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Different surrogacy approaches for stream macroinvertebrates in discriminating human disturbances in Central China

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ABSTRACT

Due to the difficulty of identifying many taxa of freshwater invertebrates to species, many researchers have assessed the utility of surrogates for species-level identifications (e.g. higher taxa) in bioassessment programs. Here, we examined the efficiency of two different approaches to species surrogacy, one using coarser taxonomic resolution and a second approach based on random aggregation ("Best practicable aggregation of species", BestAgg), in portraying patterns of stream macroinvertebrates in Central China. The main objectives were: (1) to compare the discriminatory power of biodiversity indices and assemblage structure for different levels of human disturbances based on different taxonomic resolution and on BestAgg; (2) to identify the congruence of assemblage-environment and biodiversity-indices-environment relationships for datasets at the species level versus those at surrogate levels. We found that genus-level and BestAgg datasets accurately reproduced the pattern of species-level communities, whereas family- and order-level datasets did not. Specifically, both genus-level and BestAgg approaches performed almost as well as species-level data in distinguishing sites subjected to different disturbance levels. Most of the environmental variables that were important for species-level assemblages, also emerged as significant when analyzing genera and BestAgg surrogates, as shown by both analyses of indices and assemblage composition according to distance-based ordination models. Our results suggest that genus-level taxonomy, which resulted in the least loss of ecological information relative to species-level identification, is sufficient in studies of community ecology and bioassessment of stream macroinvertebrates in Central China. In addition, the BestAgg approach, which required identification of fewer taxa than genus-level analysis, has a similar ability to depict multivariate patterns of macroinvertebrate assemblages and differentiate different disturbance levels. Applying our results could enhance speed and cost-effectiveness of freshwater biomonitoring and bioassessment programs; however, independent determination of best taxonomic level and BestAgg will be required whenever a new geographic area or habitat type is assessed.

1. Introduction

Understanding the effects on biodiversity of environmental variation, both natural and anthropogenic, is one of the main goals of research in community ecology, biodiversity conservation and environmental assessment. In most situations, species-level identification provides optimal information for quantifying assemblage responses to environmental changes, as species are the basic units for studying responses of organisms to environmental disturbances (Bevilacqua et al., 2012; Heino, 2014). However, for many taxa, identification to species-level is not always possible due to the inadequacy of taxonomic knowledge (the "Linnaean deficit"), the paucity of geographic distribution information (the "Wallacean deficit"), or presence of life-history stages that lack species-level morphological characters (Bini et al., 2006; Whittaker et al., 2005). Furthermore, species-level identification has a high demand for time, money, labor force and taxonomic expertise. Therefore, taxonomic sufficiency (i.e., identifying to a coarser taxonomic rank such as genus or family when it satisfies the objective of a study; Ellis, 1985) and taxonomic surrogacy (i.e., using higher taxa if they portray species-level patterns; Bertrand et al., 2006) are often applied in numerous studies of terrestrial, marine and freshwater ecosystems (e.g. Bevilacqua et al., 2015; Groc et al., 2010; Jiang et al., 2013; Vilmi et al., 2016). Despite slight differences between the two concepts, they are both based on the idea that datasets aggregated to

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coarser taxonomic level can often reproduce species-level patterns (Heino, 2014; Jones, 2008).

Early studies on taxonomic surrogacy focused on testing the congruence between richness of species and of higher taxa (e.g. Cardoso et al., 2004; Gaston and Williams, 1993), whereas recent studies have expanded to look at the power of coarse taxonomic resolution on perceptions of multivariate assemblage structure and assemblage-environment relationships (Heino, 2014; Jiang et al., 2013; Terlizzi et al., 2009). Examining assemblage structure and assemblage-environment relationships are deemed to be more important in community ecology, because these investigations could give more valuable information for bioassessment, e.g. assemblage heterogeneity among sites or regions, and responses of organisms to environmental gradients (Legendre, 2007; Legendre et al., 2005).

Despite the unarguable pragmatic value of identifying organisms to coarser taxonomic levels, it is still under debate whether species or higher taxa are equally useful for examination of community patterns, even though many studies have shown higher taxa to be as effective as species for descriptions of changes in assemblage structure along ecological gradients (e.g. Bowman and Bailey, 1997; Bevilacqua et al., 2012; Heino and Soininen, 2007; Milošević et al., 2014). Some authors suggest applying finest possible identification because using higher taxa could conceal spatio-temporal gradients and decrease discriminatory power in ordination processes (Hawkins and Norris, 2000; Melo, 2005; Verdonschot, 2006). In contrast, others have challenged the necessity of species-level identification and argue that economy of time, money and taxonomic experts using higher taxa outweighs harmless information loss (Jones, 2008; Marshall et al., 2006). The latter researchers also point out that the utility of taxonomic surrogacy depends on the study objective and highlight the value of using coarser taxonomical levels for rapid bioassessment programs (Bailey, 2001; Jones, 2008).

The above approaches have focused on the results of taxonomic resolution with the goal of finding the most cost/time-effective surrogates for species. However, this approach to taxonomic surrogates does not take into account the ecological relevance of the lumping or identification ease of organisms to a higher taxon, and hence would lead to unnecessary information loss of detail in community structure and limit inferences about the ecological processes originated from the observed community patterns (Jones, 2008; Terlizzi et al., 2003). A different approach for species surrogacy, namely the "Best Practicable Aggregation of Species" (BestAgg), has recently been proposed by Bevilacqua et al. (2013). This new approach goes beyond the taxonomic relatedness framework and is dependent on the construction of null models based on real ecological datasets, aiming to define the minimum effective numbers of species aggregation (i.e., from fewest surrogates, the aggregation data that still reproduce community patterns shown at the species-level). In theory, BestAgg can reduce the efforts required for specimen identification, maximizing the ecological information of community patterns from a minimum number of surrogates. This new method has been successfully applied in marine, freshwater and transitional water systems (Bevilacqua et al., 2013; Bevilacqua and Terlizzi, 2016; Bevilacqua et al., 2015; Milošević et al., 2014).

In freshwater ecosystems, benthic macroinvertebrates are probably the most widely used indicators of environmental changes due to their dependence on local conditions and ease of quantitative sampling (Bailey, 2001; Morse et al., 2007). However, their identification to species level is often difficult because of inadequate taxonomic knowledge, presence of unidentifiable immatures or specimens missing important parts of the morphology (e.g., gills), subtle morphological characters needed in identification, and increasing risks of misidentifications as taxonomic precision increases (Jones, 2008; Yoshimura and Mayumi, 2012). These difficulties have hindered the utility of macroinvertebrates in environmental assessment, especially in regions lacking reliable species-level keys and experts. This lack is especially true in China and other East Asian countries (Morse et al., 2007). Compared with increasing studies concerning taxonomic surrogacy of lotic and lentic macroinvertebrates in Europe (Heino, 2014; Milošević et al., 2014), North America (Bailey, 2001; Greffard et al., 2011) and other continents (da Silva Giehl et al., 2014; Marshall et al., 2006), few such studies have been carried in East Asia (Jiang et al., 2013), even though the change in rates of anthropogenic disturbance are probably greatest in this part of the world. There is an urgent need to assess the efficiency of higher taxonomic levels as surrogates for benthic macroinvertebrate species in bioassessment programs in this region.

Here we evaluate the effectiveness of different approaches, one based on classic taxonomic sufficiency and one using BestAgg surrogates for species, in describing macroinvertebrate assemblages in Central Chinese streams. We address three questions: (1) how strongly do biodiversity indices and assemblage structure based on species-level datasets correlate with those based on coarser taxonomic resolutions (genera, families, orders) and the random aggregation approach (BestAgg)? (2) how does the ability of biodiversity indices and assemblage structure to distinguish different levels of disturbances vary among different surrogates? (3) how do different surrogates influence the assemblage-environment and indices-environment relationships?

2. Materials and methods

2.1. Study area and sites

Data come from a previous study on 44 stream sites in upper and middle reaches of the Du River Basin (Jiang et al., 2014). Being the largest tributary of the Han River, the Du River (31°25′–32°48′ N, 109°10′–110°45′ E) is located in a transition zone between northern-subtropical and warm-temperate regions. Stream sites were representative of a suite of environmental conditions selected based on an environmental disturbance score that is a composite of 6 variables including two water quality variables (total phosphorus, total nitrogen), two land use variables (agricultural and urban land cover), flow regulation and historical point-source pollution, to classify sites into three disturbance levels: least-disturbed (=good, 13 sites), moderately disturbed (=fair, 17 sites), and severely disturbed (=poor, 14 sites) (see Table S1 in Supplemetary file, see also Jiang et al., 2014).

2.2. Macroinvertebrate and environmental data collection

In late March 2011, we sampled three quantitative replicates of macroinvertebrates in principal habitats (usually riffle, run and pool) at each site using a Surber sampler (30 × 30 cm, 500 μm mesh). The specimens were then manually sorted from sediment in white porcelain trays and preserved in 10% formalin. Specimens were identified to the finest possible taxonomic level according to the relevant references (Brinkhurst, 1986; Dudgeon, 1999; Epler, 2001; Morse et al., 1994; Wiggins, 1996; Zhou et al., 2003), and were counted. Nematoda and Turbellaria were excluded from subsequent analyses because we were unable to identify them more finely than these coarse taxonomic ranks.

At each site, a series of environmental variables were measured before macroinvertebrate sampling. Altitude (using a Unistrong MG721W system), channel width (Ranger laser Finder instrument), water depth and current velocity (LJD-10 flow-meter) were averaged from 7 to 10 locations across the transect. A YSI6680 Multi