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Incorporating Traits in Aquatic Biomonitoring to Enhance Causal Diagnosis and Prediction

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ABSTRACT

The linkage of trait responses to stressor gradients promises to expand biomonitoring approaches beyond traditional taxonomic-based assessments that identify ecological effect, to providing a causal diagnosis. Traits-based information may have several advantages over taxonomic-based methods. These include providing mechanistic linkages of biotic responses to environmental condition, consistent descriptors or metrics across broad spatial scales, more seasonal stability compared with taxonomic measures, and seamless integration of traits-based analysis into assessment programs. A traits-based biomonitoring approach does not require a new biomonitoring framework because contemporary biomonitoring programs gather the basic site by species composition matrices required to link community data to the traits database. An impediment to the adoption of traits-based for biomonitoring relates to the availability, consistency, and applicability of existing trait data. For example, traits generalizations among taxa across biogeographical regions are rare and there is no consensus related to the required taxonomic resolution and methodology for traits assessment. Similarly, we must determine if traits form suites that are related to particular stressor effects, and whether there is significant variation of traits among allopatric populations. Finally, to realize the potential of traits-based approaches in biomonitoring, a concerted effort towards standardizing terminology is required with the establishment of data-interoperability infrastructures to ease the sharing and merging of broad, geographical trait information.

Key words: Traits, Biomonitoring, Bioassessment, Causal Diagnosis and Prediction

INTRODUCTION

Biomonitoring uses biota to assess the ecological condition of the environment and has traditionally incorporated the taxonomic composition of communities as an indicator of ecological change. Following this assessment process, samples are collected from potentially impacted and reference sites, identified and enumerated. Differences in taxonomic composition among samples are then compared quantitatively using various multivariate and metric approaches to infer the level of impairment (Fig 1). Here, species identity serves as a surrogate for the suite of attributes that a species possesses, with these attributes influenced by environmental conditions and evolutionary processes. An unstated assumption of this approach is that the presence of a species indicates that it possesses the traits necessary to cope with environmental conditions at a site (see Southwood 1977).

Alternatively, the traits of taxa present at a site can be used to indicate environmental conditions, and further, infer mechanisms by which the community composition is shaped. The use of traits to indicate causal mechanisms is possible because, after stressor exposure, traits distribution at the impacted site is predicted to shift relative to the reference site (Fig. 2, see Rubach et al, this issue, for linkage of traits to toxic effects). Thus, traits that impart resistance or resilience to the stressor are favored. This filtering of traits by environmental stressors may allow biomonitoring approaches to yield mechanistic understanding rather than our current ability to simply observe that ecological change has occurred. This novel approach allows improvement to the standard biomonitoring approach by linking the taxonomic data to the traits of the taxa identified. Differences in the traits of taxa in samples can then be used to generate additional metrics of the level of impairment, as well as for diagnosis of the causes of impairment (Fig 1).

In this paper we use traits as defined by McGill (2006), where traits are a measurable property of an organism, such as body size, longevity or feeding guild, usually measured in individuals and applied comparatively across species and at broad geographic scales. Our aim is to highlight how including traits within existing biomonitoring programs can improve assessment sensitivity and prediction, and provide insight into the mechanism causing that change. Specifically, our objectives are to:

1. Describe how traits have been previously used in biomonitoring;
2. Outline the benefits of traits-based approaches in biomonitoring;
3. Describe the challenges (opportunities and limitations) in implementing trait information into biomonitoring; and
4. Describe the availability, consistency, and applicability of existing trait data.

In addressing these objectives we focus on our experiences in stream biomonitoring applied to benthic macroinvertebrates because these systems have been the basis for significant conceptual development related to biomonitoring (Rosenberg & Resh 1994). However, a robust method for bioassessment should integrate multiple levels of biological organisation, so where appropriate, we provide examples and references to other biological groups and ecosystems to demonstrate the broader applicability of these ideas.

A BRIEF HISTORY OF TRAITS IN BIOMONITORING

The use of trait information in biomonitoring is not new. Attributes of the biota collected have long been used, usually *post hoc*, to explain patterns in biomonitoring metrics (e.g., the absence of filter feeding organisms following sedimentation of aquatic habitats). However, this application of traits information has not been articulated as a traits-based approach, but has been *ad hoc,* and often dependent on the biological knowledge of the analyst. There is a need to formalise the use of traits in biomonitoring, which will provide guidance to all users, and add greater sensitivity and diagnostic power for biomonitoring programs (see below).

The concept of biomonitoring in rivers is attributed to Kolkwitz and Marsson (1909), who's Saprobien System assessed organic contamination in German rivers. Observations of taxa restricted to polluted or unpolluted locations led to the classification of taxa based on the empirically defined trait of pollution sensitivity, thereby providing the first trait-based assessment of stream condition. The Saprobien System *per se* is no longer widely used (but see Friedrich 1990), but the notion of organism tolerance to assess environmental condition underpins many current biomonitoring methodologies.

As the science of biomonitoring evolved, a shift in ecological thinking toward equilibrium theory and diversity saw diversity indices (e.g., Shannon and Weaver 1949, Margalef 1958, Cairns and Dickson 1971) emerging as a tool for ecosystem assessment (Hellawell 1986). More recently, indices combining the Saprobien style, 'tolerance' of taxa and the abundance and diversity of those taxa, have emerged. This began with the Trent biotic index (Woodiwiss 1960) for macroinvertebrates in the UK, with similar indices subsequently developed for broader application in the UK (e.g., BMWP score, Armitage et al. 1983), North America (e.g., Hilsenhoff's index, Hilsenhoff 1987; 1988), Australia (e.g., SIGNAL Index, Chessman 1995; 2003), and elsewhere, and for other taxonomic groups (e.g., Protozoa, Jiang 2006; Diatoms, Kelly and Whitton 1995). Like the earlier Saprobien System, these newer indices are principally based on the trait of taxa sensitivity or tolerance to particular stressors.

Growing interest in environmental assessment, combined with increasing computational capacity led to the emergence of multimetric, and multivariate predictive models for bioassessment. The development and formalisation of multimetric approaches for fish (IBI, Karr 1981), and macroinvertebrates (RBP, Plafkin et al. 1989) encouraged the development of ‘non-taxonomic’ trait-based metrics, particularly those relating to functional, trophic or ecological characteristics of the biota (such as feeding guild or life history). In contrast, most multivariate models that predict a reference condition from environmental variables assess impairment through metrics derived from the taxonomic composition of assemblages (e.g., RIVPACS, Wright et al. 1993; AUSRIVAS, Simpson and Norris 2000). Although these methods remain focussed on taxonomic composition of assemblages, they provide a simple platform for the inclusion of trait information, allowing comparisons of traits between predicted and observed assemblages.

Recognizing the influence of environmental conditions on the selection and expression organism traits (Southwood 1977; Townsend and Hildrew 1994; Poff 1997) lead to the definition of a wider array of morphological, ecological and life history traits. Research by Statzner and his collegues (Doledec et al. 1994; Doledec et al. 1999; Statzner et al. 200l) has explored the relationships among this more diverse set of macroinvertebrate trait data and properties of stream systems at various spatial and temporal scales. This work provides ecological background and support for the adoption of trait information for biomonitoring, however, it has not been widely applied directly to biomonitoring applications.

The development of the SPEAR method (Liess and Von der Ohe 2005) represents a significant development in traits-based biomonitoring. The method, and its subsequent iterations (e.g., Beketov et al. 2009), incorporate various traits of macroinvertebrate taxa, such as sensitivity to toxicants, generation time, migration ability, and presence of aquatic stages to produce a metric of the proportion of ‘species at risk’ at a test site (Liess and Von der Ohe 2005).

This metric is compared to that derived at a reference site. The SPEAR method has the benefit of being underpinned by reasonably detailed toxicity databases (see below), which has allowed it to be applied to a range of stressors, and consequently to have stressor specificity. Although the database on the trait of toxicant sensitivity is relatively well developed (at least for some toxicants and taxa), data on life history or ecological traits is less so and represents a major challenge to the development of traits-based biomonitoring (see below).

BENEFITS OF USING TRAITS IN BIOMONITORING

The linkage of trait responses to stressor gradients promises to expand biomonitoring approaches beyond traditional taxonomic-based assessments that identify ecological effect, to causal diagnosis assessments. Research to develop an empirical framework for such diagnoses is underway, and already suggests that traits-based information may have several advantages over taxonomic-based methods. These advantages include 1) the ability to provide mechanistic linkages of biotic responses to environmental condition and improve sensitivity, 2) consistent descriptors or metrics across broad spatial scales, 3) more seasonal and interannual stability compared with taxonomic measures, 4) the ability to seamlessly integrate traits-based analysis into current assessment programs, and 5) greater utility of biomonitoring outputs in ecological risk assessment (see Van den brink et al, this issue)

Traits-based approaches can provide mechanistic linkages between biotic patterns and environmental condition, and in so doing, improve the sensitivity of bioassessments. Greater sensitivity is achieved because an assemblage’s trait composition may demonstrate a substantive change before its taxonomic composition does (for example, sublethal changes; shifts in body size, age structure or reproduction that occur without or prior to a loss of taxa). A corollary is that traits-based bioassessments may be able to detect changes in ecological condition at mildly impacted sites that taxonomic-based assessments miss. This hypothesis is all the more reasonable given that traits can be more strongly related to differences in land use (Dolédec et al. 2006) and other human related disturbances than is taxonomy (Dolédec et al. 1999). Furthermore, taxonomic-based bioassessments of ecosystems exposed to different human activities often result in similar expressions of ecological condition (Carlisle and Hawkins 2008). In these cases the mechanistic link between traits and stressors may be useful for further interpretation of assessment results and provide insight regarding the causes of impairment (Fig. 1). Further refinement of trait characterization may be required, however, before traits can be linked to stressors in a causal manner (Carlisle and Hawkins 2008).

Additionally, traits-based approaches may further enhance biomonitoring by increasing the spatial applicability of reference conditions relative to taxonomic methods. This is possible because traits composition can exhibit stability across large spatial areas such as ecoregions (Charvet et al. 2000; Statzner et al. 2005). Similarly, biological traits appear to be more stable among seasons than taxonomic composition (Bêche et al. 2006), a quality that could potentially reduce biomonitoring sampling effort. Biological traits are expected to be more stable than taxonomic composition among years, although this hypothesis remains largely untested.

Finally, a traits-based biomonitoring approach does not require the formulation of a new biomonitoring framework but rather, traits-based approaches can be integrated into current assessment programs without additional data collection or sampling effort. This is because contemporary biomonitoring programs, using standard sampling and analytical protocols, gather the basic site by species composition matrices required to link community data to the traits database, and existing databases may provide the trait information needed (Fig. 1). As a result, current study designs, sampling protocols and laboratory procedures can still be used and perhaps, because of the wider geographical consistency of traits, more widely applied. Current reference condition models can also be used as both multimetric and multivariate methods can readily incorporate traits-based information (e.g., Carlisle and Hawkins 2008). Indeed, the only addition to the framework prior to the analysis stage is the linking of the observed taxa to a database of taxa with their traits (Fig. 1), a step that is already a part of some aquatic biomonitoring programs that include tolerance or functional group indices (e.g., Plafkin et al 1989; Schmidt-Kloiber et al. 2006). Thus, because of the above characteristics, traits have the potential to be a more powerful and sensitive biomonitoring tool than taxonomic composition in all instances excepting programs aimed at conserving biodiversity.

CHALLENGES OF INCORPORATING TRAIT INFORMATION INTO BIOMONITORING

Incorporating trait information into the existing biomonitoring framework offers several advantages as discussed, but broad application of this approach is limited by several challenges (see also Van den Brink et al, this issue). These challenges reflect the character of trait data, including taxonomic and trait resolution, trait measurement, population variation of traits and correlation among traits. In addition, we have little knowledge of how combinations of traits may link in suites related to particular stressor effects.

Relationship of taxonomic and trait resolution

Biomonitoring programs commonly use family (e.g., Hilsenhoff 1988, Metzeling and Miller 2001, Reynoldson et al. 2001) or genus level taxonomic resolution (e.g., Carter and Resh 2001, Jones 2008), and by extension, traits-based approaches should match this resolution.

However, some argue that species level data may better detect ecological patterns and perturbations (Carter and Resh 2001, Lenat and Resh 2001, Jones 2008). Thus, the decision to include lower taxonomic identification and more detailed trait information in biomonitoring presents a particularly difficult decision for practitioners. For example, increased effort and financial resources are often required to improve taxonomic resolution in biomonitoring programs (Bailey et al. 2001, Jones 2008), especially in areas where there is limited regional taxonomic knowledge. Even if species level identification can be reasonably obtained, the corresponding basic biological information from which to derive traits data is often lacking, especially for some types of traits (e.g., physiological). This issue may not be a large concern for biomonitoring given that Gayraud et al. (2003) concluded that genus, and perhaps family, identifications for invertebrates may be adequate for traits-based approaches in river biomonitoring. It remains to be shown whether this trend holds for other taxonomic groups and aquatic ecosystems. Nevertheless, we anticipate that increased traits resolution will improve the ability to detect a response to an environmental driver up to a threshold where higher resolution results in reduced ability to detect ecological pattern. A related decision is whether to include or omit rare-taxa traits. In this case, the solution will likely mirror the well-developed arguments for the use of rare species in bioassessment (e.g., Cao et al. 1998, Marchant. 1999, Marchant 2002). Parenthetically, this decision may be less critical for traits-based analyses if traits composition is more temporally and spatially stable than taxonomy-based analyses (Charvet et al. 2000; Statzner et al. 2005).

Trait representation and measurement

Biomonitoring programs may not only differ with respect to taxonomic resolution but also in the number of taxonomic groups they consider (Carter and Resh 2001). For traits-based approaches to be effectively incorporated into monitoring programs, the effect of taxonomic bias toward a subset of taxa, such as known sensitive (e.g., Ephemeroptera, Plecoptera and Trichoptera) or easily identifiable taxa, must be understood. The use of a narrow range of taxa for biomonitoring could also limit the suite of traits available for identifying the type and level of environmental impact. It is important then that biomonitoring programs incorporate adequate taxonomic diversity in order to provide the trait diversity to make a traits-based approach effective. However, only a small range of traits may be needed for targeted monitoring.

Biomonitoring practitioners must also determine the way in which traits are quantified, e.g., on a categorical or continuous scale, with some traits being naturally categorical (e.g., foraging mode) and others continuous but coded as categorical (e.g., body size). Given the coarse nature of biomonitoring data, categorical trait data may be adequate for environmental assessment (e.g., see Dolédec et al. 1999, Bonada et al. 2006). A particular trait can often be measured in a number of ways, especially across taxonomic groups, and it is important that particular traits are measured consistently. For example, several conventions can be applied to the determination of body size for many organisms, including length, mass and volume. By determining the appropriate means of quantifying particular traits, we anticipate an improvement in causal diagnostic power of traits-based assessment. Finally, a detailed definition of each trait and its related modalities must be provided with metadata detailing how the information was classified and measured so trait data can be consistently added for new taxa (Baird et al. this issue).

Trait correlations and combinations

The range of traits that can be selected for inclusion in a biomonitoring program depend on the type and amount of trait information available (see above). However, in the selection of particular traits, it is important to recognize that many traits are not independent, i.e., they are correlated to each other (Resh et al. 1994, Poff et al. 2006). For example, long adult lifespan is correlated with semi-voltinism in lotic insects and flow preferences are correlated to several traits including body shape, armouring and attachment (see Poff et al. 2006). Trait correlations often reflect phylogenetic relationships between taxa, representing their shared evolutionary history (Blomberg et al. 2003, Buchwalter et al. 2008). Trait correlations can complicate the nature of environment-trait relationships when strong environmental selection for one trait causes other, linked traits to also respond (Poff et al. 2006).

Correlated traits may confuse inference in the trait-stressor relationship of interest to the biomonitoring program, and this can be magnified in multi-stressor conditions. We need better information on the relative sensitivity of individual and correlated traits to different stressors. In some cases, correlated traits may simply be redundant and not add to the overall information gained from using only selected traits (Poff et al. 2006). Conversely, recognition of phylogenetically correlated traits may provide a way to derive traits for understudied taxa and thus allow identification of groups of taxa that respond in a similar way to a particular stressor (Buchwalter et al. 2008). Information on trait correlations is currently available for some datasets, (lotic insects, Poff et al. 2006), but for other taxonomic groups and habitat types this information may not yet be available.

The inter-correlation among traits (with phylogenetic signature) means there are a limited number of possible trait combinations (or syndromes; Poff et al. 2006, Horrigan and Baird 2008) that actually exist in nature. This raises the possibility that the suite of traits possessed by an organism could be used to examine response to environmental stressors as an alternative to traits examined individually, depending on the stressor and environmental management goals (i.e. life history strategies; Verberk et al. 2008a, b). In this way, the multivariate character of the trait response may also be matched by the multivariate nature of the environmental stressors.

Population variation in traits

Traits currently available and used in a biomonitoring context are frequently treated as static values, in that they do not allow for potentially important variation displayed by a population (Brown 1995, Jones et al. 2009). The variability/range of trait values within a population at a site may differ from that of populations of the same organism at different locations, possibly confounding the inferences that can be made from assigning all of a particular taxon to a fixed set of traits. Population variation may be the result of phenotypic plasticity, a genotypic response to the environment, or ontogeny (Sagnes et al 2008, Petchey et al. 2004). A clear example may be if populations are asynchronous, leading to differences in developmental stages in populations at different locations. The various sources of population variation may act disproportionately on selected traits which may result in some traits possessing more variation than others (see Blanck and Lamouroux 2007). The variation of traits within a population is an important evolutionary mechanism to allow organisms to cope with environmental change. As a result, population variation may occur in widely distributed species as a result of geographical shifts in ecological preferences (Buffagni et al., 2009) and as well for invasive species.

Ontogeny is an important source of population variation, especially for some invertebrate groups that possess different developmental pathways. Larval stages may differ in their life history characteristics and can even change from one larval stage to another (Sagnes et al. 2008). In freshwater biomonitoring, which typically uses insects and other invertebrates as metrics, traits are usually applied on the basis of the mature larval stages because taxonomic knowledge is in most cases also restricted to identification of mature larvae (see above; Merritt et al. 2008).

Some traits show clear ontogenetic change (e.g., predaceous insects are often detritivores as early instars), and failure to capture this detail can potentially limit trait applications, particularly if early life stages are disproportionately sensitive to a particular environmental stressor. However, this could be considered a limitation of taxonomy as well, since all organisms with the same taxonomic identity are generally assumed to possess the same characteristics, sometimes coarsely designated into adult versus immature categories, for example adult and larval stages of aquatic Coleoptera. Similarly, population variation could arise from sexual dimorphism and species showing multiple trait states depending on life cycle stages (e.g., sexual and asexual reproduction).

A better understanding of the sources and extent of trait variation as well as its importance for defining sensitivity to environmental stressors should lead to improved trait-based inferences. In some cases, however, variation in particular traits may even be useful or diagnostic of particular environmental stressors (Hodkinson and Jackson 2005). For example, morphological variation and certain life history characteristics have been used to detect stressors such as chemical contamination (Lenat et al. 1993) and thermal shifts (Hogg and Williams 1996).

Trait-environmental linkage

Few traits were initially described with the intention of representing a clear mechanistic linkage or response to environmental stressors (Poff et al. 2006). In fact, some traits exist simply as a result of the types of information available for particular taxa (Statzner et al. 2004). Yet, a clear mechanistic linkage between environmental gradient and biological traits has been demonstrated for the primary biological elements used for biomonitoring: benthic invertebrates (e.g., Pollard and Yuan 2009), fish (e.g., Lamoroux et al. 2002), macrophytes (e.g., Thiebaut et al. 2002) and phytoplankton (e.g., Litchman et al. 2007).

Where a mechanistic linkage between traits and environmental stressors can be established the relationship can often be complex. Some traits might respond to multiple features of the environment. For instance, several authors have provided mechanistic explanation of morphological traits in stream invertebrates as an adaptation to flow (e.g., Hynes 1970; Dolédec *et al*. 2007). However, Horrigan and Baird (2008) demonstrated that in a multi-stressor environment, selected trait modalities were influenced exclusively by changes in flow conditions and were not responsive to thermal and oxygen stress while other traits were simultaneously responsive to the multiple stressors, and consequently had reduced diagnostic power. Similarly, life cycle strategies can provide an useful indicator of community condition, but their diagnostic power is limited because many taxa alter their life cycle in response to a multitude of stressing conditions (e.g., Füreder et al. 2007; Diaz et al. 2008, Richards et al. 1997, Doledec et al. 2006). Identifying stressor-specific traits (i.e., trait suites) based on the understanding of the causal relationship between trait occurrence and stressor level should be the focus of next generation traits developments.

AVAILABILITY, CONSISTENCY AND APPLICABILITY OF TRAITS DATA

Traits-based approaches require the association of taxa and their traits (Fig. 1), which usually requires the development of new databases or compilation of existing ones. Traits information is available for a variety of traits and taxonomic groups through published and online data, or it can be obtained from publishing authors. Table 2 provides a range of examples that illustrate the variety of available databases, traits and approaches, and the variability of geographical and taxonomic coverage. We restrict our reporting to: (1) trait databases that minimally apply to ecoregions, with the caveat that many other databases can be found for smaller geographical areas; and (2) trait databases which are of potential use in biomonitoring.

Consistency of trait description and classification is critical if the full potential of traits-based approaches is to be realised. Such consistency begins with a conceptual framework of trait definitions that are valid across different taxonomic groups and ecosystems. Unfortunately, such frameworks are still evolving for individual taxonomic groups, and traits generalizations among taxa across biogeographical regions are rare except for a limited number of traits (e.g., body size, basal metabolic rate, life duration). For biomonitoring purposes, consistency must be achieved for the taxonomic group and resolution at which the assessment is undertaken. Here, consistency refers to the (1) applicability of trait modalities to all taxa, for example some physiological traits may not be compatible across higher taxonomic groups with very different physiologies, and (2) adequate knowledge of traits differences related to taxonomic resolution (e.g., trait states of insect families and genera similar and well described).

A first step towards building such a global trait description for species is the use of a standard nomenclature. Although there are no established requirements and protocol for a nomenclature database source, a taxonomic basis is essential. Future database development will likely include molecular markers as these may be a useful foundation from which to reference existing traits information (see Baird et al, this issue). Similarly, there are no specific requirements to create a comprehensive trait and environmental database as advocated by Statzner et al. (2007), but efforts should be oriented towards developing data inter-operability standards (see Baird et al, this issue).

Several studies have grouped traits into broad categories such as life history, mobility, morphology and ecology (e.g., Lamouroux et al. 2002, Poff et al. 2006; Litchman and Klausmeier 2008; Stevenson et al., 2008), but a common categorization and vocabulary is lacking. A point in case is the broad list of traits categorized as “ecological” by several authors. For example, the set of traits used by Poff et al. (2006) includes four trait categories: life history, mobility, morphology and ecology. This last category includes traits for both habitat preference and behaviour (e.g., locomotion types). Carlisle and Hawkins (2008) similarly use the category of ‘ecological traits’ to include the functional attributes as defined by Poff et al. (2006), and stressor tolerance values (i.e., requirements for specific environmental parameters). The use of ecological requirement for environmental conditions is considered a trait by several authors (e.g., Poff et al. 2006; Stevenson et al. 2008; Buffagni et al., 2009), despite these preferences potentially being driven by multiple biological traits. In order for traits-based approaches to develop more fully, a concerted effort towards standardizing terminology and a theoretical framework is urgently required. Such developments are fundamental to producing a shared ontology and establishing broad geographical trait databases.

Finally, a number of analytical methods have been used in the study of traits. These may be for the definition of the traits themselves, exploration of the relationships amongst traits, the definition or calibration of trait-environment relationships, and their subsequent validation. Statistical methods used include correlation (Horrigan and Baird 2008), regression (Cowlishaw et al. 2009), ordination (Dray and Legendre 2008), and cluster analysis (Poff et al. 2006). Unfortunately, univariate correlations do not result in the direct production of a model, and are unable to disentangle multiple stressor-trait relationships, especially where traits interact. Consequently, they may have limited applicability in establishing linkages between traits and environmental conditions. Regression and multivariate (ordination, clustering) approaches have been widely used in traits analysis, with a key difference being that regression models usually consider traits as explanatory variables, while the multivariate models treat traits as response variables. This distinction can be important when turning relationships into indices and management objectives.

CONCLUSIONS AND SUMMARY

Trait information has long been used in biomonitoring programs, but its full potential is yet to be realized. Traits-based approaches have the potential to expand the outputs of biomonitoring programs from the identification of impact to include a causal diagnosis. Importantly, this can be achieved with little change to existing monitoring programs, except the linking of the observed taxa to a database of taxa with their traits. Traits-based approaches have a number of desirable attributes, such as greater stability of assessment outcomes and broader applicability of reference conditions, which are likely to broaden their range of application and increase their sensitivity. Indeed, we have outlined many of the benefits that traits-based biomonitoring can provide such as the potential to develop consistent descriptors or metrics across broad spatial scales. However, there a number of challenges to be met for the full potential of traits-based approaches to be realized, central to which, is the establishment of effective and accessible trait databases (see Baird et al, this issue). While some databases already exist, their remains a paucity of traits data for many taxonomic groups and many types of traits, which is a clear and immediate research need. A concerted effort towards standardizing terminology is required with the establishment of data-interoperability infrastructures to ease the sharing and merging of broad, geographical trait information. Research effort also need to determine whether generalizations can be made among taxa and across biogeographical regions, and on producing a consensus on the required taxonomic resolution and methodology for traits assessment. Clearly, there have been already a number of promising developments in traits-based biomonitoring approaches. It is our hope that the discussion provided here will be the stimulus for many more.

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Table 1. Selected freshwater examples for algae, aquatic plants, zooplankton, benthic invertebrates and fish that demonstrate trait-stressor linkages to several common environmental stressors.

Taxa Group	**Stressor**	**Trait**	**Trait-Stressor Linkage**	**Reference**
Algae	Nutrients	Cell size	Cell size varies with trophic status	Seip and Reynolds (1995)
	Water movement	Development Rate	Faster cell division in moving water	Reynolds (1994)
Aquatic Plants	Nutrients	Growth rate	Species with highest relative growth rate most sensitive to nutrient stress	Shipley and Keddy (1988)
	Flood disturbance	Vegetative dispersal	Type of vegetative reproduction affects re-colonization rate	Henry et al. (1996)
Zooplankton	Predation	Diapause stage	Copepods enter diapause to avoid fish	Hairston and Walton (1986)
	Predation	Body size	Zooplankton size decreases in presence of predators	Brooks and Dodson (1965)
Benthic Invertebrates	Deposited sediments	Clinger habit	Decreased abundance with increased sediment	Pollard and Yuan (2009)
	Channel reconfiguration	Mobility and development	Higher mobility and more rapid development with channel disturbance	Tullos et al. (2009)
Fish	Hydrologic Variability	Body shape	Abundance of deep-bodied fish increases with greater hydrological stability	Poff and Allan (1995)
	Habitat	Invertivores	Decreased abundance with reduced habitat quality	Goldstein and Meador (2005)

Table 2. Examples of trait databases for freshwater, marine and selected terrestrial habitats summarized for different taxonomic groups. Information for each database is provided for level of taxonomic resolution, method of coding, format in which the information is distributed and a brief description of key aspects of the database. Data not available are indicated by (na).

Habitat	**Group**	**Taxonomic resolution**	**Coding method**	**Distribution Format**	**Description of key aspects of database**	**Examples**
Stream and river	Macroinvertebrates	Variable	Fuzzy	Spreadsheet	European coverage	Tachet et al. (2002); Usseglio-Polatera et al. (2000); Statzner et al. (2007)
	Macroinvertebrates, fish, diatoms	Species	Binary or ten point assignment	Web database	Variable European and taxonomic coverage	Eurolimpacs consortium (2008)
	Macroinvertebrates	Genus	Fuzzy or binary	Spreadsheet	North American lotic insect focus	Vieira et al. (2004); Poff et al. (2006)
	Fish	Species	Binary	Spreadsheet	North American and European coverage limited to six traits	Lamouroux et al. 2002
Freshwater and marine	Phytoplankton	Na	na	na	Defines a structural framework for work in progress	Litchman and Klausmeier (2008)
	Phytoplankton	Genus/ Species	Descriptive data	na	Traits-separated for freshwater functional groups	Reynolds (2002)
	Fish	Species	Descriptive data	Web database	Well-established web-based database	http://www.fishbase.org
Freshwater-terrestrial ecotone	Riparian plants	Na	na	na	Conceptual approach focused on monitoring and management	Merritt et al. (2009)

Terrestrial	Primates	Species	Quantitative variables	Spreadsheet	Global coverage	Cowlishaw et al. (2009)
	Lepidoptera	Species	Binary and quantitative variables	na	Global coverage limited to two families only.	Garcia-Barros (2008)
	Lepidoptera	Species	Quantitative variables	na	Feeding habits of UK butterflies	Hardy et al. (2007)
Multiple habitats	Frogs	Species	Quantitative and qualitative variables	Spreadsheet	Life-history and ecological traits of Australian frog fauna	Murray and Hose (2005a, 2005b)
	Plants	Species	Quantitative variables	Web database	Well-established web-based database	http://www.try-db.org
	Mammals	Species	Quantitative variables	Spreadsheet and web database	Global coverage	http://lynx.ncl.ac.uk/utheria/; Jones et al. (2009)

LIST OF FIGURES:

Figure 1. Traditional taxonomic-based bioassessment approaches involve collecting samples from potentially impacted and reference sites, identifying the organisms in those samples, and deriving a metric from the differences in the compositions. Linking traits databases to the taxonomic data allows comparison of reference and impacted sites on the basis of the traits of organisms in those samples. This not only provides additional metrics of the level of impairment, but can also allow diagnosis of impairment cause.

Figure 2. Conceptual diagram that compares the frequency distribution of species traits at a reference and test site. After exposure to a stressor, traits at the test site are modified, or filtered, such that traits that impart resistance or resilience to the stressor are favored. This results in a shift in the frequency distribution of species traits at the test site relative to the reference distribution.

Figure 1.

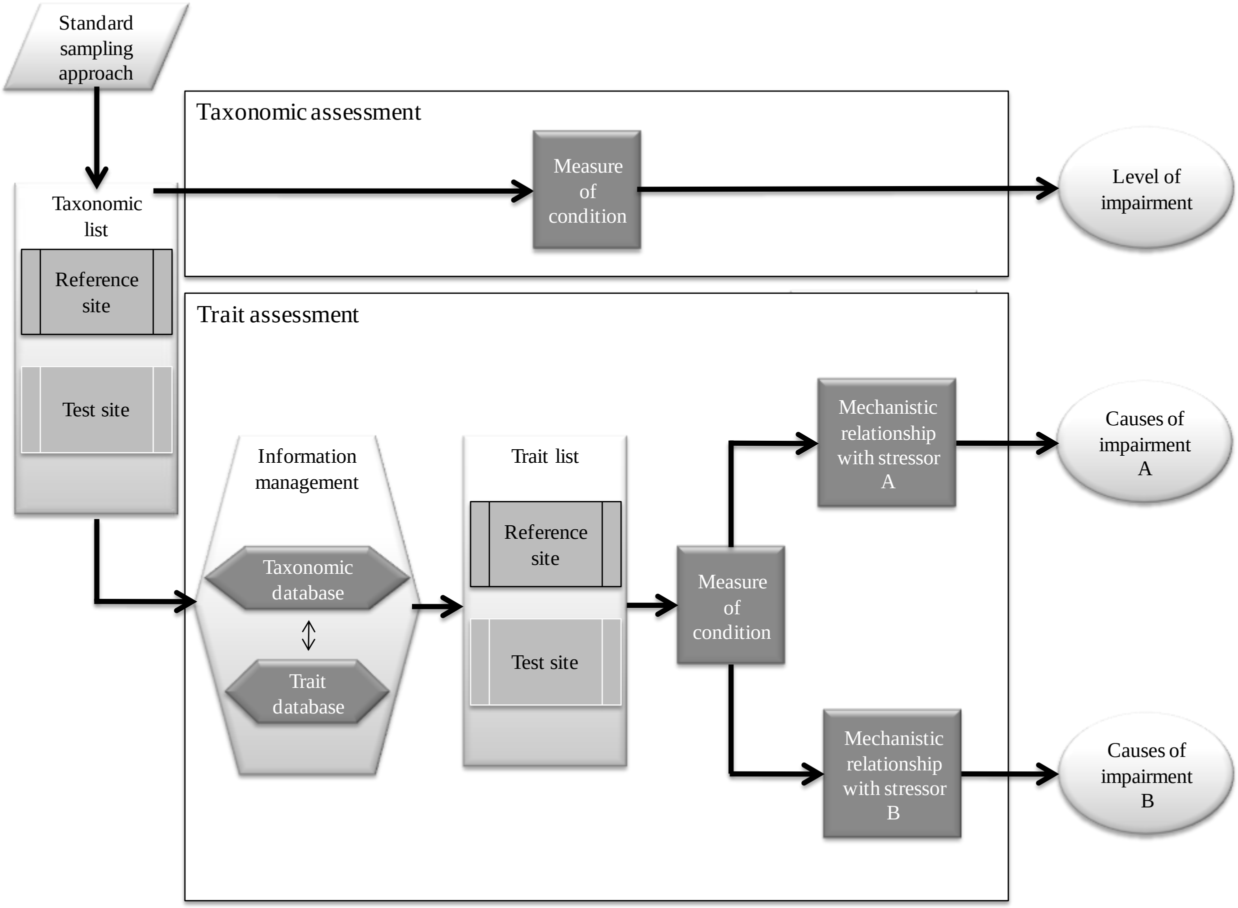
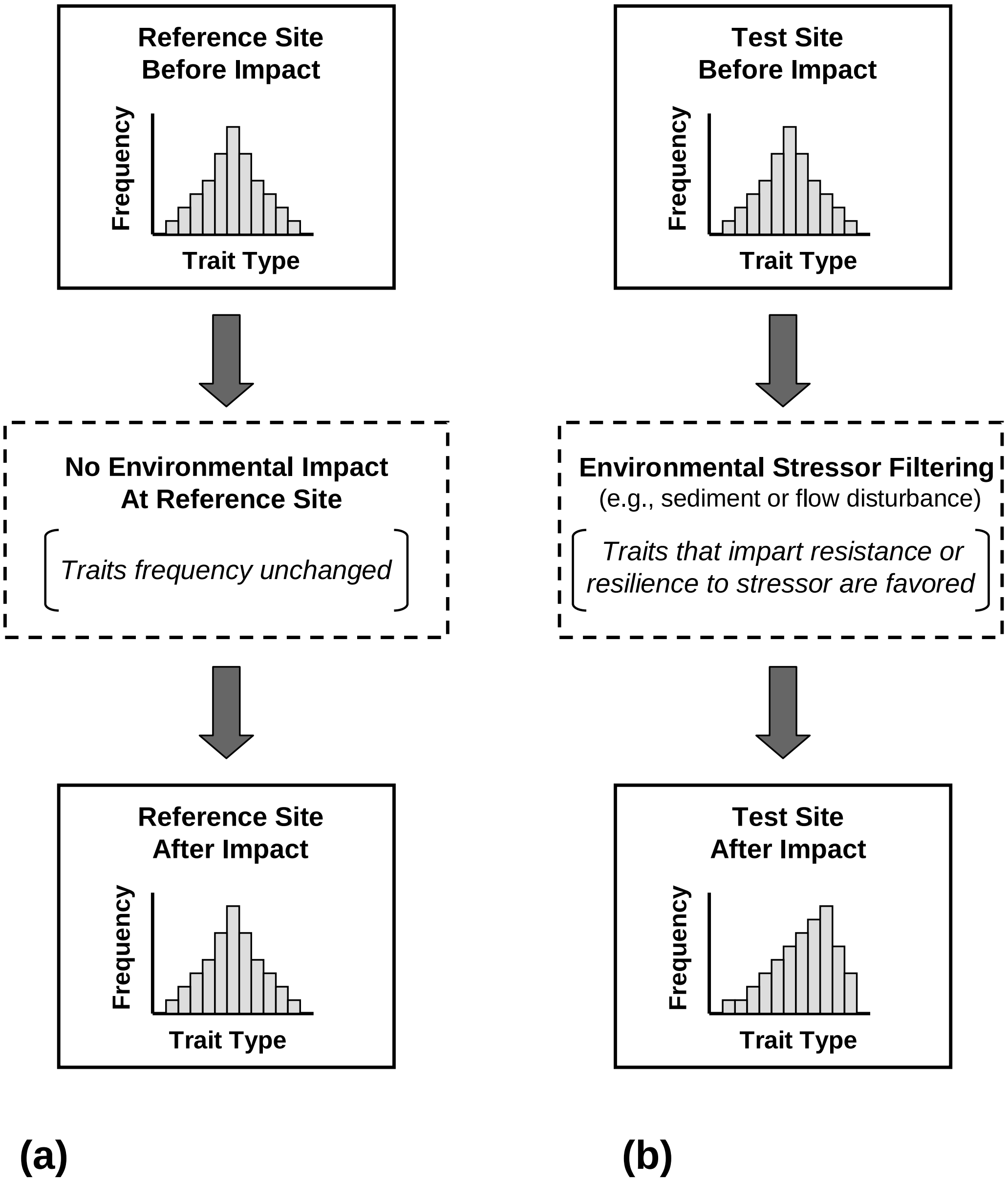

Standard sampling approach
Taxonomic assessment
Taxonomic list
Reference site
Test site
Measure of condition
Level of impairment
Trait assessment
Information management
Taxonomic database
Trait database
Trait list
Reference site
Test site
Measure of condition
Mechanistic relationship with stressor A
Causes of impairment A
Mechanistic relationship with stressor B
Causes of impairment B

Figure 2.


Reference Site
Before Impact
Frequency
Trait Type
No Environmental Impact
At Reference Site
Traits frequency unchanged
Reference Site
After Impact
Frequency
Trait Type
(a)
Test Site
Before Impact
Frequency
Trait Type
Environmental Stressor Filtering
(e.g., sediment or flow disturbance)
Traits that impart resistance or
resilience to stressor are favored
Test Site
After Impact
Frequency
Trait Type
(b)