



## Original Articles

# Cross-taxon congruence in the rarity of subtidal rocky marine assemblages: No taxonomic shortcut for conservation monitoring



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## ABSTRACT

The implementation of protection strategies such as the European Marine Strategy Framework Directive (2008/56/EC) is impeded for subtidal rock bottom habitats because of high sampling costs due to a very wide taxonomic diversity, and a lack of suitable evaluation tools to estimate their conservation importance. In this study, we seek to provide an evaluation procedure by (1) investigating the distribution of rarity among subtidal rock bottom phyla; (2) searching for potential surrogate phyla with a cross-taxon congruence approach based on their rarity; (3) proposing an appropriate multi-phyla indicator to evaluate the importance of subtidal rocky habitats for conservation. We analysed the distribution of 548 species belonging to 8 phyla sampled in 137 assemblages in subtidal rocky areas located around Brittany, Western France. We applied the Index of Relative Rarity, a flexible method which fits rarity weights to species depending on their respective phyla. We found only weak congruence in rarity patterns among phyla, which prevented any attempt to identify surrogate phyla. This finding has important implications for the conservation of subtidal rocky habitats as it means that there is no shortcut to monitor their rarity: working on a subset of phyla would imply a biased evaluation of biodiversity. Consequently, we propose a multi-phyla Index of Relative Rarity combining all phyla which allowed us to successfully describe rarity patterns across all sampled sites.

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## 1. Introduction

To mitigate the ongoing loss of marine biodiversity, the European Union has successively adopted several directives aiming at protecting and conserving marine habitats, ecosystems and biological diversity: the OSPAR convention (1998), the habitat directive (HD, 92/43/EEC, 1992), the Natura 2000 network, and more recently the Marine Strategy Framework Directive (MSFD; 2008/56/EC) (2010). Effectively preserving marine biodiversity requires the evaluation and monitoring of the diversity of different marine taxonomic groups and habitats. With respect to benthic subtidal habitats, much of the literature has focused on subtidal soft bottom habitats for which a plethora of tools is available (Van Rein et al., 2009). On the other hand, rocky subtidal habitats remain

poorly evaluated because of the difficulties and costs of sampling these diversified habitats. This lack of consideration impedes their inclusion in the implementation of European directives, in spite of their high taxonomic diversity and functional role. Consequently, researchers need to both optimise sampling procedures (Gallon et al., 2013) and identify potential surrogates that could be used to describe biodiversity based on a reduced set of data. In this study, we seek to identify biodiversity surrogates as one facet of the importance of subtidal rocky habitats for conservation, hereby not focusing on other equally important facets such as ecosystem functioning.

The concept of biodiversity surrogates has been extensively explored in the conservation literature and needs to be refined to be relevant to rocky subtidal habitats. Biodiversity surrogates fall in two main categories (Grantham et al., 2010): environmental surrogates, which use a combination of physical and biological data to estimate or predict biodiversity, and taxonomic surrogates, predominantly based on the use of one or several taxonomic groups to estimate biodiversity. We focus here on the second category, i.e.

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the identification of surrogate phyla by cross-taxon congruence, since it has been advocated as appropriate to predict patterns of marine biodiversity for conservation purposes when data are scarce (Mellin et al., 2011). The identification of surrogate taxa in marine habitats has mostly been based on species richness (Mellin et al., 2011) and, to a lesser extent, on multivariate patterns of assemblage structure (e.g., Hirst 2008; Smale 2010; Sutcliffe et al., 2012). However, it has been suggested that species richness is not appropriate because of high spatial and taxonomic variability (Su et al., 2004). More importantly, species richness is not a good enough indicator for biodiversity conservation as it does not take the identity of species into account or their varying degrees of vulnerability to extinction (e.g., Orme et al., 2005). Alternatively, surrogacy across taxa can be assessed by studying congruency of rarity across assemblages of species, an appropriate approach for taxa with limited data availability (Leroy et al., 2013, 2012). The choice of rarity as a criterion is based on the greater extinction risk of rare species relative to ecologically similar common species (Flather and Sieg, 2007; Gaston, 1994; Roberts and Hawkins, 1999), because they are appropriate indicators for other species of conservation concern (Larsen et al., 2007; Lawler et al., 2003), and because they have been shown to sometime support unique ecosystem functions unsupported by other species (Mouillot et al., 2013).

It has been established repeatedly that a large proportion of intertidal and subtidal marine benthic species exhibit narrow geographic ranges (see for instance Sanderson 1996; Chapman 1999). Therefore the frequency distributions of benthic marine species range size are typically strongly right-skewed with a large number of low occurrence species at local or regional scales (Ellingsen et al., 2007) similar to terrestrial taxa (Gaston, 1994; Gaston and Blackburn, 2000). Hence, testing the ability of the rarity of surrogate taxa to capture the rarity of other taxa may help to substantially reduce the cost of sampling protocols to evaluate the rarity of subtidal assemblages.

The methods used to measure rarity in species assemblages must be chosen carefully, because several methods have been proven to provide inappropriate results under particular conditions (Leroy et al., 2012). Hence, Leroy et al. (2012) proposed a new, flexible method to assess the rarity of species assemblages (the Index of Relative Rarity) with respect to the considered phyla. The rationale of this method is that rarity should be defined according to the taxon considered; therefore an inflexible method may bias the analysis toward a particular phylum. Indeed, the threshold of geographic range size below which species are considered rare is generally defined specifically for each particular phylum because of the large differences in range size among phyla (Grenyer et al., 2006). This rationale is especially important for subtidal rocky habitats because the diversity of their phyla may result in very different rarity patterns among phyla.

We aimed to investigate patterns of rarity and cross-taxon congruency among sessile and low-mobility animal phyla of subtidal rocky areas, based on the Index of Relative Rarity developed by Leroy et al. (2012). The opportunity for such an approach was offered by the compilation of a database from 137 inventories of assemblages of subtidal rocky habitats around the Brittany (western France) coast. These inventories were sampled between 1993 and 1998 by biologist scuba divers of the “Association pour la Découverte du Monde Marin” (Girard-Descatoire et al., 2000, 1999, 1998, 1997, 1996a, 1996b, 1996c, 1995, 1993; L’Hardy-Halos et al., 2001; L’Hardy-Halos and Castric-Fey, 2000a, 2000b, 2001) in addition to samples by our diving team from 2005 to 2009. Because this database was initially not designed for such analyses, it may contain biases that could have a negative impact on the outcomes of our study (Pearman et al., 2006). Hence, we applied a completeness metric to assess sampling quality across sites and phyla (Soberón

et al., 2007), and improved our database by applying appropriate corrections.

The objectives of this study are to (1) investigate the distribution of rarity among the sampled phyla, in order to calculate appropriate rarity metrics for each phylum; (2) search for potential surrogate phyla with a cross-taxon congruence approach on the rarity of assemblages of species; (3) propose a multi-phyla indicator and discuss its potential use to evaluate the importance of monitored subtidal rocky habitats for conservation.

## 2. Material and methods

### 2.1. Database compilation

We compiled a database on the biodiversity of benthic assemblages of species of subtidal rocky habitats around Brittany based on 122 inventories sampled between 1993 and 1998 by biologist scuba divers (Girard-Descatoire et al., 2000, 1999, 1998, 1997, 1996a, 1996b, 1996c, 1995, 1993; L’Hardy-Halos et al., 2001; L’Hardy-Halos and Castric-Fey, 2000a, 2000b, 2001), and 15 inventories sampled by our diving team from 2005 to 2009.

The inventories were grouped into 13 major sites around the Brittany coast, with 4–20 inventories per site. The 13 sites span the range of conditions around Brittany: estuaries and inland seas (Morbihan gulf, Etel ria, Brest bay, Rance estuary), open bays (Lannion bay, St Malo bay, Morlaix bay, Iroise sea), coastal sites (Granite rose coast, Crozon peninsula, Cape Sizun) and islands (Sept-Îles archipelago, Ushant island). These inventories of species presence-absence focused on benthic rocky communities between the infralittoral fringe and the nearest circalittoral, and were limited to depths of 30 m.

In this substantial inventory, eight animal taxa (conveniently called “phyla” in this paper) were kept for our analyses: Porifera, Cnidaria, Annelida, Mollusca, Arthropoda, Bryozoa, Echinodermata and Chordata, for a total of 548 species. This choice focused on only sessile and low-mobility species to minimise bias in scuba-diving surveys throughout the 13 investigated sites. The systematic nomenclature of the database was checked following the World Register of Marine Species (WoRMS Editorial Board, 2016) to avoid both orthographic mistakes and synonymies (Costello et al., 2001).

### 2.2. Database robustness and occurrence estimation

We first analysed the robustness of the database to assess and mitigate potential biases in sampling efforts, which could lead to an uneven representation of species diversity and occurrence among sites. Our analysis was divided into a three step process based on a completeness index (Soberón et al., 2007). The completeness index assesses the completeness of a set of samples by dividing the observed richness by the total estimated species richness on the basis of a richness estimator (Soberón et al., 2007). We calculated three richness estimators (Chao2, ICE and Jack1) (Hortal et al., 2006; Soberón et al., 2007) which yielded similar results; we included average values across the three estimators in the main text, and values for all three indicators in Appendix A in the Supplementary material.

Firstly, we analysed the completeness of the whole database. Secondly, all phyla pooled together, we analysed the completeness of each site in order to identify and remove under-sampled sites with a completeness threshold (see below). Thirdly, we analysed the completeness of each phylum in each site. Then we calculated the average completeness of each phylum across all sites in order to remove phyla that were on average insufficiently sampled across all sites. We applied a conservative rule to remove phyla and sites based on a threshold of completeness that we defined at 75%, i.e.

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