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Weighing the costs and benefits of reduced sampling resolution in biomonitoring studies: Perspectives from the temperate rocky intertidal

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ABSTRACT

Efficiency in biomonitoring studies is essential to maximize return (i.e. useful data) for investment (e.g. time, training, personnel). Here, we test several options for reducing data resolution when streamlining monitoring protocols, and use the results as a framework to discuss the costs and benefits of decreasing information when sampling intertidal assemblages. Specifically, we ask; (1) Is it necessary to collect species abundance data, or is species presence–absence information sufficient to differentiate sites? (2) Is it necessary to sample organismal abundance at the species-level or is coarser (higher taxon or functional group) resolution sufficient to resolve patterns of difference in intertidal community structure? and (3) How general are these patterns across different oceanic regions? We answer these questions using data from Northeast Atlantic, Northwest Atlantic, Northeast Pacific, and Southwest Pacific intertidal monitoring studies. Results show that compared to species-level sampling, genus-level sampling requires knowledge of 25% fewer taxa, but results in only a 5% difference in the ability to discern between-sample similarities. Likewise, family-level sampling involves 50% fewer taxa, and is accompanied by only an 8% difference in between-sample similarities. Species lists and functional groups were variable in performance, working well for some regions, and poorly for others. These findings will assist in the selection of monitoring protocols with the potential for increased geographic scope and temporal frequency of sampling, resulting in longer time series of data collection, and a reduction in the required taxonomic skills for individuals involved in scientifically useful biomonitoring programs.

1. Introduction

As anthropogenic pressures on coastal zones intensify (Crowe et al., 2000; Gray, 1997; Thompson et al., 2002), monitoring for temporal and spatial changes in rocky-shore biota is increasingly important. When study objectives are well defined, biomonitoring is a useful tool for identifying changes in biodiversity and has applications in science and management (Yoccoz et al., 2001). Biomonitoring can be initiated with the end-goal of identifying and reducing the stressors that induce biotic changes, or establishing a baseline data set before impacts occur. For many coastal areas baseline information is

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lacking, which can have implications for assessment of anthropogenic impacts. This latter point was exemplified when courts were tasked to legally assess 'recovery' of nearshore assemblages after the Exxon-Valdez oil spill in Prince William Sound, Alaska (Paine et al., 1996). Further, biomonitoring will draw attention to details of how particular stressors alter biodiversity, leading to more realistic questions about linkages between biodiversity and ecosystem functioning (Duffy, 2003). Marine biomonitoring can also identify areas that are highly diverse or have unique assemblage composition for placement of marine protected areas, and assess their efficacy once established.

It may appear intuitive that monitoring of biological assemblages at the highest possible taxonomic level (i.e. species/subspecies) represents the best-case scenario. This approach involves sampling biomass, numbers or percentage cover of individual species at a fine scale (e.g. quadrat or transect). This approach is desirable for several reasons. Firstly, environmental impacts can be detected through changes in relative abundance of particular species (as opposed to local extirpations or shifts in species composition). In addition, sampling at the species level allows monitoring for the introduction of exotic species and fosters knowledge about taxonomy, nomenclature, natural history, and population and assemblage structure. However, the cost of sampling at the species-level can be considerable in terms of the time taken to collect data, and to recognize and properly identify taxa (Clarke and Warwick, 2001; Murray et al., 2006). Further, post-survey processing time can become prohibitive if the number of organismal sample vouchers requiring identification is large. As well, high-resolution data are the least likely to be reliable if collected by individuals with limited training, because traits used to identify differences between organisms are typically more subtle at the species and subspecies-level (Sánchez-Moyano et al., 2006).

Routine biological monitoring programs can be expensive and time consuming. Priorities of most academic and government research programs do not include long term rocky-shore monitoring programs, so many extant data sets are short term (<four years), or of limited spatial extent. In recent years, 'citizen science' (e.g.. non-scientist involvement in biomonitoring) has been suggested as a solution (Trumbull et al., 2000). For example, in western Canada, coastal biomonitoring programs are undertaken by volunteers under the federally organized 'Shorekeepers' program (Jamieson et al., 1999). Yet, many volunteer-based monitoring programs are viewed by the scientific community as non-rigorous and therefore of little value for demonstrating temporal change and/or spatial differences in biotic assemblages (Foster-Smith and Evans, 2003). One possible solution to these problems is to reduce the resolution of sampling. This concept has been termed 'Taxonomic Sufficiency' (TS, Ellis, 1985), and described as one way to use biodiversity "surrogates" (Oliver and Beattie, 1996; Olsgard et al., 2003; Khan, 2006). Numerous alternatives to collecting species-level abundance information are available, and in certain circumstances these approaches can offer efficient and effective options for monitoring temporal and spatial variability in biodiversity (Clarke and Warwick, 1998a; Ellis, 1985). To effectively choose sampling protocols for rocky intertidal biomonitoring programs, it is important to know the effects of reducing sampling resolution. However, these effects in hard bottom marine communities have been poorly studied (Dauvin et al., 2003; Terlizzi et al., 2003), especially in the rocky intertidal (but see Lasiak, 2003; Sánchez-Moyano et al., 2006). Here we focus on testing the influence of sampling resolution for studies that have the objective of identifying temporal or spatial differences in rocky intertidal biodiversity.

Although there is a wide array of approaches to reducing sampling resolution, we examine three here: collection of species lists, higher-taxon abundances, and functional group abundances, described as follows:

(a) Species lists – also known as inventories, species lists contain no abundance data, and document only presence or absence of species. This information can be used to calculate basic biodiversity indices like species richness and beta-diversity (Koleff et al., 2003), as well as for compositional analysis (Clarke, 1993). Newer, more sophisticated biodiversity indices such as taxonomic distinctness (Clarke and Warwick, 1998b) can also be calculated using species inventories.
(b) Higher-taxon abundances – another way to streamline monitoring protocols is to collect abundance information at a taxonomic level more coarse than species (Gaston, 2000). Numerous studies from marine environments demonstrate that mild reductions in taxonomic resolution (i.e. genus or family-level) of abundance measurements result in minimal loss of the ability to detect impacts in invertebrate assemblages (Sánchez-Moyano et al., 2006). This holds true across several habitat types including estuaries (DeBiasi et al., 2003; Dethier and Schoch, 2006), the deep sea (Narayanaswamy et al., 2003), nearshore soft-bottom subtidal areas (Olsgard et al., 2003; Somerfield and Clarke, 1995), and sandy intertidal zones (Defeo and Lercari, 2004). The use of taxonomically coarse measurements is not limited to biomonitoring, and has also been assessed for use in reserve selection (Gladstone and Davis, 2003; Vanderklift et al., 1998) and in food-web studies (Sugihara et al., 1997; Thompson and Townsend, 2000).
(c) Functional group – a third possibility for reducing sampling resolution is to amalgamate abundance measurements of taxa into groups of ecologically, morphologically, or functionally similar types (Gitay and Noble, 1997). These functional groupings often transcend taxonomic boundaries, and may be more ecologically relevant than species groupings (Statzner et al., 2001); several investigators have shown that changes in functional groups have implications for ecosystem processes (Tilman et al., 1997; Diaz and Cabido, 2001). In the context of data simplification, functional groups can greatly reduce the number of entities that require sampling, as well as the dimensionality of the data set for analysis.

These three methods present logical and practical approaches to streamlining the sampling of coastal biotic assemblages. In all cases they involve a reduction in 'cost' of data collection (i.e. reduced sampling and sample process-