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Monitoring transitional waters using reduced benthic assemblages

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Abstract

In this study, the use of reduced assemblages of benthic invertebrate taxa is proposed to describe similarity relationships between samples from transitional environments.

A data set from four different studies, made up of 641 samples for a total 203 species, was analysed using permutation randomisation tests in order to extract a pool of taxa able to approximate the full set of species. The identified "operational set", comprising 19 taxa, was capable of adequately reproduce similarity relationships between samples (Rho $>$ 0.90, $p < 0.001$). All selected taxa were easily extractable from the samples and easy identifiable by non-specialised technicians; these characteristics were considered appropriate for the development of rapid and cost-effective monitoring procedures based on benthic invertebrate assemblages.

Keywords: Biomonitoring; Lagoon of Venice; Macrobenthos; Multivariate analysis; Operational set

1. Introduction

The importance of the benthic community in quality assessment is paramount (Bilyard, 1987). Many natural and anthropogenic stressors have repercussions on benthic infauna, altering trophic interactions and community structure (Pearson and Rosenberg, 1978; Gray et al., 1990; Dauer, 1993). The limited movement capacity of benthic organisms make them subject to local stressors over long periods of time; consequently, their response to stress can provide an integrated picture of the "state of health" of the site. For these reasons, benthic infaunal assemblages have been extensively applied as indicators of marine and estuarine conditions (for a review, see Diaz et al., 2004).

Recently, attention was drawn by the European Water Framework Directive (WFD) (EU, 2000) toward macrobenthos as an instrument for evaluating environmental quality, provoking an immediate response from scientists (Borja, 2004; Borja et al., 2003, 2004; Muxika et al., 2005; Rogers and Greenaway, 2005; Rosenberg et al., 2004; Salas et al., 2004).

The WFD clearly indicates that the "ecological status" of a water body should be defined on the basis of deviations from "reference conditions" ("Type-specific biological reference conditions shall be established...", Annex II, 1.3; Annex V, 1.4.1.). To do this it is necessary to be able to compare different situations. The measure of departure from "reference conditions" can be obtained by a measure of the distance (metric) or of the (dis)similarity (nonmetric).

The structure of biological assemblages is currently used to determine similarity relationships between samples. Multivariate methods are largely used to detect responses of benthic communities to environmental change and to evaluate relationships between sites on the basis of distance and similarity measures (e.g. Clarke and Warwick, 2001).

"Transitional Waters" is one among the five types of surface waters considered by WFD (article 2.6), and they include estuaries, river mouths, coastal lagoons and all brackish coastal water bodies (EU, 2000; Cullingford et al., 2003).

To monitor the habitat patchiness and temporal variability typical of wide transitional environments (Barnes, 1980; McLusky, 1981; Kjerfve, 1993), a high number of stations and frequent sampling are needed. The highly aggregated

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distribution of lagoonal benthic infauna, its seasonal variability, and the variegated micro-topography of the seabed require several replicates for reliable estimates of community parameters (Holme and McIntyre, 1984; Gray et al., 1992; Rumohr, 1999).

The rapid seasonal evolution of estuarine communities imply that time for field operations is limited, a strict timetable is necessary, and skilled technicians with knowledge of the local environment are required. In addition, the aggregation of cohesive lagoonal sediments and high contents of detritus mean that sieving and sorting are tedious and laborious tasks which, however, must be carefully carried out. It follows that routine monitoring based on a classical community approach can only be easily performed on small transitional bodies of water whereas, for larger basins, it requires very labour-intensive activities, with a large amount of work.

Efforts should concentrate on developing a framework for cost-effective biological monitoring of transitional environments focusing, as a first step, on the benthic species to monitor. Not all species influence the multivariate pattern arising from similarities between samples in the same way; their "importance" depends on the attributes used (numerical abundance, biomass, coverage), and their distribution among samples. The analysis of a small subset of the total number of species may give similar results to that of the full species analysis. This was evidenced either when the number of species analysed is reduced (Clarke and Warwick, 1998; Mistri et al., 2001) or when the species are aggregated to higher taxonomic levels (Ellis, 1985; Marchant et al., 1995; Mistri and Rossi, 2001).

The goal of this work is to find a small subset of taxa capable of reproducing similarity relationships between samples, like the original set of species. To be usable in rapid monitoring protocols, the selected taxa should be easy to identify and readily extractable from samples. A subset of taxa from the whole assemblage could compose a meaningful "profile" that summarises the original assemblage structure. As a profile is made up of traits, a benthic assemblage profile is made up of trait-species or trait-taxa. The strength of each trait will contribute to depict the whole profile. It is beyond the aim of this paper to give any evaluation of environmental quality or indication of reference conditions.

2. Materials and methods

The Lagoon of Venice is one of the largest Mediterranean transitional systems, covering a surface area of about 550 km^2, for these reasons it was chosen as representative of wide transitional water bodies.

The source of data consisted in four data sets from benthic studies carried out between 1990 and 1994, by the Magistrato alle Acque di Venezia (Water Authority of Venice)-Consorzio Venezia Nuova. The origins of data were: Dataset-1 from study "A.3.16 I" (54 samples; 61 species; executor: SGS-Ecologia, Padua, Italy; 1990); Dataset-2 from study "Aree Confinate" (161 samples; 70 species; executor: Biotecnica snc, Mestre-Venice, Italy, 1991), Dataset-3 from study "A.3. 16 II" (360 samples; 143 species; executor: SGS-Ecologia, Padua, Italy, 1992), Dataset-4 from study "AIDA" (66 samples; 64 species; executor: University of Triest, Triest, Italy, 199294). All studies were carried out inside the Lagoon of Venice (Italy) during different years and seasons, embracing a number of habitats from salt marsh edges to subtidal shoals and along transects from the mainland to the sea.

A total of 641 samples made up the data set accounting for 203 species.

Numerical abundances were analysed using multivariate techniques. The procedure adopted to select taxa was as follows;

1. From each study, similarity matrices based on the Bray–Curtis similarity index (Bray and Curtis, 1957) were calculated on numerical abundances after square root transformation.
2. Species that affect similarities between samples the most were identified by applying the BVSTEP routine (Clarke and Warwick, 1998) to similarity matrices obtained from the whole set of species. BVSTEP is a stepwise algorithm which examines possible species combinations repeating the procedure several times, starting with different initial species subsets. The BVSTEP routine (ran using default settings: 50% of variables, 5 restarts, Rho$>$0.95) enables the identification of "influential species", i.e. a small subsets of taxa responsible for assemblage multivariate pattern at a given level of Spearman's rank correlation (Clarke and Warwick, 2001). BVSTEP can identify more than one subset of "influential species" depending on the number of restarts. The strength of correlation is expressed by the Spearman rank correlation coefficient (Rho): the coefficient values fall between -1 and $+1$, extremes corresponding to the complete opposition or complete agreement between two data sets, a Rho value around zero indicate the absence of any match.
3. Among the most frequent "influential species" identified by BVSTEP from all the subsets, those which were informative, easy to identify and readily extracted from samples were selected.
4. Taxa that are difficult to identify at a species level were aggregated as a genus or family, according to the "Checklist of the Italian Fauna" (Checklist delle specie della fauna italiana, Minelli et al., 1995).
5. These taxa (hereafter called "operational taxa") form a unique restricted assemblage (hereafter called "operational set"). Numerical abundances relative only to "operational taxa" were then used to produce other similarity matrices. The new similarity matrices were searched for correlation with the original full-species matrices using the RELATE procedure (Clarke and Warwick, 1994). RELATE is an algorithm conceived to test the hypothesis of no relation between multivariate