SPECIES SELECTION FOR ASSESSING THE VULNERABILITY OF MARINE COMMUNITIES TO CLIMATE CHANGE AND TRAWLING USING TRAIT-BASED INDICES

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Introduction

Biological traits analysis (BTA) incorporates information on species' distributions and the biological characteristics they exhibit, to produce a **summary of the biological trait composition of assemblages**.

It is a valuable tool for measuring **ecosystem function** and **marine species assemblages**. Thus, it results a powerful way to **measure ecosystem health and vulnerability** to **human impacts** and **global change** on ecological functioning.

The **main objective** of this study is thus to identify the appropriate selection of species to characterize, according to their biological traits, the sensitivity of the demersal communities of Atlantic and Mediterranean shelves in the Iberian Peninsula to climate change, trawling and their interaction.

Material and methods



• Richness and abundance of nearly 1000 species identified in numerous geolocated hauls were gathered from two standardized annual bottom trawl surveys (Fig.1) conducted in the Atlantic, DEMERSALES (since 1983), and in the Mediterranean, MEDITS (since 1994).

• Information of **15 biological traits** of the most recurrent **247 demersal** species (**142 fishes (57%) and 105 invertebrate (43%), Fig.2, a**) was compiled from online databases (i.e. WoRMS, BIOTIC, FishBase or SeaLifeBase) and scientific publications.

• Traits (Fig.2, b), were selected based on the general knowledge of the effect of trawling impacts on selected species (habitat and morphology traits), their vulnerability to climate changes (related to environmental niche) or both impacts (life-history traits). Between 46.6 and 95.5% of traits in the dataset were obtained at the species level (Fig.2, b).



• Different subsets of species were determine based on the abundance and biomass of species across both data sets (**Fig 3, 4**), as well after filtering each survey database by different annual occurrence, abundance within the year and abundance per haul (**Fig 4**).

• Analysis on **Community-Weighted Means (CWM) traits** to characterize communities by combining information on species traits and distribution (by haul and year) were performed.

Results and discussion

By identifying the 10 most representative species across the two datasets, according to total **richness and biomass**, it was found that they accounted for more than 50% of the species in terms of richness and about 40% in terms of biomass for the Atlantic (**Fig. 3a**). For the Mediterranean, on the other hand, these percentages decreased (**Fig. 3b**).

For each long-term series, we obtained 4 subsets of species corresponding to 4 different filters, that acted on species annual occurrence, abundance within the year and abundance per haul (**Fig 4**).



Although the pool of species captured in each survey differs, the number of species (Figs. 4ab) doesn't significantly affect the taxonomic distribution (Phyla), which is similar for the 4 subsets chosen in both long-term series (DEMERSALES and MEDITS), fishes being the most representative group in all subsets.



Figure 5 shows the **CWM traits analyses** over the two long-term series (**DEMERSALES; Fig. 5a, and MEDITS; Fig. 5b**) for two traits (age maxima and feeding preference) and selecting two subsets of species (F1 and F3). F1 was selected after filtering each survey database by annual occurrence (we kept species that appeared at least 10 years), abundance within the year (we only kept those species that occurred at least in 12 hauls a year) and abundance per haul (by getting rid of rare species, with abundance under the first decile). On the other hand, F3, selects only the 45 species that represent the highest abundance over the entire series. In addition the mean for each trait was calculated taking into account the whole community, and on the other hand, it was calculated by selecting only those taxa for which traits are available at specie level. There is no difference in the trend shown by these traits over the years by restricting the number of species.

Our analysis confirmed that the availability of biological information is strongly biased towards abundant and large species, particularly those of fisheries importance or of conservation concern. In this sense, preliminary results indicate that a strict selection biased towards these groups of species is sufficient to characterize the sensitivity of the entire community in both areas.





