A test of the higher-taxon approach in the identification of candidate sites for marine reserves[1]

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Abstract. Alternatives to species-level identification have been advocated as one solution to the problem of selecting marine reserves with limited information on the distribution of marine biodiversity. This study evaluated the effects on selection of candidate sites for marine reserves from using the higher-taxon approach as a surrogate for species-level identification of intertidal molluscs and rocky reef fishes. These effects were evaluated by determining the % of species included in candidate reserves identified from genus-, family- and order-level data by a complementarity-based reserve selection algorithm, and by testing for correlations between the irreplaceability values of locations. Candidate reserves identified from genus- and family-level data of intertidal molluscs included a similar % of all species as the reserves identified from species-level data. Candidate reserves selected from genus- and family-level data of rocky reef fishes included, respectively, 3-7% and 14-23% fewer species than reserves selected from species-level data. When the reserve identification process was constrained by a practical planning limit (a maximum of 20% locations able to be reserved) the reserves selected from genus- and family-level data of intertidal molluscs, and genus-level data of rocky reef fishes, included a similar % of species as the reserves identified from species-level data. Irreplaceability values of locations for species, genera and families of intertidal molluscs were highly correlated, and irreplaceability values of locations for species and genera of rocky reef fishes were highly correlated. This study suggests that genus- and family-level data for intertidal molluscs, and genus-level data for rocky reef fishes, are suitable surrogates for species in the identification of candidate sites for marine reserves.

Introduction

Human activities are causing significant impacts in marine and coastal regions throughout the world (Wilkinson 2002). Marine reserves are being advocated as a management strategy to conserve biodiversity and to facilitate sustainable use of marine resources (Roberts and Hawkins 2000) and networks of marine reserves have been systematically selected in many countries and regions (Kelleher et al. 1995; Walls 1995; Yurick 1995; Thackway 1996; ANZECC 1999; Gladstone et al. 2003). The efficient and goal-orientated identification of candidate sites for marine reserves is potentially constrained by incomplete taxonomy; lack of information on distribution and abundance of marine biodiversity; and poor understanding of the role of ecological processes in maintaining biodiversity (Zacharias and Roff 2000; Ponder et al. 2002; Hutchings and Ponder 2003). In addition, the nature of marine and coastal environments presents difficulties of access that often hamper systematic efforts to survey and study biodiversity. A potentially useful approach is the use of a surrogate (e.g. habitat, environment type, indicator group) that is more easily and quickly measured yet effectively represents species-level biodiversity. Despite this approach having potential in marine systems, where the issues of lack of biodiversity information are potentially greater than in terrestrial systems, few studies have evaluated the usefulness of biodiversity surrogates for marine reserve selection (Vanderklift et al. 1998; Ward et al. 1999; Gladstone 2002; Gladstone and Davis 2003).

One potential surrogate that has received considerable attention in terrestrial systems is the higher-taxon approach. In theory, the advantages of surveying higher taxa in biodiversity inventories include: ease of identification compared with distinguishing individual species; the reduced time and cost associated with sampling and identifying taxa; and the possibility of surveying a greater number of locations (Balmford et al. 1996a; Gaston 1996; Williams and Humphries 1994; Balmford et al. 2000; Gaston 2000). Adopting the higher-taxon approach in biodiversity surveys for the purpose of conservation planning requires its usefulness to be verified in different habitats, for different groups of flora and fauna, and at spatial scales relevant to the selection and design of reserves. At the simplest level, surrogacy value of higher taxa has been evaluated by testing for correlations between species richness and the richness of higher taxa across many locations (Williams and Gaston 1994; Pik et al. 1999; Balmford et al. 2000; Wilkinson and Davis 2000). Although fewer studies have been conducted in marine systems, results have shown significant correlations between richness of species and higher taxa for fish (McAllister et al. 1994), molluscs (Jablonski and Flessa 1986; Roy et al. 1996), and amphipods (Myers 1997). It has also been demonstrated that assemblages can be distinguished similarly by species or higher taxa (James et al. 1995; Chapman 1998) and that higher taxa are useful surrogates for species in assessing environmental impacts (Warwick 1988; Ferraro and Cole 1990; Olsgard et al. 1998; Lasiak 2003; Gladstone and Schreider 2003).

An alternative approach to evaluating the higher-taxon approach has been to examine its value in complementarity-based reserve selection (Balmford et al. 1996b; van Jaarsveld et al. 1998; Vanderklift et al. 1998; Balmford et al. 2000). Using data on a number of vertebrate, plant and invertebrate groups in the Transvaal region of South Africa, van Jaarsveld et al. (1998) found only minor degrees of spatial overlap between reserves selected for species and genera, and species and families and concluded that reserves based on genera or families would lead to inefficient conservation of species. In contrast, using % of species included in reserves as a measure of effectiveness, Balmford et al. (2000) found reserves selected for macrofungi genera by a richness-based algorithm contained at least 98% of the species that were included in reserves selected for species. Vanderklift et al. (1998) found that marine reserves selected for assemblages defined by genera or families contained a similar proportion of species as reserves selected for species assemblages, provided the representation goal was to conserve at least 60% of assemblage occurrences. Differences in the outcomes of these studies probably reflect differences in their spatial scales; differences in the measures used for evaluating effectiveness (spatial overlap of reserves *vs* % of all species included in reserves); and differences in the taxonomic diversity of the groups examined. With the exception of the study by Vanderklift et al. (1998) most other studies have been undertaken at spatial scales much larger than the scales at which reserve selection actually occurs and the application of their results to this process is therefore uncertain. The objective of this study was to compare the higher-taxon approach in two groups (intertidal molluscs and rocky reef fishes) at a spatial scale relevant to conservation planning.

Methods

Field surveys

This study was undertaken in the Hawkesbury Shelf bioregion, south-east Australia (described in Gladstone 2002). The value of the higher-taxon approach in intertidal molluscs was assessed with mollusc data from Gladstone (2002) (hereafter called the Hawkesbury Shelf molluscs), and with data collected from surveys at 21 locations between Killcare and Bar Beach (New South Wales) (hereafter called the Central

Coast molluscs). The latter survey included all rock platforms in 85 km of coastline in the Central Coast section of the Hawkesbury Shelf bioregion and the average distance between nearest locations was 4.2 ± 0.7 km (Figure 1). Central Coast molluscs were sampled in December 2000-January 2001 and October-November 2002 at low tide in three 1 m wide transects that stretched perpendicular to the shore from the highest reaches of the intertidal to the water level (Zacharias and Roff 2001). Transects included the range of sub-habitats, including cobbles, boulders, rockpools, crevices, ledges and flat platform. All molluscs occurring in each transect were visually identified and all surveys were done by one individual (TA).

Data on rocky reef fishes were collected from 13 locations between Lion Island and Port Stephens (New South Wales), covering 140 km of coastline, with an average distance of 11.7 ± 5.3 km between nearest locations. Sampling occurred in the 'deep reef' habitat which is a sponge-dominated habitat of temperate rocky reefs at 12-18 m depth (Underwood et al. 1991). Deep reef habitat on fringing rocky reefs is patchily distributed in response to the availability of rocky substratum at suitable depth (*personal observations*) and the locations used represented most occurrences of this habitat in the study area. Sampling occurred in April-May and September-October 2002. Fishes were surveyed by divers using underwater visual census techniques in which all mobile fishes were counted in a 5 x 25 m strip and all cryptic and juvenile fishes were counted in a 1 x 25 m strip parallel to the larger strip (Lincoln Smith 1989). Transects were sampled by swimming at a constant speed so that counts of the 5 m and 1 m strips were completed in approximately 8 min. Search effort was therefore constant across all transects. Four randomly located replicate transects were surveyed in each of two sites within each location and results from sites were combined to give a total species list for each location. All surveys were done by one individual (WG).

Correlations between richness of species and higher taxa were tested by Spearman rank correlation coefficients with significance determined by randomization (Manly 1997) because of lack of independence of the data sets. Correlations were not calculated for species and class richness of intertidal invertebrates because the four classes recorded during these surveys occurred at all locations. Correlations were also not calculated for species and class richness of rocky reef fishes because there are only two classes and one of these (Chondrichthyes) was not recorded at all locations. The total areas surveyed for intertidal molluscs varied with the width of the intertidal shore and it is therefore possible that any relationship observed between richness of species and richness of higher taxa may be confounded by area differences. Therefore, regression was used to test for the existence of a relationship between area and taxonomic richness and where there was a significant regression, the residual scores were used for the correlations between taxonomic levels (Balmford et al. 1996a).

Reserve selection

Analyses were undertaken on the rocky reef fish data set for species, genera, families and orders following the taxonomy in Kuiter (2000). Analyses of intertidal molluscs were undertaken on species, genera, families and orders, following the taxonomy in Beesley et al. (1998) and Kay et al. (1998). Classes were not analysed because three of the four classes (Polyplacophora, Bivalvia, Gastropoda) occurred at all locations and the remaining class (Octopoda) occurred at four locations only. Six families of gastropod molluscs were classified within three superorders (no subsidiary orders) and 37 families were classified within 18 orders (Kay et al. 1998). For the purposes of the present study superorders and orders were treated as equivalent and analyzed as part of a common data set hereafter called orders.

The usefulness of the higher-taxon approach in reserve selection was tested with two reserve selection procedures: a greedy richness algorithm and irreplaceability analysis. A greedy richness algorithm was used to select locations to achieve the representation goal of each taxon occurring at least once in a reserve. The greedy richness algorithm sequentially selects locations by complementary richness until the representation goal is reached (Kirkpatrick 1983; Vane-Wright et al. 1991; Csuti et al. 1997; Williams 1999). This was done for data sets of species, genera, families and orders for the individual sampling periods and for the combined data sets. The % of all species included in the set of locations selected for each of the higher taxa was then determined. A higher taxon would be a suitable surrogate if the selected reserves contained a similar % of all species as reserves of the same number of locations selected from the species data set (Howard et al. 1998; Reyers et al. 2000; Gladstone 2002). The % of all species included in a reserve network of randomly selected locations was also determined, from the median of 1000 simulations, for reserve networks of the same size as the reserve network for each taxon. Analyses were done with WORLDMAP (British Museum of Natural History) software. This procedure was also done for the representation goal of 20% of locations as reserves, where the greedy richness algorithm selects the set of locations that will lead to the greatest number of species being included with the constraint that no more than 20% locations can be selected. This procedure was done to simulate the practical planning constraint that a maximum of 20% of locations were able to be declared as reserves.

There are potentially many possible combinations of locations that will achieve a required representation goal (Rebelo and Siegfried 1992; Pressey et al. 1994; Hopkinson et al. 2001). This characteristic of reserve selection is termed ‘flexibility’ (Pressey et al. 1994). The number of all such possible combinations in which a location occurs is a measure of its relative contribution towards the achievement of the representation goal, or its ‘irreplaceability’ (Pressey et al. 1994). Pressey et al. (1994) defined irreplaceability as (1) the potential contribution of an area to a representation target (e.g. a single representation of each species in a reserve); and (2) the extent to which options for a reserve system are lost if that area becomes unavailable for conservation. Pressey et al. (1994) originally quantified the irreplaceability value of an area as the percentage of alternative sets of areas in which the location occurs. Areas that are 100% irreplaceable must be included in a reserve system if the representation target is to be achieved. Areas with lower irreplaceability values will have more replacements in the region and less impact on the representation target if they become unavailable for conservation (Pressey, 1999; Ferrier et al. 2000). A more recent predictor (Ferrier et al. 2000) allows irreplaceability value to be calculated for very large data sets. In the present study C-Plan software (New South Wales National Parks and Wildlife Service; Pressey 1998) was used to calculate summed irrreplaceability values from data sets of species and higher taxa. Summed irreplaceability value was used because in all of the data sets used in this study all or most locations were irreplaceable for achieving the representation target of each taxon being represented at least once in a reserve, which did not provide a relative measure of the conservation value of each location. Summed irreplaceability is the sum of the irreplaceability values of all taxa in a location (Pressey 1998, 1999; Ferrier et al. 2000). This study tested the hypothesis that summed irreplaceability values determined using species and higher taxa were significantly correlated. Spearman rank correlation coefficients were calculated and their statistical significance determined by randomization because of the lack of independence of the data sets representing increasingly higher taxonomic levels.

Results

General results

Species richness of Hawkesbury Shelf molluscs was significantly correlated with richness of genera and families, but not orders (Table 1). Although statistically significant the correlation coefficients for genera ($\rho = 0.79$) and families ($\rho = 0.69$) were only of moderate magnitude. These relationships were not driven by area differences: there were non-significant relationships between the area of locations and richness of species ($r^2 = 0.002$, $P = 0.87$); genera ($r^2 = 0.0003$, $P = 0.95$); families ($r^2 = 0.001$, $P = 0.90$); and orders ($r^2 = 0.12$, $P = 0.20$).

Species richness of Central Coast molluscs was significantly correlated with the richness of genera and families in the first sampling, although the correlation coefficient was high only for genera ($\rho = 0.90$). These results are unlikely to be confounded by area differences: there was a significant, but poor relationship between area and species richness ($r^2 = 0.22$, $P = 0.03$) and no relationship between area and richness of genera ($r^2 = 0.10$, $P = 0.16$), families ($r^2 = 0.0004$, $P = 0.93$), or orders ($r^2 = 0.03$, $P = 0.45$). Species richness was significantly correlated with richness of genera, families, and orders at the second sampling and in the combined data set

(Table 1). The magnitude of the correlation coefficients were high only for genera ($\rho = 0.96$) and families ($\rho = 0.84$) at the second sampling and genera ($\rho = 0.96$) and families ($\rho = 0.81$) in the combined data set. Significant area effects existed at the second sampling for richness of species ($r^2 = 0.26$, $P = 0.02$) and genera ($r^2 = 0.22$, $P = 0.03$), but not for families ($r^2 = 0.07$, $P = 0.25$) or orders ($r^2 = 0.0007$, $P = 0.91$). The correlation between species and genera was still high after adjusting for the potential effects of area by correlating residual values for species and genera ($\rho = 0.93$). Significant area effects also occurred in the combined data set for richness of species ($r^2 = 0.30$, $P = 0.01$) and genera ($r^2 = 0.25$, $P = 0.02$), but not for families ($r^2 = 0.08$, $P = 0.21$) or orders ($r^2 = 0.03$, $P = 0.50$). The correlation between species and genera was still high after correlating residuals ($\rho = 0.94$).

Species richness of rocky reef fishes was significantly correlated with generic richness at the first sampling (ρ=0.95), with generic (ρ=0.97) and family richness (ρ=0.87) at the second sampling, and only with generic richness in the combined data set (ρ=0.96).

Reserve selection

The reserve set required to achieve the representation target of each taxon being represented at least once for genera, families and orders of Hawkesbury Shelf molluscs included 99%, 88% and 86%, respectively, of all species (Table 2). The reserve set identified for genera, families and orders of Central Coast molluscs included 97%, 91% and 59%, respectively, of all species at the first sampling; 97%, 97% and 77%, respectively, of all species at the second sampling; and 99%, 93% and 58% of all species, respectively, in the combined data set (Table 2). Randomly selected reserves included fewer species, except for orders of Central Coast molluscs at the first sampling when the randomly selected reserves included the same % species (59%).

The reserve sets selected to include at least a single representative of each genus, family and order of rocky reef fishes included 97%, 77% and 61%, respectively, of all species at the first sampling; 93%, 86% and 76%, respectively, of all species at the second sampling; and 97%, 81% and 54% of all species in the combined data set (Table 2). Randomly selected reserves always included fewer species than the reserves identified for each taxon; however, at the first sampling and in the combined data set the randomly selected reserves included only 4% and 3% fewer species, respectively, than the reserves identified for orders.

When the representation goal was 20% of locations as reserves, the locations identified for species, genera and families of both Hawkesbury Shelf and Central Coast molluscs included a similar % of species (Table 2). For rocky reef fishes, only the locations identified for genera included a similar % of species as the locations identified for species; locations identified for families excluded 5-11% species and locations identified for orders excluded 6-8% species.

Irreplaceability analysis

The frequency distributions of summed irreplaceability values differed for each of the taxonomic levels (Figures 2-4). The frequency of smaller summed irreplaceability values increased, and the summed irreplaceability values of locations became more similar, with increasing taxonomic level for rocky reef fishes and molluscs. This trend was especially pronounced for Central Coast molluscs and rocky reef fishes where the summed irreplaceability value of most locations for orders was 0-2.

Summed irreplaceability values of locations for species, genera and families of intertidal molluscs were highly correlated (Table 3). Although significant, the correlation for species and orders was not strong. The magnitudes of the correlations for Central Coast molluscs were greater in the second sampling period. The correlations for species and orders were significant (except at time 1 for Central Coast molluscs), but not high. Summed irreplaceability values for species and genera of rocky reef fishes were highly correlated. The correlations increased in the second sampling period with the magnitude of this increase reflected in the value for families, which changed from a low and non-significant correlation in the first sampling period (ρ=-0.07) to a significant, positive correlation in the second sampling period (ρ=0.63). Summed irreplaceability values of locations for species and orders of rocky reef fishes were uncorrelated.

Discussion

The present results suggest that species richness of intertidal molluscs in locations of 100s m^2 area, separated by km - 10s of km is highly correlated with genus and family richness. Species richness of rocky reef fishes in locations of 1000s m^2 area and separated by 10s of km is highly correlated with genus richness. These significant correlations are consistent with studies of other biota at different spatial scales and with different ratios of species:higher taxa (McAllister et al. 1994; Balmford et al. 1996a, 1996b, 2000; Olsgard et al. 2003). Interestingly, McAllister et al. (1994)

working with a much richer group of fishes (coral reef fishes) and at a much greater scale (global) than the present study also found that richness of species and genera in 2^0 grids were highly correlated, but species and family richness were unrelated.

The magnitude of some richness correlations changed between sampling periods. For example, species and family richness of Central Coast molluscs were only weakly correlated in time 1 ($\rho = 0.50$); however in time 2 they were highly correlated ($\rho = 0.84$). Changes of a similar magnitude also occurred for correlations between species and family richness of rocky reef fishes. Some results for reserve selection and irreplaceability analysis also changed between sampling times. Reserves selected for families of rocky reef fishes included more species at sampling time 2 (Table 2). Correlation coefficients of summed irreplaceability values for Central Coast intertidal molluscs and rocky reef fishes were greater for all taxonomic levels in time two (Table 3). The increased correlations of summed irreplaceability values for intertidal molluscs was associated with an increase in the number of species, genera and families in sampling time 2, whereas the increased correlations for irreplaceability values of rocky reef fishes was associated with a decrease in numbers of species, genera and families. Lack of consideration of the possibility of temporal variation could possibly lead to erroneous conclusions about the surrogate value of particular higher taxa e.g. that families might not be a reliable surrogate for molluscs (based on sampling time 1) or that families of rocky reef fishes show some promise as a surrogate for species (based on sampling time 2).

Species richness is an inefficient means of prioritising locations for conservation planning, leading to many more locations being required to achieve a representation goal compared with locations selected on the basis of complementarity (Williams et al. 1996; Margules and Pressey 2000). Furthermore, richness hotspots rarely coincide spatially across taxonomic groups (Howard et al. 1998; Reid 1998; Tardiff and DesGranges 1998; van Jaarsveld et al. 1998; Pharo et al. 2000), and rarely coincide with locations important for rare or endangered species (Kershaw et al. 1995; Williams et al. 1996; van Jaarsveld et al. 1998; Reyers et al. 2000). A more realistic test of the value of higher taxa in conservation planning is their effectiveness in reserve selection. The present study found that complementarity-based reserve networks selected for genera of intertidal molluscs and rocky reef fishes included the majority of species in each biota. Interestingly, these outcomes (in terms of % species representation) are comparable to other studies that have been undertaken in different environments, at different scales, and using different groups of organisms. For example, Balmford et al. (1996b) used data on woody plants from all remaining Sri Lankan forests and found that reserves selected for genera contained 95% of all species, which compared extremely well with the reserve network of the same size selected from species data that included 97% of all species. In another study using data on a single group (the macromycete fungi) in the local area of Sheffield (UK), Balmford et al. (2000) similarly found that reserves selected for genera included only 0.6 – 1.8% fewer species than the set of reserves selected for species. Use of families of intertidal molluscs in the present study led to the loss of 3-12% of species. These results are within the range of values recorded by Balmford et al. (1996b) for a much richer biota over a larger number of sites in a greater area. Balmford et al (1996b) found that use of families led to the loss of 7-10% of species for a data set of 777 species of woody plants from 35 sites across Sri Lanka. Use of families or orders of rocky reef fishes does not appear suitable for identifying candidate sites as it led to the loss of 14-23% and 24-45%, respectively, of species.

Genera and families of intertidal molluscs are suitable surrogates when the area available for conservation is more realistic i.e. 20% of available locations. Reserve networks of this size selected for genera or families included similar numbers of species as reserves selected for species. In contrast, for reserve networks of this size for rocky reef fishes only genera included a similar number of species as reserves selected for species. Vanderklift et al. (1998) found that only genus-level data resulted in numbers of species being included that were similar to the results for species and only at a representation level of 60% or more of the area of occurrences. However, the analysis of Vanderklift et al. (1998) used representation of assemblages that were based on more species and more habitats than the present study. Their results would therefore reflect turnover of species and assemblages between habitats and variability of assemblages within habitats. Both studies conclude that higher taxa are useful surrogates for species in the selection of marine reserves. However, the existence of practical constraints on the size of areas available to be set aside as conservation reserves suggests that surrogate performance is best evaluated at achievable conservation targets.

Conservation of species is one of the key goals of conservation planning. The State and Commonwealth governments of Australia adopted a set of principles for developing national and state systems of representative marine protected areas (ANZECC 1999). These principles include (amongst others) comprehensiveness, adequacy and representativeness. Representativeness requires that “Those marine areas that are selected for inclusion in MPAs should reasonably reflect the biotic diversity of the marine ecosystems from which they derive” (ANZECC 1999). The principle of representativeness requires inclusion of the range of community types and species present in the planning area (NSWMPAMPASWG 2001). The results from this study indicate that large areas, or multiple reserves, are likely to be required to implement the principle of representativeness. The area required (expressed as a % of the total number of locations surveyed) to include all species varied from 60-80% for intertidal molluscs and 75-90% for rocky reef fishes. These results are not likely to be a result of selective or limited sampling effort (which might lead to a greater number of single occurrences of species) because all or most examples of the relevant habitat type were sampled for Central Coast molluscs and rocky reef fishes. These results suggest that the extent of areas required to conserve taxonomic diversity is likely to be considerably larger than the areas currently being set aside.

The use of another criterion for reserve selection (summed irreplaceability value) led to similar conclusions as the results from the complementarity-based reserve selection procedures. Irreplaceability analysis has been used to test for surrogacy value in reserve selection (Pharo et al. 2000) and to schedule the selection of conservation areas in combination with a measure of vulnerability to loss (Pressey and Taffs 2001). In the present study the summed irreplaceability values of locations for species, genera and families of intertidal molluscs were significantly correlated. In contrast, the summed irreplaceability value of locations for species of rocky reef fishes was significantly correlated only with their irreplaceability value for genera. These significant correlations suggest that relative conservation value of locations can be quantified with species, genera, or families of intertidal molluscs and species or genera of rocky reef fishes.

In summary, the results of the present study indicate that richness of higher taxa of intertidal molluscs and rocky reef fishes is a useful predictor of species richness. This study has also shown that use of genera and families of intertidal molluscs and genera of rocky reef fishes in conservation planning will have similar outcomes for reserve selection as species-level data at achievable conservation targets. There is a need for further studies of biota in regions where the richness of higher taxa differs from those used in the present study to identify the conditions in which the higher-taxon approach provides no benefit.

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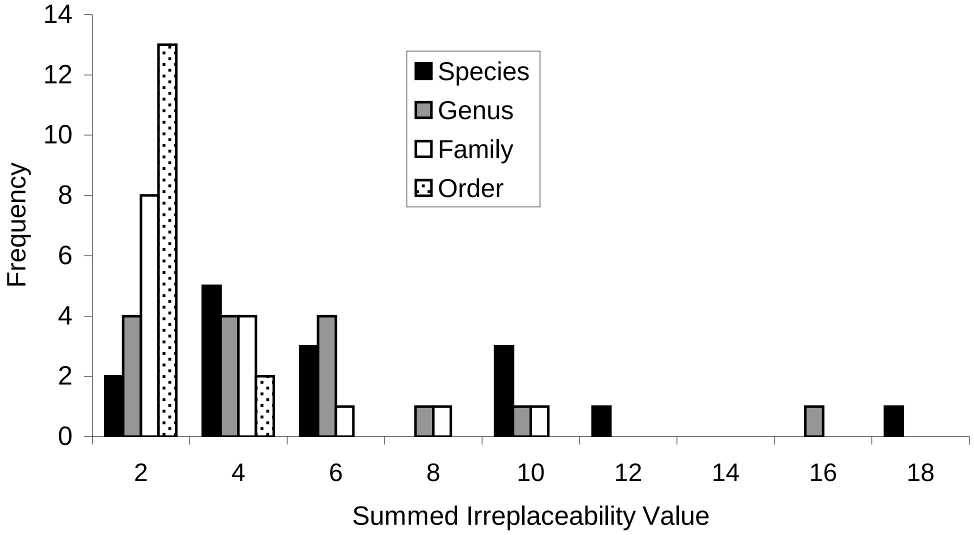
Fig.1. Sampling locations for (A) Central Coast intertidal molluscs (O) and rocky reef fishes (●); and (B) for Hawkesbury Shelf intertidal molluscs.

Fig. 2. Frequency distribution of summed irreplaceability values of locations for Hawkesbury Shelf molluscs.

Fig. 3. Frequency distribution of summed irreplaceability values of locations for central Coast molluscs at sampling time 1 (A), sampling time 2 (B), and for the combined data set of species from both sampling times (C).

Fig. 4. Frequency distribution of summed irreplaceability values of locations for rocky reef fishes at sampling time 1 (A), sampling time 2 (B), and for the combined data set of species from both sampling times (C).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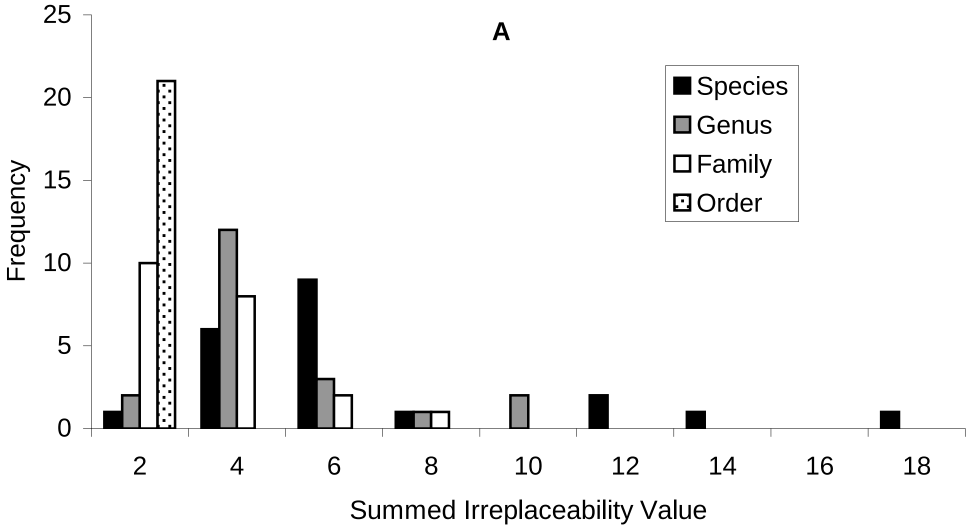
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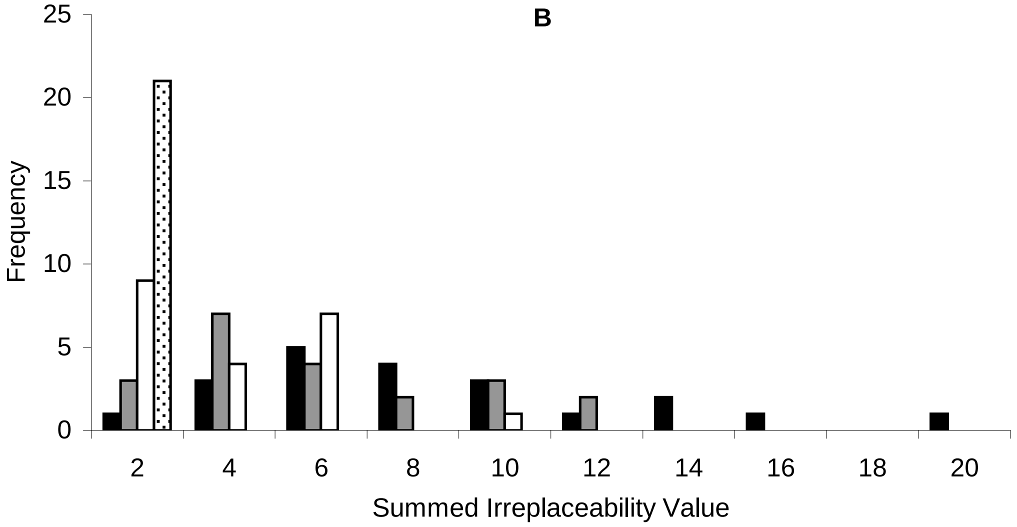
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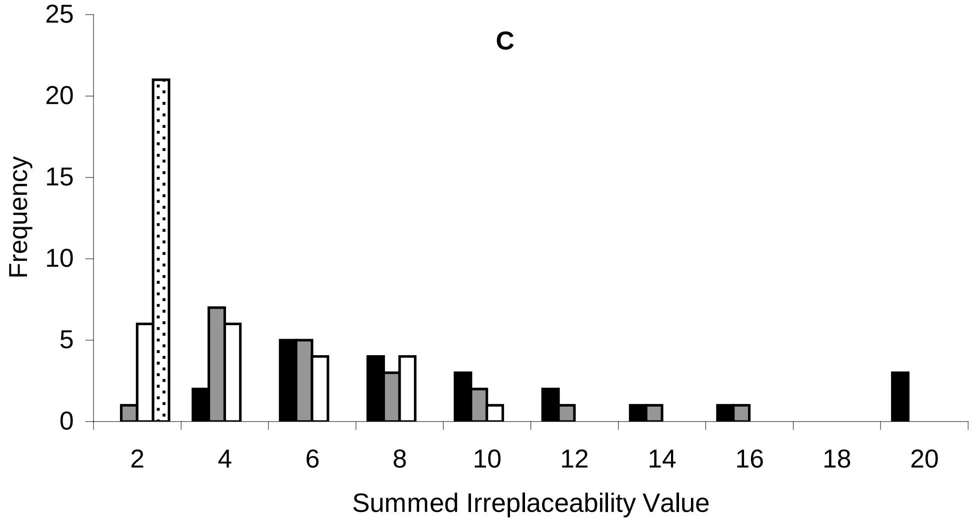
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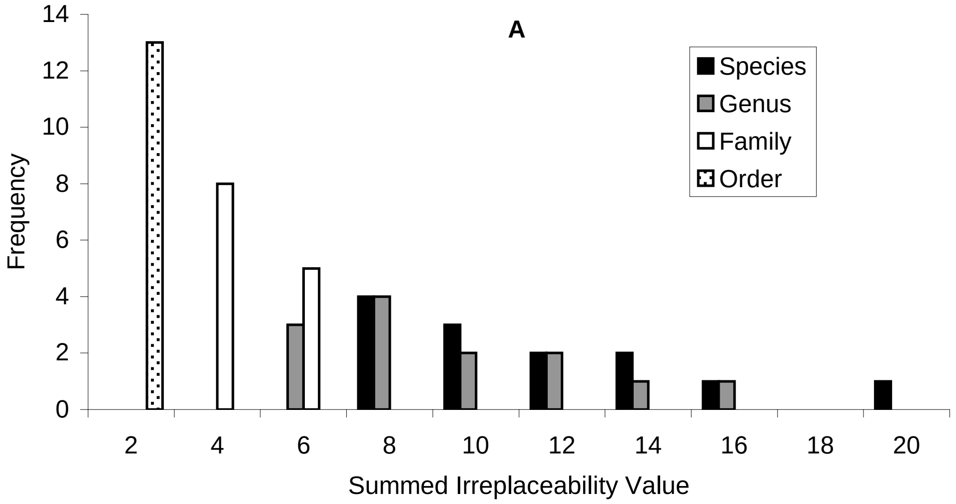
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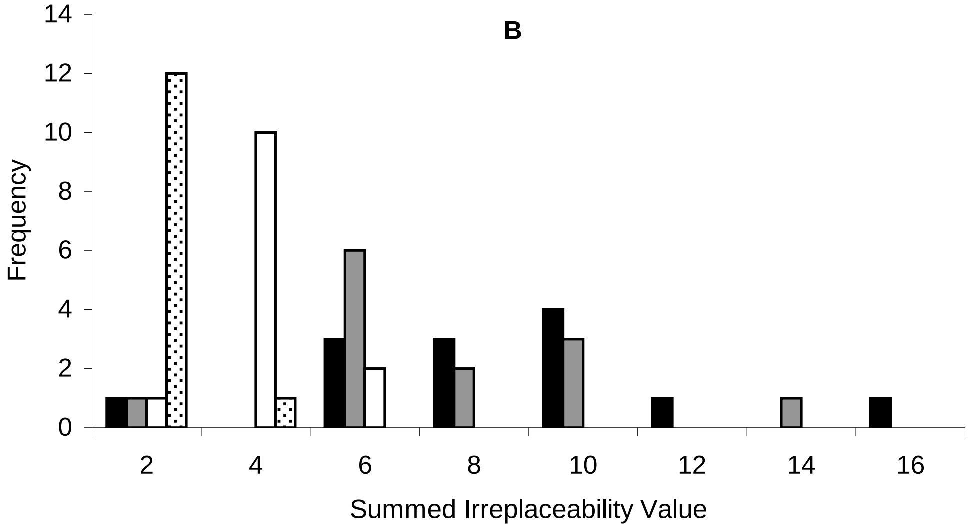
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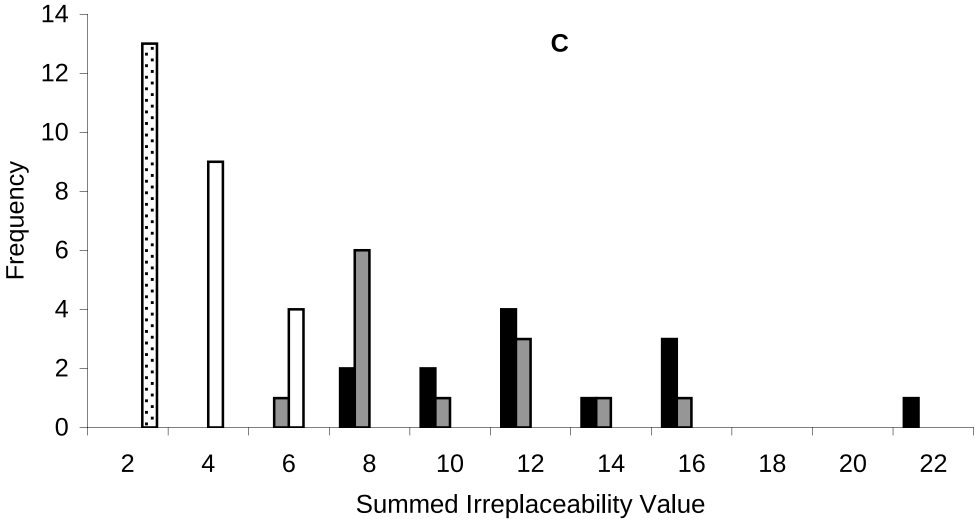
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Table 1. Numbers of taxa identified at each taxonomic level. Values in parentheses are Spearman rank correlation coefficients and their significance levels for the relationship of species richness to richness of higher taxa at each location. Hawkesbury Shelf molluscs sampled only on one occasion. Correlation coefficients for classes were not determined (see text).

Group	*Taxon*	*Time 1*	*Time 2*	*Combined*
Hawkesbury Shelf molluscs	Species	74		
	Genus	57 (0.79***)		
	Family	36 (0.69**)		
	Order	18 (0.49 NS)		
	Class	4		
Central Coast molluscs	Species	98	118	145
	Genus	72 (0.90***)	84 (0.96***)	99 (0.96***)
	Family	44 (0.50*)	54 (0.84***)	61 (0.81***)
	Order	17 (0.24 NS)	20 (0.75***)	21 (0.74***)
	Class	4	4	4
Rocky reef fishes	Species	105	74	114
	Genus	80 (0.95***)	61 (0.97***)	83 (0.96***)
	Family	37 (0.51 NS)	31 (0.87***)	38 (0.48 NS)
	Order	9 (0.21 NS)	9 (0.27 NS)	9 (0.18 NS)
	Class	2	2	2

NS *P*>0.05, * *P*<0.05, ** *P*<0.01, *** *P*<0.001

Table 2. % of species included in reserve networks selected for genera, families and orders for two representation goals. Values in parentheses are the % species included in a randomly selected reserve network of the same size as the reserve network selected for each taxon and represent the median value of 1000 random selections. No results are given for the representation goal of 20% locations reserved for orders of Central Coast molluscs (combined data) and rocky reef fishes (combined data) because the complementarity-based reserve network required <20% locations.

Biota	Taxon	Representation goal		
		Each taxon in at least one reserve		20% locations reserved
		% locations required	% species included	% species included
Hawkesbury Shelf molluscs	Species	60	100 (86)	84
	Genus	53	99 (84)	84
	Family	33	88 (72)	84
	Order	27	86 (68)	81
Central Coast molluscs time 1	Species	81	100 (94)	78
	Genus	67	97 (88)	78
	Family	48	91 (77)	77
	Order	24	59 (59)	57
Central Coast molluscs time 2	Species	71	100 (90)	78
	Genus	62	97 (86)	78
	Family	62	97 (86)	76
	Order	24	77 (62)	73
Central Coast molluscs combined data	Species	81	100 (93)	76
	Genus	76	99 (91)	76
	Family	57	93 (82)	76
	Order	14	58 (50)	--

Table 2 cont’d.

Biota	Taxon	Representation goal		
		Each taxon in at least one reserve		20% locations reserved
		% locations required	% species included	% species included
Rocky reef fishes time 1	Species	92	100 (97)	66
	Genus	85	97 (94)	65
	Family	38	77 (70)	61
	Order	23	61 (57)	58
Rocky reef fishes time 2	Species	77	100 (92)	70
	Genus	62	93 (85)	70
	Family	46	86 (77)	66
	Order	31	76 (66)	64
Rocky reef fishes combined data	Species	92	100 (98)	73
	Genus	77	97 (93)	71
	Family	38	81 (75)	62
	Order	15	54 (51)	--

Table 3. Correlations between summed irreplaceability values of locations at higher taxonomic levels and irreplaceability value based on species. Values shown are Spearman rank correlation coefficients and their significance level.

	Genus	*Family*	*Order*
Hawkesbury Shelf molluscs	0.97***	0.92***	0.68**
Central Coast molluscs			
- time 1	0.82***	0.59**	0.24 NS
- time 2	0.92***	0.83**	0.59**
- combined	0.94***	0.86***	0.52*
Rocky reef fishes			
- time 1	0.82**	-0.07 NS	0.04 NS
- time 2	0.93***	0.63*	0.39 NS
- combined	0.90***	0.38 NS	0.005 NS

NS *P*>0.05, * *P*<0.05, ** *P*<0.01, *** *P*<0.001