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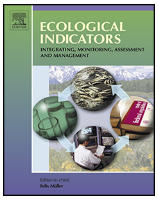

A sediment-specific family-level biomonitoring tool to identify the impacts of fine sediment in temperate rivers and streams

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ABSTRACT

Anthropogenic modifications of sediment load can cause ecological degradation in stream and river ecosystems. However, in practice, identifying when and where sediment is the primary cause of ecological degradation is a challenging task. Biological communities undergo natural cycles and variation over time, and respond to a range of physical, chemical and biological pressures. Furthermore, fine sediments are commonly associated with numerous other pressures that are likely to influence aquatic biota. The use of conventional, non-biological monitoring to attribute cause and effect would necessitate measurement of multiple parameters, at sufficient temporal resolution, and for a significant period of time. Biomonitoring tools, which use low-frequency measurements of biota to gauge and track changes in the environment, can provide a valuable alternative means to detecting the effects of a given pressure. In this study, we develop and test an improved macroinvertebrate, family-level and mixed-level biomonitoring tool for fine sediment. Biologically-based classifications of sediment sensitivity were supplemented by using empirical data of macroinvertebrate abundance and percentage fine sediment, collected across a wide range of temperate river and stream ecosystems (model training dataset $n = 2252$) to assign detailed individual sensitivity weights to taxa. An optimum set of weights were identified by non-linear optimisation, as those that resulted in the highest Spearman's rank correlation coefficient between the index (called the Empirically-weighted Proportion of Sediment-sensitive Invertebrates index; E-PSI) scores and deposited fine sediment in the model training dataset. The family and mixed-level tools performed similarly, with correlations with percentage fine sediment in the test dataset ($n = 84$) of $r_s = -0.72$ and $r_s = -0.70$ $p < 0.01$. Testing of the best performing family level version, over agriculturally impacted sites ($n = 754$) showed similar correlations to fine sediment ($r_s = -0.68$ $p < 0.01$). The tools developed in this study have retained their biological basis, are easily integrated into contemporary monitoring agency protocols and can be applied retrospectively to historic datasets. Given the challenges of non-biological conventional monitoring of fine sediments and determining the biological relevance of the resulting data, a sediment-specific biomonitoring approach is highly desirable and will be a useful addition to the suite of pressure-specific biomonitoring tools currently used to infer the causes of ecological degradation.

1. Introduction

Streambed deposited fine sediment (<2 mm) is an important, natural component of freshwater ecosystems and is critical for habitat heterogeneity and ecological functioning (Owens et al., 2005; Wood and Armitage, 1997; Yarnell et al., 2006). However, anthropogenic activities can alter sediment delivery and dynamics contributing to ecological degradation (Vörösmarty et al., 2003; Walling and Fang, 2003). Fine sediment can directly impact on stream biota by subjecting them to abrasion, scour or burial; by clogging gills or feeding appendages; by limiting light penetration; as well as indirectly by introducing toxic contaminants sorbed to the surface of fine sediment particles, and reducing oxygen concentrations in the substrate (reviewed in Bilotta and Brazier, 2008). In practice, identifying when and where sediment is the primary cause of ecological degradation is a challenging task. Biological communities undergo natural cycles and variation over time, and respond to other physical (e.g. changes to flow and temperature),

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chemical (e.g. pH, heavy metals, pesticides, nutrients) and biological pressures (e.g. invasive species), (Clews and Ormerod, 2009; Liess and Schulz, 1999; Moore and Ramamoorthy, 2012; Sousa, 1984; Townsend, 1996). The use of conventional (non-biological) monitoring approaches to attribute cause and effect necessitates measurement of multiple parameters, at sufficient temporal resolution, and for a significant period of time (Grove et al., 2015; Harris and Heathwaite, 2012). Biomonitoring tools, which use changes in the presence, abundance or behaviour of biota to indicate, gauge and track changes in the environment (Friberg et al., 2011; Gerhardt, 2000; Wright et al., 1993), can provide a valuable lower-cost alternative to conventional monitoring. Ideally, for reasons discussed in more detail in the following paragraphs, biomonitoring tools should, where possible: (i) have a biological basis, (ii) be easily integrated into standardised biological sampling and recording methods, (iii) be developed and tested over sites from the full range of river and stream ecosystems to which they are intended to be applied, and (iv) have a strong relationship with the pressure of concern.

1.1. Biological basis

There is an emerging consensus among those involved in developing biomonitoring tools, that more reliable tools have a biological basis, i.e. they use biological and ecological traits that influence the tolerance of organisms to a given pressure, and are linked to ecological niche theory (Bonada et al., 2006; Friberg et al., 2011). One of the reasons for this is that these types of tools are not vulnerable to statistical artefacts that may affect purely statistical models. The biological traits (e.g. respiration, locomotion, dispersal, feeding) of taxa in a community reflect the spatial and temporal variations in the environmental factors of a habitat, that act as "filters", with successful combinations of traits enabling survival and reproduction (Poff, 1997; Statzner et al., 2001b; Townsend et al., 1997). Certain traits or combinations of traits can result in sensitivities/tolerances to particular environmental pressures and therefore these traits have the potential to be used in biomonitoring to discriminate between types of human disturbance (Statzner et al., 2001a). If taxa are selected for inclusion and their sensitivities weighted based on the biological and ecological traits, which influence their sensitivity to a given pressure, the resultant biomonitoring tool will have a mechanistic linkage (rather than a purely correlative linkage) between the pressure of concern and the biotic response (Friberg, 2014).

1.2. Easily integrated into standardised biological sampling and recording methods

One of the many benefits of biomonitoring as opposed to conventional monitoring of multiple environmental parameters is that the biological data collected from the same biological sample can be interpreted by an array of different biomonitoring tools to identify potential pressures. In order for this efficiency and cost-effectiveness to be realised, the biomonitoring tools must be able to make use of data collected using standardised biological sampling methods and recorded to standardised, minimum taxonomic levels. Monitoring agencies in different countries commonly carry out invertebrate identification and recording at different taxonomic levels. For example, within Europe the level of invertebrate taxonomic knowledge varies between countries, as do resources, resulting in different taxonomic resolutions and a lack of comparability between data (Hering et al., 2010; Schmidt-Kloiber and Hering, 2015). Within the UK, England and Wales recently moved from family level invertebrate recording to a mixed level,[1] consisting of family-, genus- and species-level identifications, with the majority of taxa being identified to species (Davy-Bowker et al., 2010). However, Scotland and Northern Ireland currently record at family-level.[2] A family-level tool is not only essential for those countries that record at this taxonomic level, but is also crucial for those countries which have recently switched to a higher taxonomic resolution, as it will allow for retrospective analysis of historic family-level data. This ability to assess the historic conditions at sites is particularly important when attempting to distinguish between natural temporal variations (Resh et al., 2005) and those caused by anthropogenic activities, as this can require numerous years of baseline data. Furthermore, a lower-cost family-level biomonitoring tool is likely to be highly desirable for non-regulatory work (e.g. river restoration projects, aquatic research and citizen science programmes) where budgets and taxonomic expertise may be more limited.

1.3. Developed and tested over the full range of different rivers and streams

There are a number of reasons why biomonitoring tools should be developed and tested using data from sites across the full spectrum of rivers and streams to which they are designed to be applied. Firstly, biological communities and species distributions vary naturally, partly as a result of environmental gradients, biotic interactions (McGill et al., 2006) and their ecological requirements (Schmidt-Kloiber and Hering, 2015). As such, a biomonitoring tool must incorporate a range of taxa to ensure that any sampled site will have the potential to include a sufficient number of taxa with sensitivity weightings. Secondly, it cannot be assumed that biological communities will respond uniformly to the same pressure in different rivers and streams. Not only may the pressure of concern occur alongside other, different pressures (potentially having synergistic or antagonistic effects), (Folt et al., 1999), but differences in environmental characteristics (e.g. habitat complexity) may also affect a biological community's resistance and resilience to a specific pressure (Dunbar et al., 2010a,b; Lake, 2000).

1.4. Strong relationship with pressure of interest

Given the implications of incorrect assignment of ecological status of streams for both water and land managers (from unjustified burdens being placed on the users of water resources, to environmental damage going undetected), it is important that biomonitoring tools have a strong relationship with their pressure, in addition to the previous three criteria. Nevertheless, a strong correlation does not rule out the possibility of the tool indicating other aquatic pressures or variables that may occur in parallel with the pressure of concern. A statistical approach may yield strong correlations to the pressure of concern, but these can be the result of statistical artefacts e.g. an inadvertent relationship with an associated pressure (Table 1). Although a biological basis provides a mechanistic linkage for a correlation, biological traits are not always unique to a particular pressure, and as such the influence of confounding pressures also cannot be ruled out (Schuwirth et al., 2015).

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[1] This mixed level identification is referred to as TL5 by the Environment Agency.

[2] This family level identification is referred to as TL2 by the Environment Agency.