1. Introduction

The current policy of European Union on protection and management of coastal marine water bodies involves the assessment of the state of the physical environment as well as the quality of the biological component of ecosystems (EC, 2000). This last aspect represented a step forward for European legislation, namely the characterization of the ecological status of marine systems in order to define effective strategies for the enhancement of ecosystems’ health. A critical issue in such a challenging task concerns the identification and/or the implementation of suitable methods able to classify different levels of ecological quality and to recognize the effects of different sources of human disturbance (Salas et al., 2006a).

Ecological indicators are likely to constitute the mainstream tools in this framework, as they condense composite biological information into single measures, which might be more understandable for the general public and easier to deal with compared to the classical indices. Suitable ecological indicators, however, are also expected to satisfy defined requirements, such as, for instance, sound ecological meaning, handling easiness, cost-effectiveness, broad applicability (Salas et al., 2006b), and should associate high sensitiveness and relevance to
manageable human activities with a relative insensitivity to other sources of variation (Ware et al., 2009).

A variety of approaches, ranging from the use of richness and relative abundances of species to species-specific sensitivity/tolerance to environmental stress, have been adopted in the attempt to express multivariate community response to human impacts through univariate metrics (Rosenberg et al., 2004; Ware et al., 2009). The performances of indices based on species richness and evenness in highlighting the effects of both natural and anthropogenic disturbance often depend on multiple factors, which could vary under different environmental settings (e.g. Patrício et al., 2009). Most of these classical indices are strongly affected by sample size, sampling effort, natural environmental variability and do not have monotonic responses to anthropogenic disturbances (Gray, 2000; Maguran, 2004; Rogers et al., 1999). They often confound the effects of two components, namely equitability and number of species, which requires further analyses to determine which component drives the observed patterns. For small samples, indices like the Shannon index (\(H\)), can significantly underestimatethe true species diversity (e.g. Bowman et al., 1971) and has poor discriminant ability (Maguran, 1988). The Shannon formula, in particular, is, at least in information theory, strictly defined only for infinite population and the minimum variance unbiased estimator of it does not exist, an issue which poses serious limit to the use of \(H\) in ANOVA contexts (Hubálek, 2000).

Assessing the effects of environmental perturbations using such measures requires time–expensive procedures to collect species-level abundance data in the investigated site(s) and in multiple comparable unperturbed controls, since their values do not allow identifying univocally the state of a biological system but need to be compared with reference conditions. Other recently developed indices are more cost-effective and apparently do not necessitate a formal comparisons with unperturbed situations, because they are structured on selected subsets of tolerant/sensitive species as indicators of environmental perturbations (e.g. Borja et al., 2000, 2003; Mistri and Munari, 2008). A major problem with such indices relies, again, on their sensitivity to natural variability (Tataranni and Lardicci, 2010), and restricted usage, which is limited to particular habitat types (e.g. soft sediments) and source of disturbance (e.g. organic enrichment), not easily extensible to a wider array of environmental conditions (Salas et al., 2006b; Simboura and Zenetos, 2002).

In this framework, the use of taxonomic distinctness (\(\Delta^*\)) proposed by Warwick and Clarke (1995) and, above all, its form based on presence/absence data, namely average taxonomic distinctness (\(\Delta^*,\) Clarke and Warwick, 1998), coupled with its complementing index, variation in taxonomic distinctness (\(\Lambda^*,\) Clarke and Warwick, 2001), might represent a promising approach due to their appealing properties. \(\Delta^*\) and \(\Lambda^*\) are independent from the number of species, which makes them virtually not influenced by sample size and sampling efforts and, thus, potentially usable over a broad range of environmental contexts, even when analyzing historical (e.g. Cusson et al., 2007) and simple presence–absence data (e.g. Price et al., 2006) or comparing data sets from different studies (e.g. Somerfield et al., 2009). Moreover, the use of \(\Delta^*\) and \(\Lambda^*\) does not necessarily need contrasting their values among impacted versus control conditions to test for significant differences, providing a statistical framework based on simulations from existing reference taxonomic lists against which taxonomic distinctness values of any specific area, habitat or impacted site can be checked or formally tested (Leonard et al., 2006).

In marine systems, taxonomic distinctness indices have been applied across a broad spectrum of geographic areas, ranging from polar (Conlan et al., 2004; Włodarska-Kowalczyk et al., 2005) to temperate (e.g. Machias et al., 2004; Nicholas and Trueman, 2005) and tropical (e.g. Graham et al., 2006, 2007; Miranda et al., 2005) regions. Most studies have focused on soft bottom macro-benthic assemblages and individual organisms (e.g. Arvanitidis et al., 2005; Brewin et al., 2009; Munari et al., 2009; Reiss and Kröncke, 2005), and to a lesser extent, on fish (Graham et al., 2007; Lekve et al., 2005; Stobart et al., 2009) and, recently, hard substrate benthic assemblages (e.g. Anderson et al., 2005; Terlizzi et al., 2005a) and modular organisms (Bevilacqua et al., 2009a; Fioerl et al., 2009; Voultsiadaou, 2009).

Although in many cases such metrics have shown higher sensitivity than classical indices in discriminating among perturbed and unperturbed sites (e.g. Arvanitidis et al., 2005; Leonard et al., 2006; Munari et al., 2009; Warwick and Clarke, 1995, 1998), some caveats still remains. Taxonomic distinctness indices are presumed to be more sensitive to impacts with respect to classical indices since they incorporate more information and, particularly, information about taxonomic relatedness among species (e.g. Clarke and Warwick, 1998; Somerfield et al., 1997; Warwick and Clarke, 1995). In this reasoning it is assumed that such indices could be less influenced by natural environmental variability because natural variations in assemblages could occur mostly by species replacements, whereas, disturbed assemblages, are likely to show change also at higher taxonomic ranks and should tend to comprise a range of more closely related taxa than undisturbed ones (Warwick, 1993; Warwick and Clarke, 1995). A number of studies on different habitat types and taxonomic groups showed that \(\Delta^*\) and \(\Lambda^*\) can also vary along natural gradients, thus reducing their ability to discern human-driven variations from natural variability (e.g. Bevilacqua et al., 2009a; Ellingsen et al., 2005; Mouillot et al., 2005), and suggesting further examination about the usefulness of such indices in elucidating the effects of anthropogenic disturbance on marine assemblages.

In this study, we employed \(\Delta^*\) and \(\Lambda^*\) to analyze four data sets from impact assessment studies on marine mollusks and polychaetes from Mediterranean soft sediments and hard substrates. Specifically, we test their response in detecting the effects of different sources of anthropogenic disturbance (i.e. offshore methane extraction and sewage discharge) through classical univariate statistical analyses (i.e. ANOVA). We also applied the statistical framework based on simulations associated to \(\Delta^*\) and \(\Lambda^*\) to assess their ability in discriminating perturbed and unperturbed sites. Finally, we test the hypothesis that habitat type does not influence patterns of taxonomic relatedness of species (i.e. species characterizing different habitats are random subsets of the regional pool of species).

2. Materials and methods

2.1. Data sets

Four data sets were analyzed to investigate the performance of \(\Delta^*\) and \(\Lambda^*\) in detecting assemblages’ variations related to anthropogenic impacts across different organisms and habitat types. Such data sets were selected because they highlighted significant differences among impacted and control conditions in multivariate patterns of assemblages, and taxonomic identification was available at species level for all individuals.

Two data sets, “Offshore platform mollusks” and “Offshore platform polychaetes”, have been extracted from a larger study assessing the impact of offshore gas production platforms on soft bottom macro-benthic assemblages in the Ionian Sea (SW Italy) (Terlizzi et al., 2008), and referred to an eight-legs platform located on mud flats at 90 m in depth. Sampling was carried out at increasing distances from platforms (300, 1000, and 3000 m) in five sites randomly selected at each distance, with three 0.1 m² van Veen grabs in each site, sieved on 1 mm mesh.
The other two data sets, “Sewage outfall mollusks” and “Sewage outfall polychaetes”, came from two studies investigating the impact of the same sewage outfall on mollusk (Terlizzi et al., 2005a) and polychaete assemblages (Musco et al., 2009) in subtidal rocky reefs (Ionian Sea, SE Italy). In both study cases, sampling was carried out in the impacted location (I) and in two control locations (C1 and C2), with three sites within locations and nine replicates in each site. Samples were collected by scraping into a 0.4 mm mesh bag all organisms from a 20 cm × 20 cm surface of rocky substrate, and applying a suction-sampler before and after the scraping. A summary of data sets’ information has been provided in Table 1.

### 2.2. Calculating Δ* and A*

Since the reference list of species is critical for the performance of taxonomic distinctness indices, it should be as representative as possible of the biodiversity existing in the studied area (Warwick and Clarke, 1998). For this purpose, four reference lists, one for each data set, were built including all species we found in the present and previous studies we carried out in the same habitat type and geographic area (see Table 1 for further details). Data matrices coupled with the corresponding reference list were used to calculate the values of Δ* and A* for each sample. For each data set, Δ* and A* values were calculated also on the whole assemblages present in each site. Finally, Δ* and A* values were calculated for the whole pool of species characterizing each of the two targeted habitat types. In this last case, indices were calculated on the basis of the whole pool of species characterizing each of the two targeted habitat types. In this last case, indices were calculated on the basis of the whole pool of species characterizing each of the two targeted habitat types.

### 2.3. Univariate statistical analyses

ANOVA was then employed to test for differences in sample mean values of Δ* and A* among distances, for offshore platform data sets, and between impacted versus control locations, for sewage outfall data sets. In the former cases, the analyses involved the factors Distance (fixed, 3 levels) and Site (random, 5 levels, nested in Distance), with n = 3, whereas, in the latter, the analyses were asymmetrical and included the factor Location (with one impacted and two control locations) and Site (random, 3 levels, nested in Location), with n = 9. For each data set, ANOVA was conducted on sample species richness also. Prior to analyses the homogeneity of variance was tested using the Cochran C-test. The analyses were done using the GMAV 5 computer program (University of Sydney, Australia).

### 2.4. Simulation test of Δ* and A*

For each data set, Δ* and A* values of sites were plotted against the corresponding number of species. To test the departure from expectations of these values, the 95% confidence ‘funnel’ was generated for both indices on the basis of the corresponding reference list (see Warwick and Clarke, 1998 and Clarke and Warwick, 2001 for the technical details of the procedure). In this statistical framework, the null hypothesis is that assemblages are composed of random subsets of the same number of species from the regional pool (i.e. the reference list). As a consequence, unperturbed assemblages could have naturally high or low values of Δ* and A*, which should fall within expectations generated by random simulations from the reference list (i.e. the 95% confidence funnel). Human impacts, in contrast, would select subsets of species significantly more closely related taxonomically than what expected by chance, leading to indices values that should fall below random predictions. Using the same rationale underlying the construction of funnels, a scatter plots of simulated Δ* against the Δ* values can be created, allowing to generate a combined 95% confidence contour for a specified number of species (‘ellipse’, Clarke and Warwick, 2001). This bivariate approach was used to test at the same time the departure from expectations of both Δ* and A* values calculated on the whole mollusk and polychaete assemblages present in each habitat type. All analyses were run using the TAXTEST routine from PRIMER 6 β package.

### 3. Results

For both mollusks and polychaetes, ANOVA on sample values of Δ* and A* did not detect significant differences among assemblages at increasing distance from platform (Table 2), indicating that the platform did not significantly affect patterns of taxonomic relatedness among species. The same results were obtained for analyses on sample indices’ values of assemblages between impacted location and controls in the sewage outfall study cases (Table 3), showing that sewage discharge did not lead to assemblages less taxonomically related than those in control locations.

### Table 1

Summary of data set information. For each data set, the habitat type, number of samples, number of species, literature used to build reference taxonomic lists and the number of species present in each list are given.

<table>
<thead>
<tr>
<th>Data set</th>
<th>Habitat type</th>
<th>No. of samples</th>
<th>No. of species</th>
<th>Taxonomic reference list</th>
<th>No. of species in the reference list</th>
</tr>
</thead>
<tbody>
<tr>
<td>Offshore platform mollusks</td>
<td>Continental shelf mud flats</td>
<td>45</td>
<td>38</td>
<td>Terlizzi et al. (2008)</td>
<td>218</td>
</tr>
<tr>
<td>Offshore platform polychaetes</td>
<td>Continental shelf mud flats</td>
<td>45</td>
<td>33</td>
<td>Terlizzi et al. (2008)</td>
<td>90</td>
</tr>
<tr>
<td>Sewage outfall mollusks</td>
<td>Subtidal rocky reefs</td>
<td>81</td>
<td>151</td>
<td>Terlizzi et al. (2003, 2005a)</td>
<td>204</td>
</tr>
<tr>
<td>Sewage outfall polychaetes</td>
<td>Subtidal rocky reefs</td>
<td>81</td>
<td>105</td>
<td>Giangrande et al. (2003) and Musco et al. (2009)</td>
<td>176</td>
</tr>
</tbody>
</table>

### Table 2

Species richness (S), average taxonomic distinctness (Δ*), and variation in taxonomic distinctness (A*) for offshore platform data sets. Mean ± SE (n = 15) was calculated for each of the three distances (N = 300 m, M = 1000 m, F = 3000 m). Summary of ANOVAs was also reported. Results of post hoc pair-wise comparisons (SNK test) were given when appropriate. ns = not significant.

<table>
<thead>
<tr>
<th>Distance</th>
<th>S</th>
<th>Δ*</th>
<th>A*</th>
</tr>
</thead>
<tbody>
<tr>
<td>Offshore platform mollusks</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>N/M/F</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>N</td>
<td>6.40 (±1.11)</td>
<td>82.72 (±1.52)</td>
<td>175.78 (±37.68)</td>
</tr>
<tr>
<td>M</td>
<td>4.20 (±0.86)</td>
<td>66.57 (±0.89)</td>
<td>82.93 (±30.14)</td>
</tr>
<tr>
<td>F</td>
<td>4.60 (±0.57)</td>
<td>79.41 (±5.88)</td>
<td>145.45 (±27.47)</td>
</tr>
<tr>
<td>ANOVA</td>
<td>ns</td>
<td>ns</td>
<td>ns</td>
</tr>
<tr>
<td>SNK</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>

| Offshore platform polychaetes     |      |      |      |
| N/M/F  |      |      |      |
| N    | 5.67 (±0.63) | 57.43 (±4.19) | 132.34 (±30.24) |
| M    | 9.20 (±0.94)  | 61.29 (±0.65)  | 139.17 (±17.90) |
| F    | 10.47 (±0.67) | 61.59 (±0.23)  | 148.98 (±10.84) |
| ANOVA | ns   | ns   | ns   |

**P < 0.01.**
Analyses on sample species richness revealed significant differences among distances from platform for polychaete assemblages only, whereas, as far as the outfall, any significant difference attributable to sewage discharge emerged for both investigated taxonomic groups (Tables 2 and 3).

When analyzing data using the 95% confidence funnel for $\Delta^+$ and $\Delta^-$, no significant departure from expectations ($P > 0.05$) were generally identified. Mollusk assemblages around the gas platform showed site values of $\Delta^+$ lying close to the expected mean for all distances (Fig. 1a), whereas, $\Delta^-$ values were in most cases above the mean, with some exception (i.e. one site at 3000 m, and two sites at 30 m) falling outside the upper limit of funnel (Fig. 1b). For polychaetes, although always within the confidence funnel, assemblages of different sites were generally characterized by values of $\Delta^+$ above the mean and of $\Delta^-$ below the mean and values of $\Delta^+$ above the mean, independently of distance from platform (Fig. 1c and d).

Mollusks at sewage outfall exhibited site values of $\Delta^+$ very close to the expected mean value, except for two sites in C1, which fall above expectations, indicating significantly higher ($P < 0.05$) taxonomic distinctness of assemblages characterizing one control location (Fig. 2a). Associated values of $\Delta^-$, for either the impacted or control locations, were generally above the expected mean and within the 95% confidence funnel in all sites, except for one impacted site falling above the upper limit (Fig. 2b). For polychaetes, analyses on sewage outfall showed low $\Delta^+$ values in all sites, especially for C1 and I, although in most cases they lay within expectations. In C1, however, one site fell below expectations, indicating an assemblage characterized by a group of species significantly closely related than what expected by chance (Fig. 2c). All sites, instead, showed high values of $\Delta^+$ very close to the upper limit of funnel or in some cases (i.e. in two sites of C1 and one site of I) falling above expectations (Fig. 2d).

Mollusk assemblages characterizing soft sediments showed a high value of $\Delta^+$, which lay outside expectations, coupled with a high value of $\Delta^-$ close to the 95% limit of the ellipse, indicating that they were composed by species significantly more taxonomically distinct, though quite unevenly distributed among higher taxa (Fig. 3a). For hard substrates, mollusks showed a value of $\Delta^+$ within expectations but, again, a significantly high value of $\Delta^-$ ($P < 0.05$) (Fig. 3a). As far as polychaetes, $\Delta^+$ and $\Delta^-$ values of soft sediment assemblages fell within or close to expectations (Fig. 3b). In contrast, for hard substrate, polychaete assemblages were characterized by a significantly lower value of $\Delta^+$ accompanied by a significantly higher value of $\Delta^-$, indicating the presence of closely related taxa characterized by low evenness in species distribution among them (Fig. 3b).

### 4. Discussion

Several studies discussed the efficacy of both $\Delta^+$ and $\Delta^-$ in detecting variations among different levels of perturbation, suggesting that such indices based on taxonomic relatedness among species are likely to better discriminate ecological states at the extremes of environmental gradients, but less prone to identify moderately perturbed conditions (e.g. Salas et al., 2006b; Schratzberger et al., 2009). Here, we considered areas historically interested by high levels of anthropogenic disturbance, which has been demonstrated to strongly affect multivariate patterns of macro-benthic assemblages both on hard (Musco et al., 2009; Terlizzi et al., 2002, 2005b) and soft substrates (Terlizzi et al., 2008), even at taxonomic levels higher than species (Bevilacqua et al., 2009b; Musco et al., 2009). Our results, however, showed that neither classical univariate analyses on taxonomic distinctness indices revealed significant differences imputable to the investigated sources of impact, nor the associated statistical framework was able to discern among perturbed and unperturbed sites, highlighting a low sensitiveness of such metrics in detecting assemblage variations related to anthropogenic disturbance.

As $\Delta^+$ and $\Delta^-$ are metrics based on presence/absence data, and assume impacts being likely to induce variations in taxonomic structure of assemblages, they could experience reduced discriminating power when anthropogenic disturbance mostly affect relative abundances of organisms rather than the compositional structure of the assemblage. The consequence is that, when human perturbations mainly acts by influencing the evenness component of the assemblage diversity as observed for both mollusk data sets and polychaetes of sewage outfall (Musco et al., 2009; Terlizzi et al., 2005a, 2008), $\Delta^+$ and $\Delta^-$ could fail in detecting significant variations related to disturbance. Analogous reductions in sensitiveness of taxonomic distinctness indices could raise also when human perturbations affect assemblage composition, such as in the soft sediment polychaete example, where the significant decrease of species number detected in sites close to the platform remained unnoticed analyzing $\Delta^+$ and $\Delta^-$. Thus, compositional variations in assemblages driven by anthropogenic disturbance could not necessarily imply variations in taxonomic relatedness among species, in contrast with the assumption that the effect of species replacement within higher taxa is typical of natural disturbance, whilst human impacts likely induce changes among higher taxonomic ranks. A further issue in the application of taxonomic distinctness indices concerns their potential to less influence by natural variability, although most evidences of this appreciable property derive from studies focusing on soft sediments, which are likely to be less subject to high regimes of natural disturbance. In other habitats, such as, for instance, exposed rocky shores, higher environmental heterogeneity and natural disturbance regimes could increase the confounding effects of natural variability, possibly affecting the performance of $\Delta^+$ and $\Delta^-$ in identifying variations related to anthropogenic disturbance (Bevilacqua et al., 2009a). However, no substantial differences in the performance of $\Delta^+$ and $\Delta^-$ between hard substrates and soft bottoms emerged in the present study for both mollusks and polychaetes, suggesting that such measures could be more influenced by natural variability than expected across a range of environmental contexts.

In contrast with the idea that $\Delta^+$ and $\Delta^-$ values could vary among areas and habitats, but unless they are perturbed in some way their values should fall within expectations (Warwick and Clarke, 1998), our results also showed that habitat type could strongly affect taxonomic relatedness of species within assemblages, and that this effect varied among organisms. Indeed, taxa belonging to a given phylum could result more or less associated to specific environments, with strong implication on taxonomic relationships among species characterizing a given habitat type. This
could be the case of marine polychaetes of hard substrates, which are mostly represented by few speciose families (e.g. Syllidae, Cinar, 2003; Musco and Giangrande, 2005), leading to assemblages with low taxonomic breadth and high clustering of species within a single taxon. This particular taxonomic structure might explain the significantly low value of $\Delta^+$ and high value of $\Delta^-$ detected of polychaete assemblages on rocky reefs. In contrast, mollusk assemblages in both habitat types and polychaete assemblages of soft sediment, being characterized by species more or less evenly distributed among a wide range of high taxa, showed values of $\Delta^+$ and $\Delta^-$ within or very close to expectations. Thus, when analyzing assemblages in a putatively impacted site based on a reference list including all species from different habitats, the departures from expectation of $\Delta^+$ and $\Delta^-$ values might not be univocally attributable to human perturbations, possibly also depending on habitat effects. In this respect, some doubt raises about the appropriateness of testing against expectations built on regional lists incorporating all species irrespectively of habitat preference. Restricting reference lists to species inhabiting specific habitat types, depending on the taxonomic group of organisms considered, could represent a profitable strategy.

The response of taxonomic distinctness indices to anthropogenic disturbance supposes that impacts might reduce taxonomic breadth of assemblages by selecting set of taxonomically closely related species, which implicitly entail a general functional homogeneity of species within high taxonomic rank (e.g. family) (Warwick, 1993). However, functional responses of species, such as tolerance or sensitivity to environmental stress (e.g. Giangrande et al., 2005; Gray and Pearson, 1982; Pearson and Rosenberg, 1978; Lenat and Resh, 2001), and life traits, as feeding habits (e.g. Dugan et al., 2000; Fauchald and Jumars, 1979; Giangrande et al., 2000; Paine, 1962) or reproductive strategies (e.g. Heinz-Dieter, 1999), can largely vary within the same taxon. To what extent structural and functional traits identifying taxonomic units are related with natural or human-driven environmental changes and, ultimately, how taxonomic diversity links functional diversity, still remains a basically unsolved issue (Hooper et al., 2005), making controversial the assumption at the base of taxonomic distinctness indices.

Taxonomic distinctness indices provide a deeper insight into the composite of assemblages (Price, 2002; Rogers et al., 1999), including in their metrics elements related to the taxonomic relationships among species, which are crucial to better address the wide concept of biological diversity (Purvis and Hector, 2000). Such indices allowed a great advance in the study of spatial and temporal distribution of marine organisms, providing exceptional tools in identifying patterns of biodiversity (e.g. Price et al., 1999, 2006) and testing hypotheses about processes behind (e.g. Brewin et al., 2009; Somerfield et al., 2009). However, the effectiveness of taxonomic distinctness measures in disclosing the effects of human disturbance is unclear, leading to inconsistent outcomes across different environmental contexts, although their potential to highlight patterns obscured by the analysis of other indicators suggest them as...
Fig. 2. Average taxonomic distinctness ($\Delta^+$) and variation in taxonomic distinctness ($\Lambda^+$) of assemblages in the three sites within the outfall location (black triangles) and control locations (blank squares = C1, blank circles = C2), plotted against the corresponding total number of species characterizing each site. For both indices, the expected mean (dotted line) and the 95% confidence limits (crossed lines) were also plotted (details in the text). (a) $\Delta^+$ and (b) $\Lambda^+$ values for mollusk assemblages, (c) $\Delta^+$ and (d) $\Lambda^+$ values for polychaete assemblages.

Fig. 3. Average taxonomic distinctness ($\Delta^+$) of the whole assemblage present in the two investigated habitat types plotted against the corresponding value of Variation in taxonomic distinctness ($\Lambda^+$), for (a) mollusks and (b) polychaetes. SM = soft sediment mollusks, HM = rocky reef mollusks, SP = soft sediment polychaetes, HP = rocky reef polychaetes. Numbers in brackets are the total number of species in each habitat type. The relevant 95% probability contours (ellipse) for ($\Delta^+$, $\Lambda^+$) paired values, obtained from 1000 independent simulations of random subsets of species from national checklists (details in the text), were also plotted. For mollusks, ellipse was built for random subsets of 200 (grey), 210 (light grey), and 220 (blank) species. For polychaetes, ellipse was built for random subsets of 90 (dark grey), 120 (grey), 150 (light grey), and 180 (blank) species.
valuable complementary tools in impact assessment (Heino et al., 2005; Stobart et al., 2009).

Over the past decade, increased efforts have been dedicated to develop, refine and assess ecological indicators, but the effects of habitat affecting their performance is still largely unknown. The development of indicators is still focused on soft bottoms, largely neglecting hard substrate habitats, in spite of their recognized ecological value (e.g. EU Habitats Directive 92/43/EEC, 1992). Taxonomic distinctness indices are the few ones unconstrained to a set of specific environments and potentially relevant also in the assessment of ecological quality of hard substrate sessile assemblages, but their application in this framework stands far to be fully explored (e.g. Bevilacqua et al., 2009a; Floerl et al., 2009). Much more efforts are required in this direction, as well as in structuring new suitable tools (e.g. Ballesteros et al., 2007), able to ensure novel insights on the separate and combined influence of natural and human disturbance on coastal rocky habitats.

References


