Freshwater mussel abundance predicts biodiversity in UK lowland rivers

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ABSTRACT

1. Indicator taxa are widely used as a valuable tool in the assessment of freshwater biodiversity. However, this approach to identifying sites of conservation priority requires surveyors to possess expert taxonomic knowledge. Furthermore, sorting and microscopic examination of material can present logistical and financial constraints.

2. Comparisons were made between the taxon richness and the density of freshwater mussels (Bivalvia: Unionidae) from 30 sites in seven UK lowland rivers, ranging from *ca* 3 m to 50 m width and *ca* 0.5 m to 4 m depth. Where mussels occurred, taxon richness of other invertebrates was strongly correlated with both mussel density and mussel biomass. Overall mussel density was a better predictor of taxon richness than the density of any individual mussel species.

3. It is suggested that this association arises from the 'keystone' role that mussels play in many freshwater ecosystems. Local biota can benefit from the mussels' filtration, excretion, biodeposition and physical presence.

4. Using mussel abundance as a surrogate provides a rapid and straightforward alternative to conventional methods of assessing freshwater biodiversity. No expert knowledge is required and any standardized sampling technique can be used. Freshwater mussels are found throughout the world's lentic and lotic fresh waters and this approach therefore has the potential for widespread utility, especially where rapid comparisons of biodiversity are required between biogeographically similar regions. In addition, the results highlight the ecosystem-level consequences of allowing the global decline of freshwater mussels to remain unchecked.
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INTRODUCTION

The limited resources available to most conservation organizations has led to the widespread use of indicator taxa as a means of identifying sites of conservation priority. By successfully conserving a large proportion of the indicator taxa, it is hoped that a large proportion of the local biodiversity also can be protected. There has been considerable discussion on how best to select indicator taxa for different habitats (e.g. Noss, 1990; Pearson, 1994). Important criteria include choosing organisms that are readily surveyed and broadly distributed. It is also essential that there is some evidence that patterns observed in the indicator taxon are reflected in other unrelated taxa (Pearson, 1994).

The greatest use of indicator taxa has been in terrestrial ecosystems, especially tropical regions where patterns of species richness are poorly known (e.g. Kremen *et al.*, 1998; Rolstad *et al.*, 2002; Basset *et al.*, 2004). In freshwater ecosystems, macroinvertebrate indicator taxa are widely used to assess the quality and pollution status of a water body (Reynoldson, 1984). Benthic invertebrates are particularly favoured because they are relatively sedentary and therefore representative of local conditions (Cook, 1976). While numerous biotic indices and score systems have been developed to assess overall water quality and conservation status based on the suite of invertebrate taxa present (e.g. Biological Monitoring Working Party (BMWP) score, ISO, 1984; System for Evaluating Rivers for Conservation (SERCON), Boon *et al.*, 1997; Chadd and Extence, 2004), little effort has been made to identify a single taxon useful to predict overall freshwater biodiversity.

Suggested single indicator taxa for fresh waters include the Odonata (Davis *et al.*, 1987; Sahlen and Ekstubbe, 2001; Briers and Biggs, 2003), Coleoptera (Foster *et al.*, 1989) and the Limnephilidae (Trichoptera) (Briers and Biggs, 2003). However, biodiversity assessment using this approach still requires expert knowledge to identify the specimens at least to the family level. In addition, samples must often be sorted, preserved and assessed with a microscope, which may present logistical and financial problems. Furthermore, the taxonomy of aquatic invertebrates in many areas of conservation interest may be poorly known.

An ideal indicator taxon would be one whose abundance strongly correlates with overall taxon richness. By using a standardized sampling procedure to assess the bioindicator's relative abundance among sites, biodiversity 'hotspots' could be identified rapidly without the need for any expert taxonomic knowledge or microscopic examination. A 'keystone taxon' meets these criteria; elimination or reduction in abundance of such a taxon from the ecosystem could cause a significant fraction of the species in the ecosystem to be extirpated (Jain and Krishna, 2002).

This study tested the abundance of freshwater mussels (Bivalvia: Unionidae) in UK lowland rivers as a tool for rapid biodiversity assessment. Freshwater mussels are the dominant filter feeders in many of the world's lakes and rivers, and are widely considered to be a 'keystone taxon' (MacIsaac, 1996; Vaughn and Hakenkamp, 2001; Gutiérrez *et al.*, 2003). In the River Thames, UK, unionid mussels comprise >90% of the benthic biomass (Negus, 1966). They can directly affect nutrient dynamics in freshwater systems through excretion as well as biodeposition of faeces and pseudofaeces (mucus-bound material that is ejected without ingestion). Mussels can directly impact benthic processes as they burrow through sediments, and the physical presence of their shells creates habitats for epiphytic and epizoic organisms, and refugia for benthic fauna (Vaughn and Hakenkamp, 2001; Gutiérrez *et al.*, 2003). A single unionid mussel can filter about 40 L of water per day (Tankersley and Dimock, 1993); such filtering helps to maintain water clarity and encourages establishment of macrophytes (Phelps, 1994). The 'keystone' role that freshwater mussels can play is exemplified by the shifts observed in freshwater communities following the establishment of non-native filter feeders such as the invasive Asian clam (*Corbicula fluminea*) and zebra mussel (*Dreissena polymorpha*) (Phelps, 1994; MacIsaac, 1996). Furthermore, Horvath *et al.* (1999) and Mayer *et al.* (2002) found that the presence of zebra mussels on artificial substrates locally increased macroinvertebrate abundance.

METHODS

Study sites

Data were collected during July 2002 from 30 sites in seven rivers in the counties of Cambridgeshire and Somerset, UK. The sites ranged from a width of *ca* 3 m to 50 m and a maximum depth of *ca* 0.5 m to 4 m. The rivers chosen were representative of lowland rivers across much of the UK, with a relatively sluggish summertime flow, silty benthos and macrophytic vegetation dominated by *Phragmites communis*, *Glyceria maxima*, *Nuphar lutea* and *Sparganium* spp.

Invertebrate sampling

At each site a standard 1-min sample was collected 1 to 3 m from the bank using a standard square-framed Freshwater Biological Association net (frame width 25 cm, mesh size 250 μm). Preliminary surveys had revealed that most taxa had been collected by 1 min and that macroinvertebrates were most abundant at 1 to 3 m from the bank. All available habitats were sampled in proportion to their occurrence following the protocol of Furse *et al.* (1981). All taxa were identified to the lowest level possible, i.e. recognizable taxonomic units (RTUs); for most taxa this was to the family level. The use of RTUs as a measure of richness is widely accepted (e.g. Oliver and Beattie, 1993; Altaba, 1996; Krell, 2004).

Mussel sampling

The freshwater mussel populations were surveyed at each site using 0.5×0.5 m quadrats. The number of quadrats needed to provide an acceptable estimate of mussel abundance at each site was determined by preliminary surveys. Hand sampling was carried out within 15 randomly placed quadrats positioned 1–3 m from the bank at each of four UK lowland rivers (River Nene and Old West River (Cambridgeshire), River Brue and South Drain (Somerset)). The quadrats were subdivided into 25 sectors, which were systematically searched by hand to ensure that all large mussels were collected. The appropriate number of quadrats was calculated according to the method of Elliott (1971), by identifying the number of replicates necessary for the coefficient of variation (the ratio of the standard error to arithmetic mean) to be $\leqslant 0.2$ (a reasonable error in most benthic samples; Elliott, 1971).

At each of the 30 study sites eight random quadrats, placed 1–3 m from the bank, were sampled by hand. Mussels were identified to species, measured along their longest axis with Vernier callipers and returned to the river at the point of collection. The mussel biomass m^{-2} at each site was estimated from conversion factors derived from Müller (2003) (wet mass of Anodontinae $= 0.0003 \cdot (\mathrm{Length})^{2.714}$; Unioninae $= 0.0004 \cdot (\mathrm{Length})^{2.631}$).

RESULTS

Mussels were relatively homogeneously dispersed within 1–3 m of the banks of all four rivers. The coefficient of variation (CV) was $\leqslant 0.2$ at all sites after $\leqslant 8$ quadrats had been sampled (Figure 1). Therefore eight quadrats were deemed sufficient to characterize the mussel population at each further sampling location.

Eighteen of the 30 sites contained unionid mussels. All five British species were collected: *Anodonta anatina*, *Anodonta cygnea*, *Pseudanodonta complanata*, *Unio pictorum* and *Unio tumidus*. There was no significant difference in the number of taxa found in sites that contained mussels (mean 14.83 ± 1.15 SE) compared with the sites that did not contain mussels (12.92 ± 1.23) ($t = 1.14$, df $= 25$, $p = 0.266$; unionid mussels were excluded from taxon counts). Similarly, there was no difference in the BMWP score
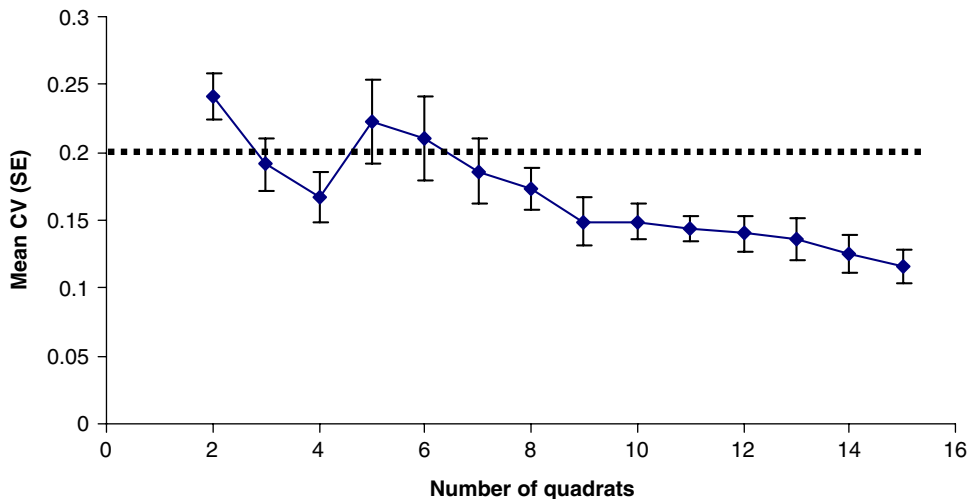
Figure 1. Coefficient of variation (CV; the ratio of standard error to arithmetic mean) in mussel density as a result of sampling from progressively more $0.5 \times 0.5\,m$ quadrats. Mean CVs are calculated from sampling within four different UK lowland rivers. The dotted line indicates the point at which CV = 0.2; Elliott (1971) suggests that an acceptable level of error in benthic samples is where CV $\leqslant 0.2$.

(a measure of the water quality based on the indicator taxa present; ISO, 1984) between the sites that contained mussels (39.28 $\pm$ 3.49) and those that did not contain mussels (42.00 $\pm$ 5.21) ($t = 0.43$, df = 20, $p = 0.669$; unionid mussels were excluded from BMWP scoring).

A relatively high proportion of mussel sites also contained Lymnaeidae (Gastropoda), Viviparidae (Gastropoda) and Asellidae (Isopoda). A relatively high proportion of sites without mussels contained Dytiscidae (Coleoptera), Elmidae (Coleoptera), Simuliidae (Diptera), Plecoptera and Caenidae (Ephemeroptera) (Table 1).

Taxon richness was strongly correlated with mussel density ($r_s = 0.635$, $n = 18$, $p = 0.005$; mussels were excluded from taxon counts; Figure 2). BMWP scores also were strongly correlated with mussel density ($r_s = 0.599$, $n = 18$, $p = 0.009$; mussels were excluded from BMWP scores; Figure 3), but the average score per taxon was not correlated with mussel density (ASPT = BMWP/number of taxa; $r_s = 0.242$, $n = 18$, $p = 0.333$).

No single mussel species was collected at all 18 sites and no species' abundance gave as good a correlation with taxon richness as did total mussel abundance. There was no significant correlation between mussel species richness and the richness of other taxa ($r_s = 0.346, n = 18, p = 0.159$), nor was there a correlation between mussel diversity (Simpson's Index) and the richness of other taxa ($r_s = 0.144, n = 18, p = 0.568$).

Mussel biomass was highly correlated with taxon richness ($r_s = 0.589$, $n = 18$, $p = 0.010$; mussels were excluded from taxon counts). This correlation was not any stronger than that between mussel abundance and taxon richness.

DISCUSSION

Assessing the abundance of freshwater mussels provides a valuable and effective short-cut to estimating aquatic biodiversity in UK lowland rivers. In particular, sites with relatively low mussel abundance can be expected to contain especially low taxonomic richness. Unlike previous approaches to using indicator taxa in fresh waters, comparisons of relative mussel abundance between sites can be undertaken without the

Table 1. Percentage of sites in which each macroinvertebrate taxon occurred. For sites containing unionid mussels $n = 18$ and for sites without mussels $n = 12$. BMWP scores are given in parentheses, unless the taxon has not been assigned a BMWP score (ISO, 1984) or the taxon has not been identified to a sufficient level to enable the allocation of a score. Occurrence of a taxon is significantly different between mussel and non-mussel sites when denoted by ** (Fisher exact test, significant with Bonferroni correction) and * (Fisher exact test, significant without Bonferroni correction).

Common name	Taxon (BMWP score)	% occurrence (mussel sites)	% occurrence (non-mussel sites)
Bivalve molluscs	Sphaeriidae (3)	78	75
Gastropod molluscs	Planorbidae (3)	44	25
	Physidae (3)	17	33
	Lymnaeidae (3)	89	41*
	Valvatidae (3)	17	0
	Viviparidae (6)	50	0*
Crustaceans	Asellidae (3)	89	42*
	Gammaridae (6)	50	50
Mites	Hydracarinae (—)	89	92
Leeches	Glossiphonidae (3)	72	33
	Hirudidae (3)	50	58
	Piscicolidae (4)	33	8
Worms	Oligochaeta (1)	61	50
Dipteran flies	Simuliidae (5)	0	67**
	Chironomidae (2)	28	33
	Dixidae (—)	83	100
	Ceratopogonidae (—)	22	0
Caddisflies	Hydropsychidae (5)	0	8
	Rhyacophilidae (7)	17	25
	Phryganeidae (10)	6	0
	Molannidae (10)	11	33
Beetles	Dytiscidae (5)	28	75*
	Elmidae (5)	6	42*
	Haliplidae (5)	44	67
	Hydrophilidae (5)	6	8
Bugs	Corixidae (5)	50	42
	Notonectidae (5)	22	8
	Pleidae (5)	6	0
	Nepidae (5)	0	8
Alderflies	Sialidae (4)	22	0
Mayflies	Caenidae (7)	22	92**
	Baetidae (4)	39	33
Stoneflies	Plecoptera (—)	6	50*
Dragonflies	Anisoptera (—)	6	0
Damselflies	Zygoptera (—)	6	0

need for taxonomic knowledge. Furthermore, assessment of mussel abundance can be carried out rapidly and entirely in the field using any standardized sampling technique (see Strayer and Smith (2003) for a review of sampling methodologies).

Freshwater mussels are widely distributed throughout the world's fresh waters, occurring in both lotic and lentic systems (Bauer and Wächter, 2001; Killeen *et al.*, 2004). However, as this study shows, there are some systems where mussels do not occur, but where taxon richness is high. Consequently, this technique for predicting taxon richness can be applied in many systems, but only where mussels are present.

Unionid mussels are likely to serve as effective bioindicators for four reasons. First, they are relatively sensitive to pollution, scoring 6 out of a possible 10 in the BMWP scoring system (ISO, 1984). As such, their
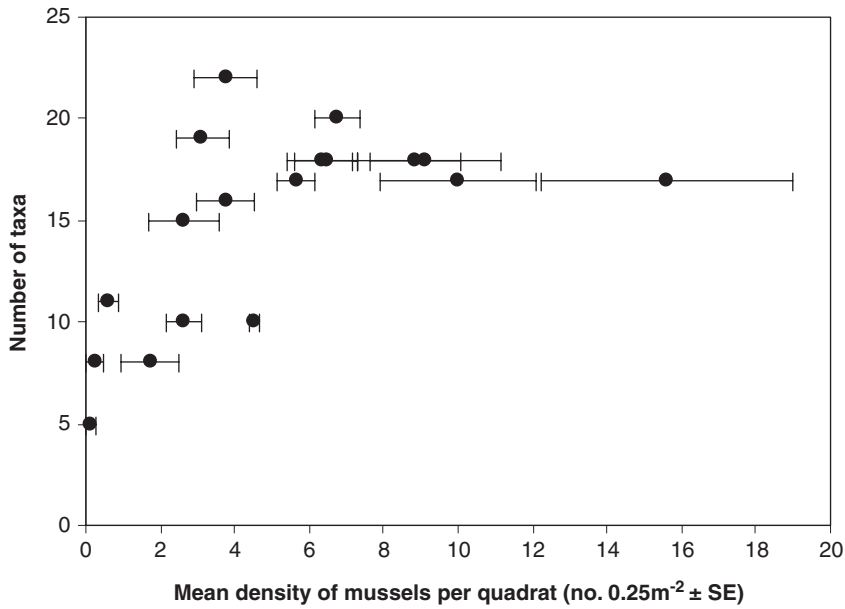
Figure 2. Relationship between number of taxa (excluding unionid mussels) and unionid mussel density (all species combined). Data are shown only for sites where unionid mussels were found.
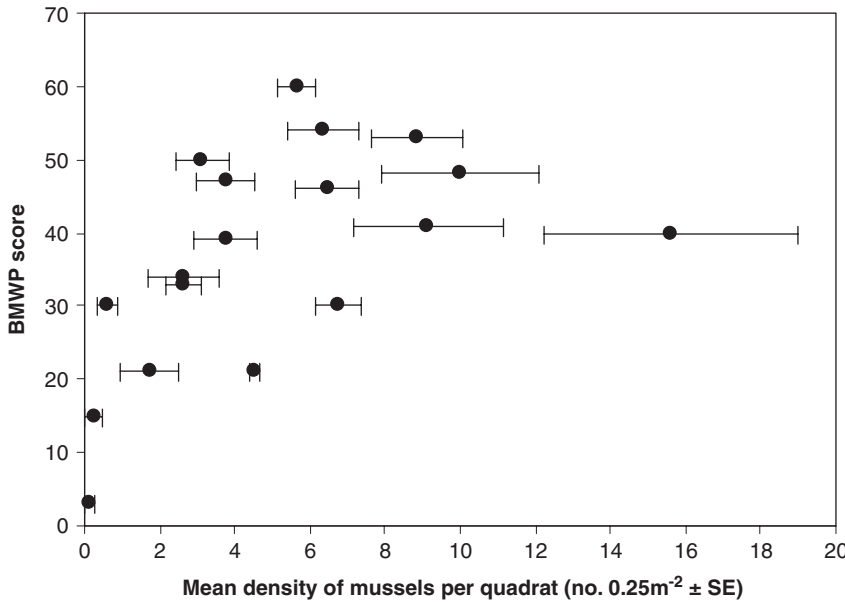

Figure 3. Relationship between BMWP score (excluding unionid mussels) and unionid mussel density (all species combined). Data are shown only for sites where unionid mussels were found.

presence is indicative of water quality that can support a relatively wide taxonomic richness. Second, the glochidia (larvae) of almost all freshwater mussels are obligate ectoparasites on fish hosts (Kat, 1984). Therefore, a recruiting population of mussels is indicative of an adequately abundant fish population.

Third, freshwater mussel density and species richness are related to landscape features of catchments (Arbuckle and Downing, 2002), which in turn will affect taxonomic composition.

The fourth, and most important, reason why mussel abundance functions as a good predictor of taxonomic richness is that mussels can be 'keystone fauna', that create habitats for other organisms (Vaughn and Hakenkamp, 2001). While the filtration of water by mussels (Tankersley and Dimock, 1993) may have a broad impact on an ecosystem's phytoplankton (Phelps, 1994; Smith *et al.*, 1998) and zooplankton (Pace *et al.*, 1998; Jack and Thorp, 2000) communities, the excretion, biodeposition and physical presence of live and dead mussels can positively affect organisms at a much more localized scale. For example, Sephton *et al.* (1980) found that native bivalve molluscs locally increased the numerical abundance of chironomid larvae and other non-bivalve detritivore species in a Canadian reservoir. However, Sephton *et al.* (1980) were unable to identify a specific cause for the increased invertebrate abundance.

More detailed studies have shown that following the establishment of the invasive zebra mussel (*Dreissena polymorpha*) in Lake Ontario, USA, increases were seen in annelids, gastropods, amphipods and crayfish (Stewart and Haynes, 1994). These results strongly parallel results for Lake Erie (Dermott *et al.*, 1993), Lake St Clair (Griffiths, 1993) and the Hudson River (Strayer *et al.*, 1998). The increases in these taxa have been attributed to enhanced habitat structure and complexity (in the case of amphipods, leeches, triclads, snails, mayflies, caddisflies and true flies) or enhanced food supply (in the case of crayfish and annelid worms) (MacIsaac, 1996). We would predict that the relatively high presence of Viviparidae, Lymnaeidae (snails) and Asellidae (isopod crustaceans) at mussel sites in our study are a result of increased habitat availability and complexity. However, it is important to note that *D. polymorpha* can have particularly profound impacts on habitat complexity owing to its epifaunal, clustering habit and its laying down of byssus threads, which unionid mussels typically do not produce.

The low overlap of sites containing mussels and Caenidae (mayfly larvae) may reflect the different habitat requirements of these taxa; Caenidae are often found in muddy substrates (Giller and Malmqvist, 1998), while unionids, except *A. cygnea*, are rarely found in such habitats (Killeen *et al.*, 2004). Furthermore, muddy substrates are especially associated with lentic habitats, which are sites favoured by the Dytiscidae (beetles) and this may explain their lack of sympatry with mussels. Conversely, the low representation of Simuliidae (blackfly larvae) and Elmidae (beetles) in the mussel sites may reflect their requirement of swift-flowing waters, which would preclude them from many sites in which mussels were found during this study.

While most studies that have investigated the impacts of bivalves on other taxa have recorded an increase in invertebrate abundance, few have investigated the impact on taxon richness. Exceptions include Stewart and Haynes (1994) who found that, following the *D. polymorpha* invasion in Lake Ontario, invertebrate taxon richness increased from <23 to between 27 and 32 in a cobble site and from <16 to between 19 and 26 in an artificial reef site. However, MacIsaac (1996) criticises this study for lack of a control and points out that there was a wide-scale coincidental increase in taxon richness at other sites within the Great Lakes, whether or not they contained *D. polymorpha*.

If unionids play a central role in enhancing local biodiversity, it would be predicted that absolute biomass of mussels would have served as a better predictor of taxon richness than did mussel density. A population of many small mussels may modify the local environment to a lesser extent than a similar number of large mussels. This study found mussel abundance and biomass to be equally well correlated with taxon richness, and this is possibly because mussels were of a similar size at all sites. Studies of the size–frequency distributions of *D. polymorpha* have shown that populations dominated by smaller mussels consumed significantly less algae and produced significantly less pseudofaeces than populations of the same numerical abundance but dominated by large mussels (Young *et al.*, 1996). As a consequence, the practical use of mussel abundance as an indicator of taxon richness should take note of any major differences in size–frequency distributions among sites. The relative importance of large mussels in structuring local

communities means that sampling regimes that may select only for the largest mussels (e.g. hand sampling and dredging; D. Aldridge, pers. obs.) are very suitable for predicting taxon richness.

The results of this study suggest that using mussel abundance as a surrogate for taxon richness has considerable utility. In particular, rapid comparisons can be made between sites within a single river so that biodiversity 'hotspots' can be identified which contain a relatively large proportion of the river's biota. Furthermore, this study suggests that comparisons can also be made between sites in different rivers, especially if the rivers are biogeographically well-matched. This study looked only at lowland rivers in the UK, which are relatively homogeneous environments in terms of flow, substrate and mussel distributions (McIvor, 1999; Müller, 1999). It is likely that the method would have similar utility in other parts of the world where the river environments are relatively homogeneous and the different mussel species share broadly similar habitat preferences to one another. For example, similar correlations would be predicted in European lowland river systems which display a similar environmental homogeneity and suite of unionids to those in this study.

More caution may be needed when comparing among sites with notably different physical and chemical features, as a weaker correlation may be expected between mussel abundance and taxon richness. Therefore, the method may be useful in comparing the taxon richness of similar sites in fast-flowing, cold-water, British streams by recording the relative abundance of the pearl mussel, *Margaritifera margaritifera*, but extending these comparisons to include lowland sites containing unionids may not be appropriate. The same caution may be necessary when applying the method to single rivers embracing a diverse range of habitats or a high diversity of mussel species. Such rivers occur in North America, where one often finds a high unionoid richness, belonging to numerous genera, and exhibiting markedly different habitat preferences. This can result in a highly patchy distribution of mussels which would require a far greater sampling effort to determine accurately the mussel abundance at a site (Strayer and Smith, 2003). Not only may this place logistical constraints on the utility of the method, but extensive sampling may be damaging to the ecosystem.

Some authors have suggested that there can be problems using very long-lived organisms as indicator taxa, because they may take a relatively long time to recover following a pollution or disturbance event, and populations under stress may persist without reproducing (e.g. Meffe and Carroll, 1997). Certainly, the Margaritiferidae fall into this category (Bauer, 1992; Beasley *et al.*, 1998), although it would still be expected that the presence of non-recruiting freshwater mussels locally would enhance taxon richness. The unionid mussels are shorter-lived than margaritiferids (e.g. Aldridge, 1999), can reach reproductive maturity at three years (D. Aldridge, pers. obs.), and are quick to establish in newly created water bodies (D. Aldridge, pers. obs.). Unionids therefore represent good indicator taxa.

This study indicates that in many freshwater systems mussel populations may be playing a central role in supporting both local and ecosystem-level biodiversity. The ultimate extirpation and extinction of such mussel populations may therefore have profound effects on the wider ecosystem. The results emphasize the importance of conserving the world's freshwater bivalve populations, which are declining at an alarming rate through habitat destruction, pollution, declines in host fish and the invasion of non-native biota (Altaba, 1990; Bogan, 1993; Aldridge, 2000, 2004).

PRACTICAL APPLICATION

It is pertinent to consider under what conditions a mussel abundance index may provide a practical tool in freshwater conservation, and how such an index may be generated. Frequently, managers may desire to identify 'hot spots' of biodiversity so that conservation efforts can be focused appropriately. In addition, managers will often wish to minimize the damage caused to an ecosystem when necessary management or disturbance must take place, such as dredging of the river bed, identifying the precise location for an

abstraction/discharge point, or positioning an access point for cattle, river crossings, moorings, etc. Under such circumstances, managers will rarely consider undertaking a full invertebrate survey because of the logistical and financial constraints of commissioning a specialist survey. Therefore, key zones of biodiversity may be unwittingly damaged.

A rapid bioassessment using the surrogate of mussel abundance can be carried out quickly and by a non-specialist. Surveys can concentrate on the marginal 0–3 m of the water body, as it is here that unionid mussels are most abundant (McIvor, 1999; D. Aldridge, unpublished data). Sampling can therefore be carried out from the bankside. While it is preferable to use a sufficiently replicated, quantitative technique to account for the patchiness in distribution of mussels, even a rapid qualitative survey is likely to provide a crude estimate of relative mussel abundance and help reduce the risk of damaging sites of highest biodiversity.

As a rule, in a UK lowland river, a reliable estimate of mussel abundance can be gained by taking at least 10 2-m-long sweeps of a standard FBA net spaced at 2 m apart along the bank, or at least 10 standardized dredges using a 'naturalist's dredge', or conducting a timed hand-sample within the water body for at least 10 min within 0–3 m of the bank (D. Aldridge, pers. obs.). All unionid mussels collected, irrespective of size or species, should be counted and then returned to the site of collection as soon as possible. Mussels are relatively mobile (Aldridge, 2000) and so they can be gently thrown back to the water without the need for 'replanting'. Those sites with especially high mussel abundance can be considered to support a relatively high proportion of invertebrate taxa compared with those sites supporting few mussels, and should thus be protected as much as possible.

It is likely that this technique can be applied to lentic systems in the UK with equal success because riverine and lacustrine mussels in the UK display similar patterns of abundance and patchiness. Furthermore, the technique should also have utility in other countries, in other freshwater ecosystems, and using other mussel families because a high abundance of large bivalves can be expected to play an important structuring role in any ecosystem (Gutiérrez *et al.*, 2003). However, it should be noted that the greater patchiness of mussels in more speciose regions, such as parts of North America, and in some mussel families, such as the Margaritiferidae, may require a more extensive sampling effort to provide a reliable estimate of relative mussel abundance (e.g. Strayer and Smith, 2003).

The technique may have especially important utility in regions where the taxonomy of the invertebrate fauna is poorly understood. Under such circumstances, the use of relative mussel abundance, irrespective of mussel species, may provide the only opportunity of identifying sites of conservation priority.

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