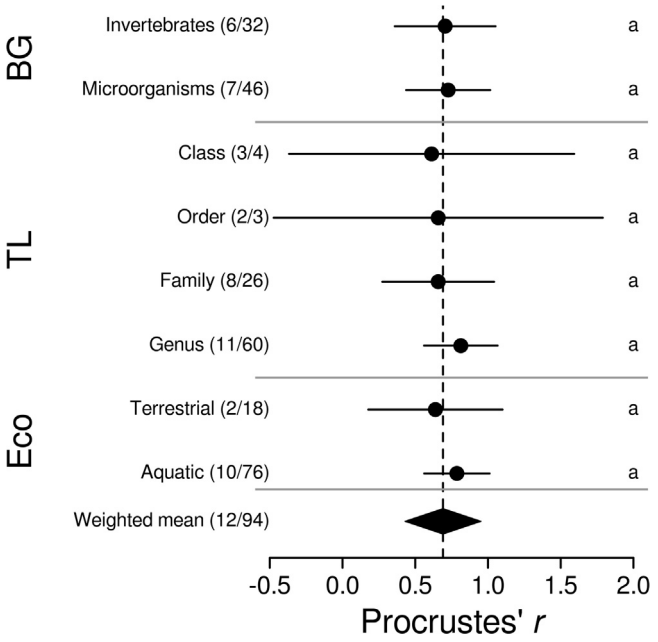

Fig. 6. Variation of the effectiveness of the Higher Taxon Approach in relation to ecosystems type, taxonomic level and biological groups for the studies that carried out Procrustes tests (r_p). Eco: Ecosystems; TL: Taxonomic level; BG: Biological groups. The dashed line represents the cumulative mean effect size for all studies (r_p = 0.78). See the description in Fig. 2 for other definitions.

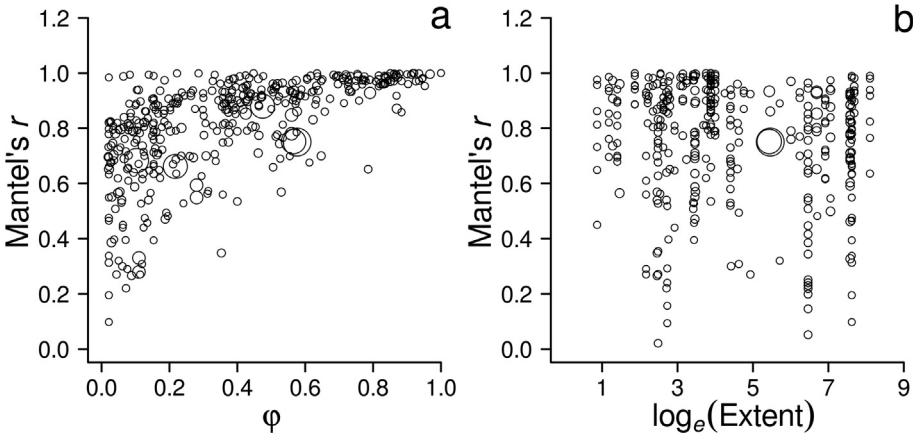

Fig. 5. Relationships between the effectiveness of the Higher Taxon Approach (Mantel correlation) and (a) the ratio between higher and lower taxonomic levels (φ) and (b) the spatial extent (km) for studies focused on composition data. The size of the circles is proportional to the weight of each effect size.

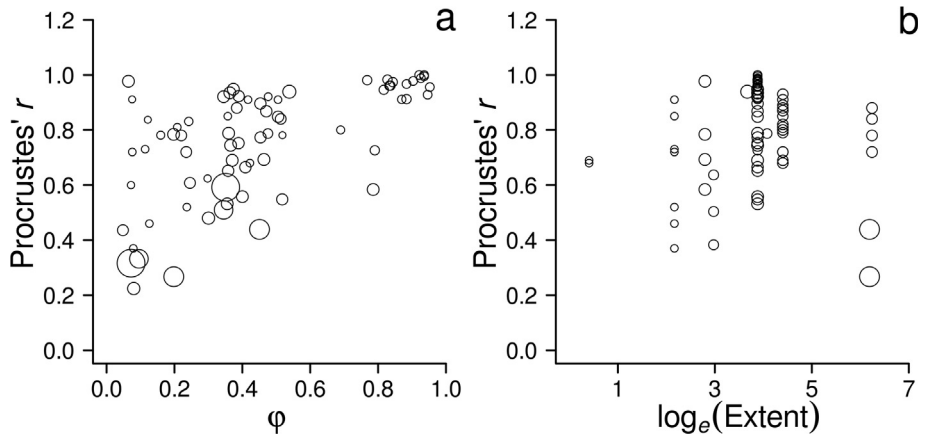

Fig. 7. Relationships between the effectiveness of the Higher Taxon Approach (Procrustes' *r*) and (a) the ratio between higher and lower taxonomic levels (φ) and (b) the spatial extent (km) for studies focused on composition data. The size of the circles is proportional to the weight of each effect size.

grouped into family. Therefore, the results of our meta-analysis indicate that the HTA can be equally effective in biomonitoring programs based on taxa composition (beta diversity). Also, we did not find differences between types of ecosystems (aquatic and terrestrial) or biological groups, independently of the type of effect size (*z*, r_m or r_p). Thus, the HTA tended to be similarly effective in both types of ecosystems and for different biological groups. However, it is worth mentioning that the reliable use of the HTA requires an a priori analysis of the ratio between the richness of different taxonomic levels (e.g., using pilot studies) because low values of the ratio φ could invalidate the use of the HTA. We also found that the HTA effectiveness increased with spatial extent, after controlling for the effects of other moderators. Thus, the reliability of the HTA is likely to increase with the spatial extent of a study.

The statistical significance of the correlation between data with higher and lower taxonomic levels is a necessary but not sufficient outcome to validate the use of HTA because statistical significance is directly related to both the sample size and the precision (Altman and Krzywinski, 2017). In addition, positive and significant correlations between species and genus richness (or other taxonomic levels) are expected due to the hierarchical structure of the taxonomic classification (Gaston, 2000). Thus, studies evaluating concordance among biological communities, which is another shortcut for biodiversity analyses, suggest that only high correlations (e.g., $r > 0.7$) would justify the use of a group as a surrogate for a second biological group (de Morais et al., 2018; Heino, 2010). Even critics of the HTA agree that high correlation values would justify its use in applied studies (Bertrand et al., 2006). In this context, our results are in line with those found in primary studies because, as expected, they showed significant correlations between species and higher-taxon richness (e.g., Balmford et al., 1996a,b; Bates et al., 2007; Bennett et al., 2014; Heino and Soininen, 2007). However, our meta-analysis also showed high effect sizes for both univariate (richness) and multivariate (focused on composition) analyses. This combination of results (high and statistically significant effect sizes) suggests that the HTA is, in general, a trustworthy practice.

The variability in effect sizes across studies should also be evaluated before the use of an approach that seeks to simplify biomonitoring programs. In this context, our analysis with different moderators showed in which situations lower taxonomic resolutions could be used reliably. Rosser (2017), for example, showed that ordination patterns generated with higher taxa differed from those with species data. On the other hand, Vilmi et al. (2016) found strong correlations between distance matrices obtained with different taxonomic resolutions. Similar results were obtained by Ribas and Padial (2015) for beta diversity analysis with phytoplankton, zooplankton, periphyton, and fishes in the Upper Paraná River floodplain. For the different analytical approaches (i.e., simple, Mantel, and Procrustes correlations), we did not observe significant differences between different biological groups and ecosystem types. In general, our results, along with those found in the literature, suggest that the HTA tends to be an effective strategy in different contexts.

Most of the heterogeneity in effect sizes, for richness analyses, can be attributed to the use of different taxonomic levels (genera, families, orders, and classes). Specifically, we found a strong decline in effect size with a reduction of taxonomic resolution. The correlation between species and genus richness was considerably high ($r \approx 0.96$). On the other hand, despite the statistical significance, the correlations between species and higher-taxon richness were markedly lower ($r \approx 0.86$, $r \approx 0.78$ and $r \approx 0.68$ for families, orders and classes, respectively). This decline in the effect size with the reduction of taxonomic resolution was also found in primary studies (e.g., Carneiro et al., 2010;

Table 1
Meta-regression model relating Higher Taxon Approach (HTA) effectiveness (Fisher's *z*) and spatial extent, ratio between the richness of different taxonomic levels (φ), ecosystem, biological group and taxonomic level for studies with complete information for these moderators (Dataset 2). SE: standard-error; 95% CI_l and 95% CI_u: lower and upper 95% confidence interval, respectively. Estimates are deviations from a reference level for categorical moderators. The reference levels were Aquatic (ecosystem), Vertebrates (biological groups) and Class (taxonomic level).

Parameter	Estimate	SE	95% CI_l	95% CI_u	*z*	*p*
Intercept	0.09	0.49	−0.87	1.06	0.19	0.847
Log_{10}(Spatial extent)	0.23	0.11	0.01	0.46	2.04	0.042
φ	1.71	0.28	1.16	2.26	6.15	< 0.001
Ecosystem (Terrestrial)	−0.29	0.18	−0.65	0.06	−1.63	0.103
Biological group (Invertebrates)	0.11	0.25	−0.38	0.61	0.45	0.651
Biological group (Microorganisms)	−0.12	0.33	−0.79	0.54	−0.37	0.712
Biological group (Plants)	0.28	0.29	−0.28	0.85	0.99	0.323
Taxonomic level (Family)	0.35	0.28	−0.21	0.91	1.25	0.211
Taxonomic level (Genus)	0.62	0.31	0.00	1.24	1.99	0.047
Taxonomic level (Order)	0.35	0.29	−0.21	0.92	1.23	0.217

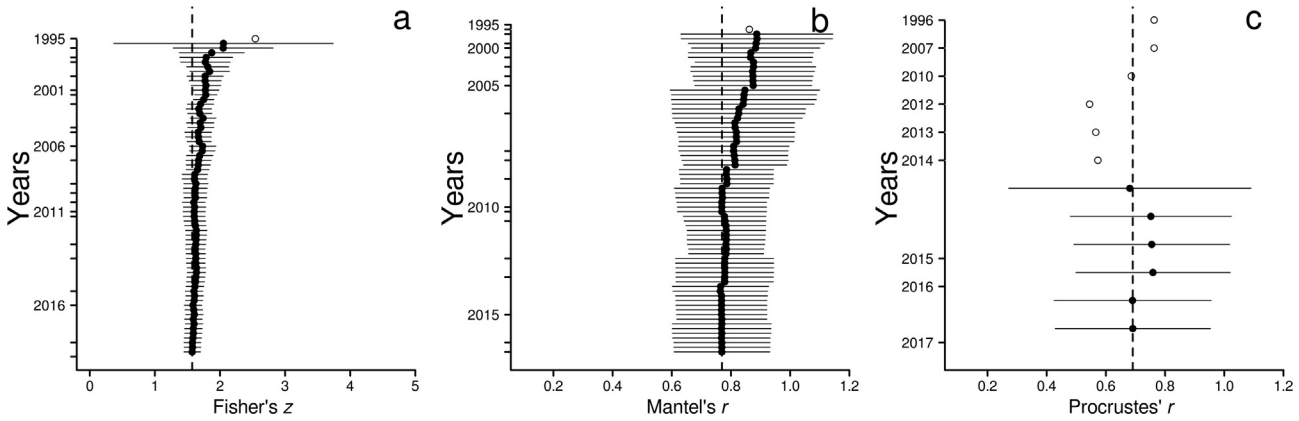

Fig. 8. Temporal variation of the Higher Taxon Approach effectiveness measured with Fisher's *z* (a), Mantel correlation (b) and Procrustes' *r* (c) (cumulative forest plot). The open circles indicates effect sizes which did not differ from zero (their 95% confidence intervals (95% CI) include zero). Closed circles indicate weighted mean effect sizes that were significantly higher than zero. The horizontal lines indicate the 95% CI of each weighted mean effect sizes. The dashed line indicates the weighted mean effect size estimated with all studies with each metric. Note that the y-axis scale is irregularly spaced because represents the amount of studies by year included following our inclusion criteria (the greatest distances between tick marks indicate a greater number of studies by year).

Kallimanis et al., 2012; Rosser and Eggleton, 2012). However, for analyses based on Mantel and Procrustes tests, the effect sizes were similar for the different taxonomic levels. Although this pattern has also been found in some studies (e.g., Bhusal et al., 2014), it differs from other primary studies that found a decline in these statistics with the reductions of the taxonomic resolution (e.g., Bates et al., 2007; Vilmi et al., 2016).

Different ecological patterns and processes are scale-dependent (Bracken et al., 2017; Rahbek, 2005). Also, the effectiveness of the HTA can be sensitive to spatial scale (Mandelik et al., 2007). Our meta-regression model showed that the effect size (Fisher's *z*) increased with spatial scale (after controlling for the effects of other moderators). Thus, based on the results of this model, the effectiveness of the HTA in biomonitoring is likely to increase with spatial extent. However, we emphasize that this meta-regression model was applied to a dataset with a small number of studies (i.e., Dataset 2) and, therefore, results should be viewed with caution. Again, we used a reduced dataset because it was necessary to have the data for all moderators, so that we were able to test a single model. The absence of information on the spatial scale of the primary studies was the main cause of missing values. Thus, we endorse Gerstner et al.'s (2017) call regarding the need to improve the description of the study area in primary research studies: "Complete reporting of spatial scale facilitates the analysis of scale--dependence of results, allows to estimate a "study area" and add additional georeferenced data which might explain observed patterns and explain the geographical reach of the meta-analysis." Other problems (e.g., lack of basic statistics) to be overcome in the primary research studies are listed in their Table 1.

We found that the φ ratio was significantly correlated with the strength of the correlation between species and higher-taxon richness. Similarly, Bevilacqua et al. (2012) observed that φ increased the correlation between different taxonomic levels of some groups of organisms. Rosser (2017) also verified that φ was an important variable in predicting the capacity of higher taxa to represent species richness and composition. The results of these studies, together with those obtained in our meta-analysis, indicate that the use of the HTA by studies seeking to describe alpha and beta diversity patterns is defensible, especially when the values of φ are greater than 0.8. Considering our results and a $\varphi \geq 0.8$, one could expect, on average, a correlation of 0.8 between different taxonomic resolutions. However, it is noteworthy that even above a φ threshold of 0.8 one can observe a high variability in Fisher's *z* (for univariate analysis). Thus, in some cases, even when $\varphi \geq 0.8$, low correlation values between species and higher-taxon richness can be expected (Fig. 3a). On the other hand, above a φ threshold of 0.8, Mantel and Procrustes correlations were always high (Fig. 5a and 7a). It is important to highlight that 75% of the primary studies in our meta-analysis had a φ lower than 0.8. Thus, for these studies, the effectiveness of the HTA was low. In short, the HTA is reliable only when φ is high.

Reduced costs and time to process the samples from biodiversity assessment studies, without the loss of relevant information, have been mentioned as important advantages of the HTA (for an opposite view, see Bevilacqua et al., 2012). For example, the reduction of survey costs of woody plants in Sri Lankan forests was estimated to be of the order of 60% when, instead of species, woody plant genera were targeted (Balmford et al., 1996a). In terms of information loss, Bates et al. (2007) found that, in comparison with species data, the changes in the similarity between samples estimated with data of genera and families were negligible (5 and 8%, respectively). Thus, assuming negligible loss of information, one could argue in favor of "citizen science" to guarantee long-term biomonitoring programs (Bates et al., 2007). This practice could reduce even more the costs of biomonitoring programs, generating short and long term benefits for conservation (Dickinson et al., 2010). It is also important to note that the resources saved could be invested to increase the spatial scale of these programs, as well as to the increase of the number of biological groups to be monitored. This would be especially important because different biological groups may have low levels of concordance, precluding cross-taxa surrogacy (de Morais et al., 2018; Westgate et al., 2014). Finally, higher taxa tend to be less affected by changes in taxonomy and, therefore, can generate more robust and comparable data in long-term ecological studies. Also, higher taxa may be more robust to changes (e.g., due to retirements and job changes) in the personnel that conduct these studies.

The HTA may be an effective strategy to decrease the costs of monitoring programs if compared with other methods (Mellin et al., 2011). For example, the use of a given taxon (i.e., surrogate group) to measure the diversity of other taxonomic group has been shown to be unreliable (de Morais et al., 2018; Rodrigues and Brooks, 2007; Sutcliffe et al., 2012; Westgate et al., 2014). Therefore, our results reinforce the advantages of the HTA in comparison to other biodiversity shortcuts that have been tested to minimize the costs of monitoring programs (e.g. cross-taxa or subset taxa surrogates; Mellin et al., 2011). Also, our cumulative meta-analysis indicated that, from 2007 to 2017, the weighted mean effect sizes were very similar to each other. Although we found a "first-year" effect, a pattern where oldest studies are more likely to report a higher effect size than more recent studies (Koricheva and Kulinskaya, 2019), there was no trend of decreasing effect sizes over the years. This lack of negative trend is particularly

important because the temporal stability of evidence supporting a conservation policy (e.g., adopting the HTA in biomonitoring programs) reinforces the reliability of this policy. Conversely, as discussed by Koricheva and Kulinskaya, (2019), "rapid temporal changes in cumulative evidence represent a real threat to policy making in conservation and environmental management and call for systematic monitoring of temporal changes in evidence and exploration of their causes".

The HTA is thought to be effective when there is a strong environmental gradient, for example, caused by an anthropogenic impact (Vanderklift et al., 1996; Warwick and Clarke, 1993). On the other hand, one should be cautious when using HTA in more natural settings or over short environmental gradients because, under these circumstances, the turnover of higher taxa due to environmental filtering is unlike. Also, our goal was to evaluate whether higher taxa data can substitute species data in applied biomonitoring studies (focused especially in richness and composition analyses), which require fast and continuous execution. Thus, we did not consider that our results could validate this approach in basic and applied ecological studies when obtaining data with refined taxonomic resolution is a necessary requirement (see also Timms et al., 2013). Thus, in these cases, we believe that species-level identification is crucial.

5. Conclusions

We found high correlations between data with high and low taxonomic resolutions. Thus, HTA is likely to be a valid strategy for studies requiring rapid and continuous biodiversity assessments. Moreover, the HTA has the potential to facilitate the work of non-specialists (e.g., of citizen scientists) and, assuming that the reduction of the time and costs of biomonitoring programs is an inescapable necessity, we favor this strategy over others (e.g., cross-taxa surrogates). However, we also found that the effectiveness of the HTA was dependent on the ratio between the numbers of taxa identified at low and high taxonomic resolutions and spatial extent. Thus, the use of HTA should be avoided for taxonomic groups with low values of this ratio, when the studies are planned to cover small spatial extents and when even small differences in species richness or composition are believed to be important.

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Declarations of interest

None.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.ecolind.2019.105994.

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