



Original Articles

Selecting indicators based on biodiversity surrogacy and environmental response in a riverine network: Bringing operationality to biomonitoring

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ABSTRACT

An efficient indicator group should fulfill operational and performance-related criteria, including reasonable taxonomic knowledge, costs, response to environmental changes and strong proxy-capacity for biodiversity groups. However, in the real world many trade-offs are involved in the selection of an indicator group, and a single group rarely satisfies all criteria. We investigated cross-taxon congruence of assemblage composition patterns using both quantitative and qualitative data between adult dragonflies and aquatic insects (midges, Ephemeroptera-Plecoptera-Trichoptera (EPT), beetles and entire aquatic insects assemblage). Also, we tested whether environmental and spatial variables were important drivers for cross-taxon congruence. Finally, we developed a set of guiding criteria that avoid arbitrariness in the selection of the best indicator group. We sampled adult dragonflies and aquatic insects in 41 streams and rivers along a riparian vegetation loss gradient in a Neotropical riverine network. We used Procrustes analyses to verify surrogacy between groups and the association of each group with environmental and spatial predictors. The criteria used involves both operational and performance aspects to select an indicator group. Our results showed that adult dragonflies were weakly congruent with the entire aquatic insects assemblage and aquatic insect subgroups were moderate (beetles) to strongly (EPT and midges) congruent with the entire assemblage. Comparisons between EPT, midges and beetles were also weakly congruent, with the exception of midges-EPT. The association between assemblage patterns and overall environmental predictors was significant for all groups, while with spatial patterns, only midges and entire assemblage showed significant results. Numerical resolution slightly improved the congruence results. Incidence data could be used instead of abundance, due to higher congruence values compared to abundance data. Based on cost-benefit, EPT was selected as the best indicator group for monitoring the effects of riparian vegetation loss on aquatic biodiversity, and its use could be viable in biomonitoring programs.

1. Introduction

Efforts to conserve and understand the effect of anthropogenic impacts on biodiversity are still inadequate considering the multiple anthropogenic threats to biodiversity (Secretariat of the Convention on Biological Diversity, 2014). In freshwater systems, habitat degradation, species invasion, over-exploitation, water pollution and flow modification have resulted in wildlife population declines, loss of biodiversity (Dudgeon et al., 2006; Vörösmarty et al., 2010), and high levels of threat to water security (Vörösmarty et al., 2010). Under such circumstances, conservation and biomonitoring practices are highly advisable (Dudgeon et al., 2006). Among the latter, the selection of

indicators is a key step in the detection of anthropogenic impacts and for implementing biomonitoring programs (Balmford et al., 2005; Bonada et al., 2006).

A variety of invertebrate groups have been selected to indicate environmental changes in aquatic ecosystems (e.g. Ephemeroptera, Plecoptera and Trichoptera, also known as EPT). However, some of them may display strong concordance, also termed as cross-taxon congruence, in space or time (Heino, 2010). Instead of sampling an entire aquatic assemblage, which is time consuming and fund-demanding, cross-taxon congruence creates the opportunity to sample a small subset of organisms that are representative of the entire assemblage (Heino, 2010). For example, EPT assemblage showed congruent

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patterns with entire aquatic invertebrates in Amazonian streams along a deforestation gradient (Brito et al., 2018). Detecting cross-taxon congruence may lead to the selection of surrogates, thus simplifying critical biomonitoring issues, including financial resources and number of experts needed, plus time required for sample processing (Gardner et al., 2008). Testing cross-taxon congruence using different data types (qualitative vs quantitative – numerical resolution) is another consideration when seeking to improve biomonitoring methods, since quantitative data require more processing time than qualitative ones. Thus, cross-taxon congruence may allow selection of surrogates and so optimize biomonitoring programs and conservation planning (Lawton et al., 1998; Lewandowski et al., 2010).

Congruence between different taxonomic groups may occur due to variety of different mechanisms, including biotic interactions, common responses to environmental variables and dispersal limitation (Gaston, 2000; Heino, 2010). Biotic interactions between taxa, such as predator-prey, may result in congruence patterns, because they reciprocally affect abundance while often occupying the same area. Common or different, but correlated, responses of species to environmental variables may result in congruent patterns. Dispersal limitation could also create congruent patterns between different groups, especially when species are spatially restricted and cannot disperse to their preferred patches. Although disentangling these possible explanations is challenging, assessing common responses of different taxonomic groups within the same ecological gradient and spatial pattern may provide evidence concerning the mechanism structuring cross-taxon congruence (Heino, 2010).

Despite efforts to find appropriate biodiversity surrogates, cross-taxon congruence is scale and context-dependent, and no satisfactory generalizations have been achieved so far, both globally (Westgate et al., 2014; Westgate et al., 2017) and for Neotropical aquatic systems (Siqueira et al., 2012). In riparian zones, congruence patterns could potentially be even more complex compared to patterns within a neighboring aquatic or terrestrial system, since organisms living in terrestrial-aquatic interface, such as aquatic insects, are affected by both terrestrial and aquatic environmental conditions. For example, Roque et al. (2017) assessed cross-taxon congruence between frugivorous butterflies, dung beetles and aquatic insects in Neotropical riparian zones and showed incongruent richness and assemblage composition patterns. Similarly, benthic macroinvertebrates assemblage pattern were weakly concordant with spiders, beetles and plants community patterns in central Germany (Tonkin et al., 2016), and with birds and plants in Canadian wetlands (Rooney and Bayley, 2012).

Among riparian communities, adult dragonflies (hereafter comprising both Anisoptera and Zygoptera suborders – sensu Corbet, 2004) have been reported as reliable bioindicators of riparian deforestation, land use conversion and urbanization (Kutcher and Bried, 2014; Luke et al., 2017; Simaika and Samways, 2011). These anthropogenic impacts affect important adult dragonflies niche conditions, such as sites for thermoregulation, reproduction, oviposition and feeding (Saito et al., 2016; Valente-Neto et al., 2016). Adult dragonflies can also be used as surrogates of larval stages along a deforestation gradient, resulting in their use being recommended in biomonitoring programs (Mendes et al., 2017; Valente-Neto et al., 2016). In addition, genus level was found to be sufficient to capture assemblage composition patterns for both adult species and genera larval dragonflies (Valente-Neto et al., 2016), this being another practical way to optimize biomonitoring programs (Buss and Vitorino, 2010; Melo, 2005). Although such results indicate the use of adult dragonflies to has strong potential for detecting and monitoring anthropogenic impacts in aquatic and riparian systems, members of this group comprise a small fraction of the biodiversity of riverine systems (Kalkman et al., 2008; Smith et al., 2007). Thus, it is needed to assess the congruence between adult dragonflies and aquatic insects groups, since the latter is long-established in biomonitoring protocols worldwide (Buss et al., 2015), are sensitive to both in-stream and riparian conditions (Roque et al., 2010), and some of them cannot

easily disperse from a disturbed to a suitable patch (Bilton et al., 2001). This is a potential extension of the effectiveness use of adult dragonflies as bioindicators (Smith et al., 2007).

Accordingly, our goal was to investigate cross-congruence assemblage composition patterns between adult dragonflies and four aquatic subgroups: Ephemeroptera-Plecoptera-Trichoptera (EPT), beetles (Coleoptera), midges (Diptera), and entire aquatic insects assemblage (hereafter called AIA). Additionally, to shed light into possible mechanism behind cross-taxon congruence patterns, we assessed the congruence between assemblage patterns and two set of predictors (environmental and spatial). Based on the relationships of each group with environmental variables described in the previous paragraphs and the higher dispersal ability of adult dragonflies compared to aquatic insects, we expected a higher level of congruence between aquatic insect subgroups compared to each comparison between adult dragonflies and aquatic insects groups. We also expected the concordance of the AIA with environmental variables, and some subgroups more dispersal limited (beetles and midges) with both environmental and spatial variables. In contrast, the higher dispersal ability of adult dragonflies and their dependence on vegetation structure suggest congruence only with environmental predictors. Finally, we developed a set of criteria to guide us in the selection of one indicator based on cost-effectiveness criteria.

2. Methods

2.1. Study area

We carried out the study in the Betione riverine network, located in the Bodoquena Plateau, southwest Mato Grosso do Sul, Brazil. We selected 41 streams and rivers to sample adult dragonflies and aquatic insects. The sites were selected to follow a gradient of riparian vegetation loss, from lotic system with near-pristine riparian vegetation to varying amounts of native vegetation remnants, including open-canopy stream (Fig. 1). Indeed, vegetation cover loss is the main impact in the study region, mainly due to native vegetation conversion to agriculture and cattle ranching. Typically, streams and rivers of the Betione network have karstic waters and they did not receive any sort of sewage disposal.

2.2. Adult dragonflies and aquatic insect sampling

As focal groups, we used adult dragonflies, AIA (comprising the orders Odonata, Diptera, Ephemeroptera, Plecoptera and Trichoptera, Coleoptera and Hemiptera), and the following groups to test congruence patterns: EPT (Ephemeroptera, Plecoptera and Trichoptera), beetles and midges. We used EPT as a group, because they have similar collective responses to anthropogenic impacts and have long been recognized as bioindicators (Bonada et al., 2006; Rosenberg and Resh, 1993). Genus was the taxonomic resolution used in this study, since, for most aquatic insects, species-level identification is scarcely achieved.

For adult dragonflies, we used 41 sites from the dataset resulting from sampling by Valente-Neto et al. (2016). They were sampled once at each site using a fixed-area scan method (100 m transect) during 1 h (De Marco et al., 2015; Monteiro-Júnior et al., 2015).

We sampled aquatic insects using a multi-habitat approach (Barbour et al., 1996), consisting of the sum of 20 sampling units per stream/river proportionally distributed between all available major habitats. We used three reaches of 10 m to estimate the proportion of the following habitats: rock outcrops, rock cobble, gravel, sand, mud silt, organic matter, wood, aquatic vegetation, leaf litter and roots. We then calculated the mean for the 30 m reach and proportionally distributed the sampling units among habitats. Each sampling unit consisted of 1 m length using a kick net (0.5 mm mesh size; covering 0.3 m²), totaling a sampling effort of 6 m² of stream/river bottom.

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