



Unravelling the drivers of aquatic communities using disparate organismal groups and different taxonomic levels



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ARTICLE INFO

Article history:

Received 29 April 2015

Received in revised form 11 June 2015

Accepted 18 June 2015

Keywords:

Bacteria
Bioassessment
Diatoms
Macroinvertebrates
Taxonomic surrogacy
Higher-taxon approach

ABSTRACT

Bioassessment and monitoring methods should be as cost-efficient as possible. Limiting the number of sites is not a practical solution to face the financial challenges related to bioassessment. Hence, it is highly important to find inexpensive ways to assess and monitor human-impacted environments. Suggestions have been made to use coarser taxonomic levels because they require less expertise and time, or to use single surrogate taxonomic groups that indicate the overall state of ecosystems. In this study, we examined the level of within-taxon and cross-taxon congruence of aquatic bacterial, diatom and macroinvertebrate communities, while simultaneously assessing the chemical, physical and spatial drivers of community structure in these organismal groups. Our study area was an extensively sampled large lake system with high connectivity between sites. Thus, we ensured that spatial processes, if they existed, were well portrayed in our data. Our aim was to find out the taxonomic levels sufficient for the purposes of bioassessment and to detect possible surrogate taxonomic groups. We found that bacterial communities were best associated with pure effects of water chemistry, whereas diatom and macroinvertebrate communities were varyingly related to chemical, physical and spatial variables. Macroinvertebrates were the only group related to small-scale spatial variables, while bacteria and diatoms were associated with variables illustrating spatial relations among sites at large and intermediate scales. Overall, the three organismal groups were mainly related to different chemical parameters. Also, the three organismal groups showed only weak, if any, congruent patterns in their community structure. Thus, we do not recommend the use of only one biological group as a surrogate in bioassessment. However, we found that higher taxonomic levels of all three studied organismal groups could be used as surrogates for finer-level taxonomic assignments. Our findings are promising for the possible use of bacteria in future bioassessment and monitoring. Owing to the characteristics of very large lake systems, our findings may be applied to similarly highly connected ecosystems, such as marine coastal systems.

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1. Introduction

Species are considered the main units of biodiversity (Gaston, 2000). Bioassessment is also often based on species-level information (Birk et al., 2012; but see Jones, 2008), as the responses of organisms to changes in the surrounding environment are assumed to be most visible at that taxonomic level (Warwick, 1993; Bevilacqua et al., 2012). However, depending on the biological group, the use of species-level information usually takes

more time, money and expertise than that of coarser taxonomic levels (Warwick, 1993; Bertrand et al., 2006). These ideas centre on the concepts of *taxonomic sufficiency* and *taxonomic surrogacy*. Taxonomic sufficiency means that organisms are identified to the taxonomic level needed to meet the requirements of the study (Ellis, 1985), and there is thus usually no point in using more effort than needed to get a result reliable enough for bioassessment (e.g. Bailey et al., 2001). Taxonomic surrogacy, on the other hand, means the degree to which higher taxonomic levels actually represent species-level patterns (i.e. within-taxon congruence; Bertrand et al., 2006). There are a number of studies showing that higher taxa (i.e. genera or families) show similar patterns to those of species-level data (Heino and Soininen, 2007; Terlizzi et al., 2009; Mueller et al., 2013a). However, the success of taxonomic surrogacy can be dependent on the spatial scale, the identity of the region

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examined (Terlizzi et al., 2009; Heino, 2014) or the investigated taxonomic group and the extent of the studied environmental effects (Mueller et al., 2013a). At its best, the use of taxonomic surrogates can enhance bioassessment because costs of the assessment can be minimised and, hence, more extensive surveys can be conducted (Warwick, 1993; Heino and Soininen, 2007; Terlizzi et al., 2009).

The use of taxonomic surrogates has encountered some criticism stating that it lacks justification due to the fact that taxonomic classifications are human-made and thus artificial (Bertrand et al., 2006). In addition, it is important to acknowledge the value of species-level information especially for conservation actions (e.g. Bailey et al., 2001). Nevertheless, if higher taxa show similar responses to environmental gradients compared with species, then it generally would be cost-efficient to utilise higher taxa in bioassessment. However, this idea does not necessarily apply to all organisms. For instance, DNA-based assignment of organisms to fine taxonomic resolution is equally expensive as assigning them to coarser levels. Overall, these issues regarding both taxonomic surrogacy and taxonomic sufficiency should be considered when planning environmental monitoring and bioassessment programmes, especially when they are based on macroscopic or microscopic organisms. For DNA-based taxonomic assignments, acknowledging within-taxon congruence provides insights into the taxonomic group itself, but it also gives valuable information for the applications of sequencing and bioassessment methods.

In the past, taxonomic surrogacy has mostly been studied using richness measures, but also community composition has been used to assess these issues more recently. The community–environment relationships among various taxonomic levels have thus recently gained more attention (Heino, 2014), and the metacommunity context (Leibold et al., 2004; Logue et al., 2011) offers a suitable framework to study these surrogacy issues even further (Siqueira et al., 2012). A common assumption underlying most bioassessment approaches is that biological communities are primarily products of local environmental conditions, pertaining to the species sorting paradigm of metacommunity ecology (Leibold et al., 2004). These bioassessment approaches, however, largely ignore the influence of biotic interactions and spatial processes (Heino, 2013; Friberg, 2014; Siqueira et al., 2014). By separating the roles of local environmental (i.e. species sorting) and dispersal-related processes (e.g. mass effects, dispersal limitation) to the variation in community structure, it is possible to better understand how biological communities are structured (e.g. Cottenie, 2005) and, consequently, how well they could perform as bioindicators (Siqueira et al., 2014). Acknowledging metacommunity processes is also essential in studies examining taxonomic resolution. Higher taxa may be less responsive to dispersal-related mechanisms because they are likely to show less dispersal limitation and mass effects owing to their wider distributions than those of species along ecological gradients. The higher-taxon approach may also overcome the effects of numerous rare species typical of species data matrices (Warwick, 1993). Rare species are difficult to model because they often appear at only few sites by chance, without their occurrence being related to environmental conditions. At the genus level, these rare species are pooled together and, hence, the prediction of the distributions of genera can be easier.

In addition to studying congruence between various taxonomic levels within a biological group, it is useful to examine cross-taxon congruence between different biological groups (Heino, 2010). In freshwater ecosystems, rather weak but significantly congruent community patterns have been reported between various taxonomic groups (Johnson and Hering, 2010; Özkan et al., 2014). This taxonomic congruence may be due to similar responses to environmental gradients or due to interactions among biological groups (Johnson and Hering, 2010; Padial et al., 2012). Padial et al. (2012) found high temporal variation in cross-taxon congruence, with

predictability being too low for the use of surrogates in biomonitoring. Tolonen et al. (2005) neither found any good surrogate taxon for overall biodiversity in a large lentic ecosystem. Heino (2010) stated that cross-taxon congruence may be commonly weak in aquatic ecosystems and, thus, the use of multiple taxonomic groups is advisable for biomonitoring and conservation purposes as biological groups may react in different ways to natural environmental conditions and different anthropogenic pressures (Hering et al., 2006; Marzin et al., 2012). Consequently, community patterns of various organismal groups do not necessarily correlate strongly.

We examined the effects of taxonomic resolution in the context of assessing the ecological drivers of aquatic communities. We used data for littoral bacteria, diatoms and macroinvertebrates to answer our study questions. Specifically, we asked: (1) What are the main ecological drivers of bacterial, diatom and macroinvertebrate community structures at different taxonomic resolutions? (2) Which taxonomic level best portrays the environmental conditions of littoral sites, i.e. best meets the requirements of bioassessment? (3) Do the different taxonomic levels show congruent patterns within organismal groups? (4) What is the strength of cross-taxon congruence between the three taxonomic groups examined? (5) Which taxonomic group best portrays variation in water quality? In particular, we were interested in finding out if bacteria were better as water quality indicators than the traditional biological indicators, e.g. diatoms and macroinvertebrates.

Our study area comprised a large lake system in which dispersal limitation of bacteria and diatoms – efficient passive dispersers – is not likely to occur (Telford et al., 2006; Kristiansen, 1996). Macroinvertebrates should also be able to freely disperse within our study area, as it contains no evident barriers for dispersal. Special features of our lake system are the large areal extent (305 km²) and the assumed considerable connectivity between the study sites. Thus, our findings can also be applied to similarly highly connected systems, such as other large lakes, stream networks and marine coastal systems.

2. Materials and methods

2.1. Study area

The study area, Lake Kitkajärvi, is a large lake system located in north-eastern Finland. The lake system was originally oligotrophic, but an increase of recent anthropogenic stress has led to an ongoing eutrophication process (Vilmi et al., 2015). In September 2013, we sampled 81 similar stony littoral sites for bacteria, diatoms and macroinvertebrates. The sites were located across the whole lake system and were as evenly distributed as possible. One sampling site was a 10-metres stretch along the shoreline. However, bacterial DNA could be extracted from the samples of 36 sites only, and thus bacterial community data are available from a subset of sites (Fig. 1). To facilitate comparisons, we used diatom and macroinvertebrate data from only the same subset of 36 sites. The sites including data from all of the three organismal groups were evenly distributed around the lake system. All sampling was carefully planned and executed to rule out sampling-related effects or seasonal variations.

2.2. Biological sampling, laboratory procedures and data processing

2.2.1. Bacteria

At each site, bacterial samples were taken from the surfaces of 10 cobble-sized stones collected from water depths of approximately 40 cm. At each site, new sampling equipment (a piece of foam plastic (4 cm × 4 cm × 4 cm), and a pair of disposable gloves), which were packed in to small plastic bags in advance in the

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