Marine Environmental Research 200 (2024) 106631

Contents lists available at ScienceDirect

Marine Environmental Research

journal homepage: www.elsevier.com/locate/marenvrev

Unveiling the role of taxonomic sufficiency for enhanced ecosystem monitoring

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ARTICLE INFO

Keywords:
Epifaunal assemblages
Artificial substrates
Artificial Seaweed Monitoring System
Taxonomic sufficiency
Ecosystem monitoring

ABSTRACT

The use of Artificial substrates (AS) as sampling devices addresses challenges in macrofaunal quantitative sampling. While effectively capturing biodiversity patterns, the time-intensive identification process at the species level remains a substantial challenge. The Taxonomic Sufficiency approach (TS), where only taxa above species level are identified, arises as a potential solution to be tested across different environmental monitoring scenarios. In this paper, we analyzed three AS macrobenthic datasets to evaluate the odds of TS in improving the cost-effective ratio in AS monitoring studies and establish the highest resolution level to detect assemblage changes under different environmental factors. Results indicated that the family level emerged as a pragmatic compromise, balancing precision and taxonomic effort. Cost/benefit analysis supported TS efficiency, maintaining correlation stability until the family level. Results also showed that reducing resolution to family does not entail a significant Loss of Information. This study contributes to the discourse on TS applicability, highlighting its practicality in monitoring scenarios, including spatial-temporal studies, and rapid biodiversity assessments. Additionally, it highlights the “second best approach” of family-level practicality depending on the specific monitoring scenario and recognizes the importance of the species-level “best approach” before applying TS in monitoring studies.

1. Introduction

Artificial substrates (AS), designed to mimic the essential features of natural habitats, provide standardized and replicable sampling devices that allow quantitative sampling, enabling direct comparisons across sites, times, and studies (Baronio and Bucher, 2008; Cacabelos et al., 2010; Carreira-Flores et al., 2023; Edgar, 1991; Leite et al., 2023; Norderhaug et al., 2002; Ransome et al., 2017). Artificial Substrates could be an environmental friendly alternative solution that mitigates the detrimental effects of destructive sampling (e.g., collecting macroalgae for epifauna studies) for assessing biodiversity, especially in the context of monitoring Marine Protected Areas (MPAs). Implementing less-destructive methodologies that result in minimal to no ecosystem disturbance upon AS deployment and collection is highly desirable, in this context. However, assessing biodiversity based on AS methodologies implicates several challenges (Danovaro et al., 2016; Rice et al., 2012). AS-based monitoring studies face two primary issues. Firstly, sampling macrofauna assemblages using AS is not instantaneous like direct methods (e.g., scraping, cutting macroalgae thallus, or using underwater benthic pumps), as it requires the deployment of the AS, time for colonization by macrobenthic organisms and the retrieval of the AS (Cacabelos et al., 2010; Carreira-Flores et al., 2020; García-Sanz et al., 2014). Secondly, AS-based methodologies are subjected to the time-consuming and expertise constraints of obtaining macrobenthic

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https://doi.org/10.1016/j.marenvres.2024.106631
Received 10 April 2024; Received in revised form 27 June 2024; Accepted 1 July 2024

data at high taxonomic resolution. Therefore, an accurate taxa identification depends on the existence and disponibility of a reliable fauna description, trained expert researchers, specialized methods, and extensive laboratory work (Bacci et al., 2009).

Macrobenthic invertebrates are reliable biological indicators for monitoring programs due to their conspicuous nature, easy sampling, and rapid response to environmental changes (Aguado-Giménez et al., 2015; Salas et al., 2006; Van Der Linden et al., 2015). However, the detailed identification of macrofauna at the species level presents numerous challenges. On the one hand, the aforementioned time-consuming process of sample processing and identification (Jones, 2008; Terlizzi et al., 2003) combined with the scarcity of specialized taxonomists (Hopkins and Freckleton, 2002; Magurran and Queiroz, 2010) partly caused by the prevailing trend in funding policies favoring applied research over basic research, creates a significant limitation. This time-consuming process leads to extensive time and human resource costs in macrofauna-based monitoring studies. On the other hand, monitoring studies are frequently subject to tight submission deadlines often commissioned by government administrations. Therefore, validating and implementing monitoring methodologies that reduce time-consuming efforts and economic costs while maintaining accuracy for determined monitoring tasks is necessary.

The less-destructive monitoring approach based on the use of AS (Artificial Seaweed Monitoring System, ASMS) proposed by Carreira-Flores et al. (2023, 2021, 2020) has been demonstrated to be sensitive to scale-dependent patterns and capture the variability of macrobenthic communities over time. ASMS methodology has also been reported to be more efficient in capturing biodiversity than other more established and widely accepted AS methodologies (Leite et al., 2023). However, the high abundance of organisms captured by the ASMS resulted in the need for a high investment of time to sort and identify the organisms to the highest taxonomic resolution (species level). Therefore, the validation process of this methodology will benefit from the standardization of an efficient effort/benefit approach that obtains accurate results to carry out quick or extensive marine monitoring programs. For instance, implementing the proposed methodology in monitoring programs that require a fast detection of eventual changes in the assemblage composition (e.g. pollution discharges monitoring) could offer significant advantages. It enables quick responses in applying management solutions before reaching the point of no return, thereby facilitating proactive intervention.

To address the challenges associated with time-intensive approaches, the scientific literature suggests that studies aiming to identify benthic assemblage structure can be conducted using low taxonomic resolution data (de Oliveira et al., 2020; Gerwing et al., 2020; Terlizzi et al., 2009; Vijapure and Sukumaran, 2019). Taxonomic Sufficiency (TS) involves identifying taxa at lower taxonomic levels than species, enabling the detection of changes in assemblages exposed to different factors (e.g. environmental stressors) while minimizing the Loss of Information (Ellis, 1985). The TS approach has increased attention as a method to optimize costs and overcome time constraints in marine monitoring studies (Chapman, 1998; Pitacco et al., 2019; Vijapure and Sukumaran, 2019). Taxonomic Sufficiency has been tested in many studies focused on marine pollution (Mendes et al., 2007; Rubal et al., 2009), marine macroalgae communities (Anderson et al., 2005; Veiga et al., 2013), transition waters (Pitacco et al., 2019), hard bottoms (Vijapure and Sukumaran, 2019), benthic communities monitoring (Sánchez-Moyano et al., 2006), variation along natural gradients (Terlizzi et al., 2009), spatial distribution patterns (Dethier and Schoch, 2006; Tataranni et al., 2009), and coastal defense structures (Sedano et al., 2020). Those studies highlight the family level as the taxonomic level that gives the best balance in the cost/benefit ratio, showing a compromise between results' precision and taxonomic effort's reduction. However, none of these studies have evaluated the validity of the TS approach for monitoring benthic assemblages using AS. Even so, Magierowski and Johnson (2006) tested a subset-taxa method on macrofauna communities inhabiting artificial kelp holdfasts. Although this is not a TS method, it represents another form of taxonomic surrogacy applied to macrobenthic communities associated with AS. Their study found that the richness of crustaceans and polychaetes at the family level were good predictors of total familial richness, suggesting that higher taxonomic levels can serve as effective surrogates for biodiversity.

This paper analyzed three datasets of macrobenthic assemblages associated with two different types of AS and two species of brown macroalgae as a natural substrate reference, obtained through three different studies carried out in two Rías of Galicia (NW Spain). Dataset 1 (Carreira-Flores et al., 2020) examines the variability of macrobenthic macrofauna using two types of Artificial Seaweed Monitoring System (ASMS) and natural macroalgae as references, exploring whether ASMS with different structural complexities captures similar faunal variability over time. The hypotheses tested in Dataset 1 are: H1: ASMS and natural macroalgae will capture similar variability of mobile epifauna at different taxonomic resolutions, and H2: ASMS of different complexities will host distinct assemblages of mobile epifauna. Dataset 2 (Carreira-Flores et al., 2021) investigates differences in capturing macrofaunal assemblages between dendritic (ASMS) and crevice (ACMS) substrates across two locations, with the hypothesis: H3: Dendritic and crevice substrates will support different assemblages at different taxonomic resolutions. Dataset 3 (Carreira-Flores et al., 2023) assesses the regional scale variability of natural assemblages captured using ASMS at different locations and times, with the hypothesis: H4: the variability of natural assemblages captured by ASMS will differ between locations on a regional scale at different taxonomic resolutions. Those datasets represent variability in temporal and spatial (local and regional) assemblages captured by AS and harbored by natural macroalgae. The present study aims to: 1) evaluate the odds of the TS approach to improve the cost-effective relationship in monitoring studies based on AS, concerning different spatial and time scales, and 2) establish the highest level of taxonomic resolution without the loss of biological information that enables the detection of changes in assemblages exposed to different conditions, hypothesizing that according to the literature the family level will be the most suitable level for this purpose. The efficiency of TS was estimated by comparing the Loss of Information the cost/benefit ratio, and by multivariate analyses, taking into account five levels of taxonomic aggregation (species, genus, family, order, and class).

2. Material and methods

The three analyzed datasets correspond to three different studies carried out in the Ría de Ferrol and the Ría de Vigo (NW Iberian Peninsula) between 2017 and 2019 (Carreira-Flores et al., 2020, 2021, 2023) (Fig. 1). Both rías are SW-NE orientated and present a semidiurnal mesotidal regime. Besides, the rías are impacted by human activities such as dockyards, commercial harbors, bivalve mollusc harvesting, sewage runoff pollution, and industrial discharge (see Carreira-Flores et al., 2023).

In previous studies, three detailed datasets for two types of "Artificial Seaweed Monitoring System, ASMS" and one type of "Artificial Crevice Monitoring System, ACMS" (Fig. 2) assemblages were analyzed, demonstrating that, for the species level, the approach proposed by Carreira-Flores et al. (2023, 2021, 2020) is sensitive to scale-dependent patterns and captures the variability of macrobenthic communities over time. The present study aggregated data from the three datasets to species (considered as a high level of taxonomic resolution), genus and family (considered as a medium level of taxonomic resolution), order, and class (considered as a low level of taxonomic resolution) following the taxonomic classification of the World Register of Marine Species (WoRMS) (WoRMS Editorial Board, 2020).

Spearman's rank correlation among Bray-Curtis similarity matrices based on total abundance between each level of aggregation (species-genus, genus-family, family-order, order-class) was determined using the 2STAGE module in the PRIMER software (Clarke and Gorley, 2001).

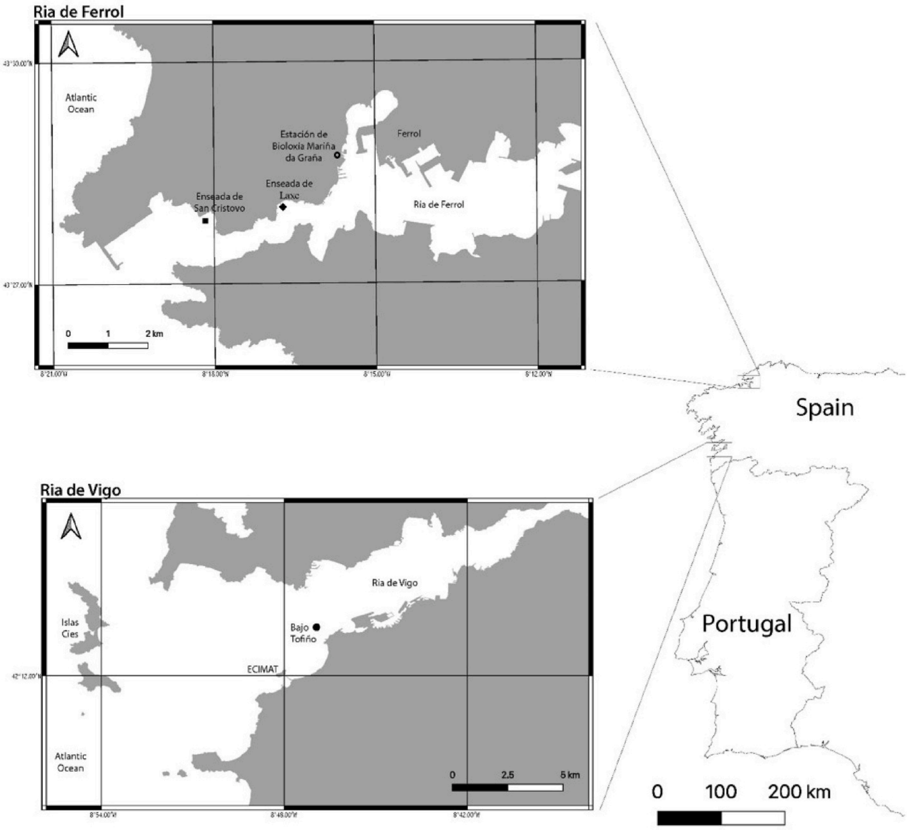

Fig. 1. Location of study areas. ■Enseada de San Cristovo, ◆ Enseada de Laxe, Ría de Ferrol; ● Bajo Tofiño, Ría de Vigo.

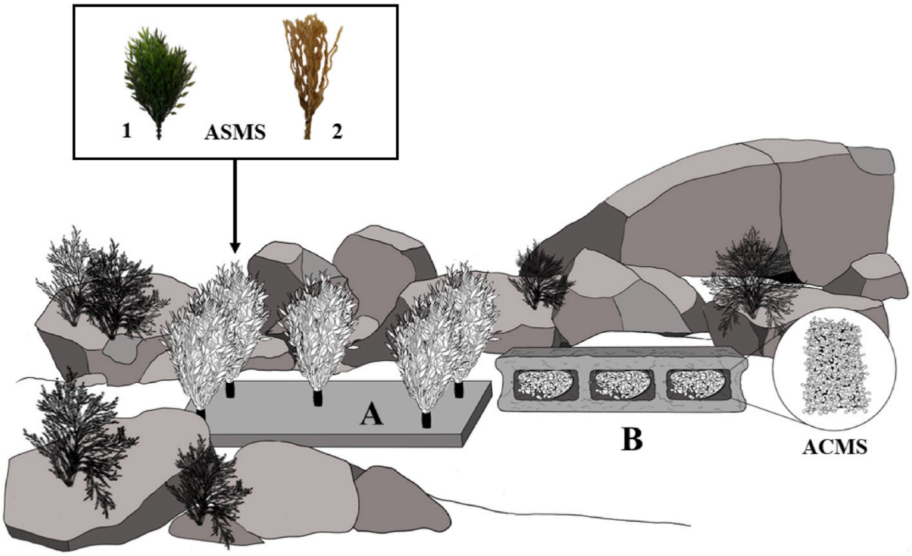

Fig. 2. Experimental scheme deployment of Artificial Seaweed Monitoring System (ASMS) (A) and Artificial Crevice Monitoring System (ACMS) (B) within the natural algae settlement of a rocky reef. Numbers 1 and 2 correspond to different ASMS types used in the experiments: ASMS 1 refers to a complex structure, while ASMS 2 refers to a non-complex structure.

Specifically, to be consistent with the previous analyses, we used square-root transformed density matrices constructed at each taxonomic level to evaluate the consistency of dissimilarity patterns among samples when taxa were aggregated to higher taxonomic levels. Multivariate analyses were conducted using Primer v.6 (Clarke and Gorley, 2001) with PERMANOVA + add-on (Anderson et al., 2008).

Variations in the taxonomic structure of benthic assemblages were analyzed according to Bacci et al. (2009) through the difference of Number of Taxa (NT): NTx – NTx+1 defined as 'Loss of Information α''. The percentage of Loss of Information value was calculated ((NTx –

NTx+1)/NTx * 100) from the lowest to the highest taxonomic level considered (species-genus, genus-family, family-order, order-class). Loss of Information values quantify the reduction in taxonomic detail when transitioning from a lower (x) to a higher (x+1) taxonomic level; higher values indicate a significant loss of information, while lower values suggest minimal information loss (Pitacco et al., 2019).

To objectively select the taxonomic level with the minimal Loss of Information and the least taxonomic effort, a cost/benefit ratio was calculated for each dataset according to the proposed formula (*sensu* Karakassis and Hatziyanni, 2000):

$$CB_L = \frac{(1 - r_L)}{\frac{S - t_L}{S}}$$

CB_L corresponds to the cost/benefit ratio at a defined taxonomic level L, r_L the Spearman's rank correlation (computed on Bray-Curtis similarity) between the taxonomic level L and the species level, t_L the number of taxa present at taxonomic level L, and S the number of species. The numerator and, therefore, the ratio tends to 0 when Spearman's correlation between L and species level is highly correlated. The denominator (the benefit) is the proportion of decrease in the taxa that needs to be identified in comparison to the number of species (see Karakassis and Hatziyanni, 2000).

Non-parametric permutational multivariate analysis of variance [PERMANOVA (Anderson, 2017);] was used to test the different hypotheses about variations in epifaunal assemblages. Before performing the PERMANOVA test, analyses of multivariate dispersion were also conducted to test for the homogeneity of the dispersions between groups of samples (PERMDISP, analysis). This verification was performed for each dataset in their respective articles (Carreira-Flores et al., 2020, 2021, 2023), confirming that significant differences were not influenced by the dispersion or variability among replicates (Permdisp, $p < 0.05$). Due to the features of the three datasets and to be consistent with previous analyses, square-root transformed density data was used to build five Bray-Curtis dissimilarity matrixes for each study (aggregated to species, genus, family, order, and class) to obtain a more 'balanced' view of the assemblages by reducing the influence of the most numerous taxa (Clarke and Gorley, 2001). When appropriate, a posteriori multiple comparisons (PERMANOVA pair-wise tests) were made to test for differences between/within groups for pairs of levels of factors. The tests were based on 9999 unrestricted random permutations of data. Besides, non-metric multidimensional scaling (nMDS) was used as the ordination method for exploring differences in the assemblage responses at every aggregation level.

For the first dataset (Carreira-Flores et al., 2020) two hypotheses were tested, (H1) ASMS and macroalgae, both with similar structures, will capture similar variability of mobile epifauna at different levels of taxonomic aggregation (complex: ASMS 1 and *Gongolaria baccata* (S.G. Gmelin, 1768) Molinari and Guiry, 2020; non-complex: ASMS 2 and *Halidrys siliquosa* (Linnaeus) Lyngbye, 1819), and (H2) ASMS of different complexity will shelter different assemblages of mobile epifauna at different levels of taxonomic aggregation. For the first hypothesis, the factors studied were: the type of substrate (fixed, 3 levels, ASMS_1 vs. ASMS_2 vs. Natural macroalgae) and time (random, two levels, "time 1" vs. "time 2"); for the second hypothesis were: the type of substrate (fixed, 2 levels, ASMS 1 vs. ASMS 2), location (random, 2 levels, Enseada de Laxe vs. Enseada de San Cristovo) and time (random, 2 levels, time1 vs time2).

The second dataset (Carreira-Flores et al., 2021) tested the hypothesis (H3) that dendritic (ASMS) and crevice (ACMS) substrates will support different assemblages at different levels of taxonomic aggregation. For this hypothesis, the factors studied were Substrate type (fixed, 2 levels, dendritic vs crevice) and Location (random, 2 levels, Enseada de Laxe vs. Enseada de San Cristovo).

The third dataset (Carreira-Flores et al., 2023) tested the hypothesis (H4) that the variability of natural assemblages captured using ASMS will differ between locations on a regional scale at different levels of taxonomic aggregation. For this hypothesis, the factors studied were Location (fixed, two levels, Enseada de San Cristovo vs. Bajo Tofiño) and Time (random, four levels, time 1 vs. time 2 vs. time 3 vs. time 4).

3. Results

The highest number of taxa for high species resolution was observed in dataset 2 for ACMS and ASMS recovered in Enseada de Laxe after 3 months of deployment in June 2018 (120 and 98 taxa, respectively) and the lowest associated with *H. siliquosa* and ASMS 2 of dataset 1 recovered in Enseada de San Cristovo in March 2018 (11 and 24 taxa respectively) (Table 1). Besides, the highest number of taxa for genera and family medium level of resolution corresponded to samples with the highest number of taxa for species high resolution, for instance: ACMS of dataset 2 recovered in Enseada de Laxe after 3 months of deployment in June 2018 corresponded to 88 taxa aggregated to genus level and 60 to family level (120 species-level); ASMS of the dataset 3 recovered in Enseada de San Cristovo after 12 months in June 2019 corresponded to 83 taxa aggregated to genus level and 65 to family level (95 species-level) (Table 1). Similarly, the lowest number of taxa for medium genera resolution and family corresponded to samples with the lowest number of taxa for species resolution, for instance: for dataset 1 recovered in Enseada de San Cristovo in March 2018, *H. siliquosoa* corresponded to 7 genera and 6 families taxa (11 species-level); and ASMS 2 correspond to 19 genera and 17 families (24 species-level). The aggregation for order and class resolution data followed the same pattern.

The Loss of Information from species to class level showed the same pattern for the three datasets, with the lowest percentages of Loss of Information from species to genus and genus to family (Fig. 3). The average of the percentages of Loss of Information from species to genus was 20.33 ± 7.43%, from genus to family was 19.79 ± 5.55, from family to order was 51.75 ± 6.65 % and from order to class was 52.43 ± 7.75%. Loss of Information from genus to family was 19.79 ± 5.5 %, with percentages ranging from 31.81 % (Dataset 2, ACMS, Enseada de Laxe) and 10.52 % (Dataset 2, ASMS 2, Enseada de San Cristovo, March 2018) indicating the presence of several families with more than one genus. Loss of Information was noticeably higher from family to order (from 57.14% - Dataset 1, ASMS 2, Enseada de Laxe, March 2018; to 37.93% - Dataset 2, ACMS, Enseada de San Cristovo, June 2018) and order to class (from 67.85% - Dataset 2, ACMS, Enseada de Laxe, June 2018) than the previous ones. In most samples of the three datasets, the highest percentage of Loss of Information was observed above the family level.

The cost/benefit ratio analysis (CBL) that depends on Spearman's rank correlation values (Rho) showed minimal values at the family level, becoming noticeably higher at the order and class level. Rho values (Significance level of sample statistic: 0.1 %) remain stable in the three datasets between species-genus and species-family but highly decreased from species-order and species-class, especially in dataset 2 (Fig. 4). Therefore, for the given datasets the cost/benefit ratio analysis showed that the family level provides the best balance between the precision of the results and the decrease in taxonomic effort.

PERMANOVA results highlighted significant differences ($p < 0.05$) in the interaction of factors at every taxonomic level for the three datasets (Table 2). For PERMANOVA post-hoc tests (pair-wise tests), the significant differences at different levels of taxonomic aggregation remained stable up to the order level (Table 2). Accordingly, nMDS plots showed a clear distinction of assemblages of the 3 datasets until the family level, at higher levels of taxonomic resolution (Order and Class), the differences became less and less distinct, presenting an undistinguishable differentiation in the nMDS (Figs. 5–8).

4. Discussion

Due to the increasing need to study human interventions in near-shore zones, there has been an intensive effort to develop standard

Table 1
Summary of the taxonomic aggregations used for hypothesis testing among datasets. The numbers correspond to the number of taxa for each taxonomic aggregation (species, genus, family, order, and class).

				Species High resolution	Genus Medium resolution	Family Medium resolution	Order Low resolution	Class Low resolution
Dataset 1	E. de Laxe	Mar. 2018	ASMS 1	58	45	37	16	6
			ASMS 2	49	43	35	15	7
			G. bac	48	39	32	15	6
		Jun. 2018	ASMS 1	89	65	49	21	10
			ASMS 2	69	54	46	22	11
			G. bac	77	59	43	21	10
	E. S. Cristovo	Mar. 2018	ASMS 1	41	34	30	13	6
			ASMS 2	24	19	17	10	5
			H. silq	11	7	6	4	3
		Jun. 2018	ASMS 1	70	52	42	19	9
			ASMS 2	60	49	41	20	9
			H. silq	46	39	33	12	7
Dataset 2	E. de Laxe	Jun. 2018	ASMS 1	98	71	53	23	12
			ACMS	120	88	60	28	9
	E. S. Cristovo	Jun. 2018	ASMS 1	67	47	38	18	9
			ACMS	54	37	29	18	8
Dataset 3	E. S. Cristovo	Sept. 2018	ASMS 1	69	61	53	24	11
		Dec. 2018	ASMS 1	97	78	65	30	13
		Mar. 2019	ASMS 1	76	65	53	25	11
		Jun. 2019	ASMS 1	95	83	65	30	15
	Bajo Tofiño	Sept. 2018	ASMS 1	69	67	47	25	11
		Dec. 2018	ASMS 1	83	67	52	28	14
		Mar. 2019	ASMS 1	86	73	54	27	13
		Jun. 2019	ASMS 1	89	73	58	26	12

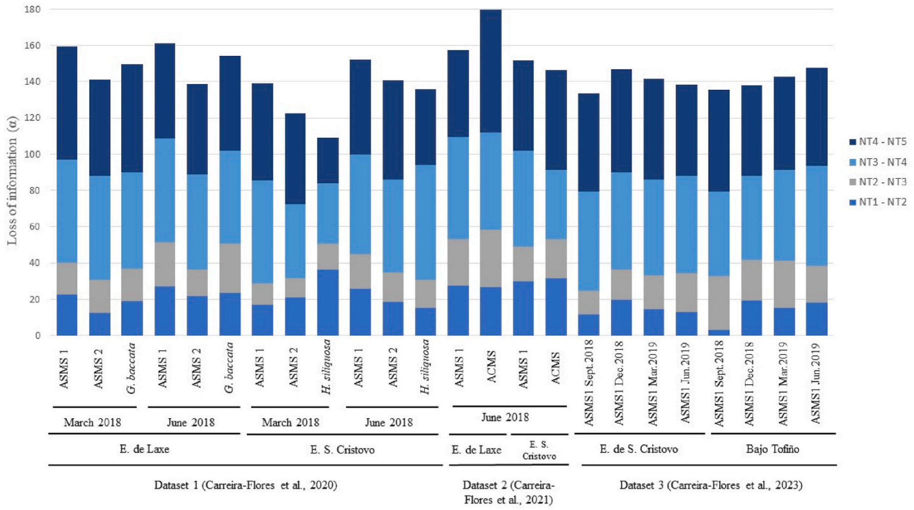

Fig. 3. Loss of Information (α), from higher taxonomic resolution to low-taxonomic resolution (NT1: species-level; NT2: genus-level; NT3: family-level; NT4: order-level; NT5: class-level) for the three datasets.

methodologies that maximize information while reducing effort and costs (Vijapure and Sukumaran, 2019). The ASMS and ACMS standard less-destructive methodology proposed by Carreira-Flores et al. (2023, 2021, 2020) has been demonstrated to capture representative local biodiversity, as the AS effectively sample the surrounding natural environment biodiversity, showing sensitivity to scale-dependent patterns and temporal variations across different factors. However, the time-intensive process of sorting and identifying macrobenthic organisms at the species levels remains a substantial challenge. The need for expedited biodiversity assessments has led to the emergence of alternative methodologies, such as the combination of ARMS and metabarcoding techniques (e.g. Obst et al., 2020; Zimmerman and Martin, 2004). While these DNA-based approaches offer accelerated biodiversity assessments, they fall short in providing detailed taxa abundance and identity data, which is crucial for understanding assemblage dynamics and function.

Contrary to the customary use of ARMS-DNA-based approaches, studies such as Leite et al. (2023) highlight the efficiency of ASMS in capturing taxa, especially regarding species lists. Although the ASMS methodology requires considerable time for taxonomic identification, it

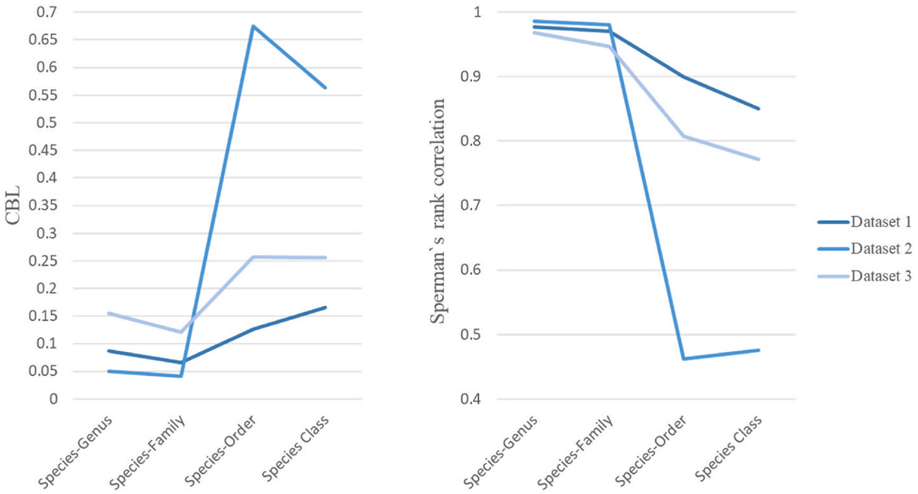

Fig. 4. Cost/benefit ratio (CBL) and Spearman's rank correlation (Rho) for different taxonomic levels for the 3 datasets.

has demonstrated its superiority in taxa capture compared to ARMS. Therefore, the challenge persists in obtaining species abundance data efficiently, improving the cost-effective ratio. TS becomes a valuable tool in this situation, allowing for information optimization while maximizing efforts and minimizing costs in monitoring studies.

Our study explores the application of TS as a complementary approach to overcome the challenges associated with time-consuming and labor-intensive taxonomic identification. The validity of using higher taxonomic levels as surrogates for detailed species-level identifications has been supported by various studies. Mellin et al. (2011) conducted a global meta-analysis demonstrating that higher-taxa surrogates, including family-level identifications, can effectively predict marine biodiversity patterns across different spatial scales. Similarly, Kokesh et al. (2022) reported that coarser taxonomic resolutions, such as family level, retained robust community-level patterns of spatial and temporal variation in the long-term monitoring of macrobenthic assemblages. In the case of using AS to capture macrobenthic biodiversity. Magierowski and Johnson (2006) reported that the family level was a good predictor of total richness, suggesting that higher taxonomic levels can serve as effective surrogates for biodiversity. These studies reinforce the potential of using higher taxonomic levels to reduce identification efforts while maintaining ecological relevance, highlighting the practical applicability of TS in marine biodiversity monitoring.

To further investigate the application of TS, we analyzed various taxonomic levels across three datasets, revealing a typical pattern in the Loss of Information. Our results agree with Sánchez-Moyano et al. (2006) suggesting that the family level provides a favorable balance between precision and taxonomic effort as indicated by the cost/benefit ratio analysis, retaining important information whereas having the advantage of being more resilient to the aforementioned challenges of species-level taxonomy. The Spearman rank correlation values (Rho) support the efficacy of TS, emphasizing the stability of Rho between species-genus and species-family levels. Therefore, our results showed that reducing the taxonomic resolution to the family level did not result in aa significant Loss of Information. This reduction still allows us to detect significant differences when they exist at the species level and reach the same conclusions for the proposed hypotheses as working with the species level dataset. Even with the reduction of taxa when applying TS, the relative abundance remains equivalent.

Loss of Information, understood as the loss of taxa richness, followed the same pattern in the three datasets. The highest Loss of Information percentage was observed between family and order, and between order and class, as reported from macrofauna assemblages in transition waters (Pitacco et al., 2019). The similar values of Loss of Information suggest comparable levels of taxonomic heterogeneity, with approximately the same number of taxa belonging to the same higher taxa among different factors across datasets. The cost/benefit ratio analysis for the three datasets showed minimal values at the family level, indicating that analysis at this taxonomic level provides the best balance between the precision of the results and decreased taxonomic effort. Our results are in accordance with Karakassis and Hatziyanni (2000). Although the information loss is relatively small at the genus level, the decrease in taxa usually is about 15–25% compared to the number of species. At higher taxonomic levels than family, the reduction in precision is not compensated by the drastic decrease in the number of taxa.

There is no agreement on how the taxonomic resolution can be reduced without loss of biological information (de Oliveira et al., 2020; Karakassis and Hatziyanni, 2000) and if the TS approach has the same effectiveness at different spatial and time scales (Anderson et al., 2005). The loss of biological information may vary depending on the local dataset used in each case, its origin, and the appropriate research context. The behavior may vary when studying different factors in diverse locations, especially if the locations have significant differences. Nevertheless, for spatial scales, the literature suggests that reducing the taxonomic resolution to the family level does not cause subtantial Loss of Information (Anderson et al., 2005; Tataranni et al., 2009). Additionally, for studies focused on monitoring and disentangling spatial patterns, identifying fauna at the family level is a reasonable alternative to the more time-consuming species level identification (Dethier and Schoch, 2006). In this study, the PERMANOVA results revealed significant differences among all three datasets for the proposed hypotheses, irrespective of the level of taxonomic aggregation until family level. The analysis confirmed that family-level identifications were enough to obtain consistent patterns of variability under different factors, allowing us to get the same conclusions as when working with species-level data for the three datasets and associated hypotheses. Accordingly, nMDS plots showed that the dissimilarity patterns among the assemblages obtained using the data analyzed at the species, genus, or family level were remarkably similar for the three datasets, as reported in other studies of TS for benthic invertebrates (Anderson et al., 2005; Bacci et al., 2009; Sánchez-Moyano et al., 2006). Studies focused on the detection of changes in marine assemblages stated that changes in community composition can be detected at levels above species (Sánchez-Moyano et al., 2006; Warwick and Clarke, 1991). Spearman's rank correlation computed between Bray-Curtis dissimilarity matrices transformed at species, genus, and family levels was very high in both datasets. Thus, the identification at the family level seems to have enough resolution accuracy to discriminate ecological patterns in the community structure collected by ASMS/ACMS. Higher taxonomic levels of data aggregation lead to redundant information to describe

Table 2
PERMANOVA and post-hoc results for the proposed comparisons according to the proposed hypotheses for the 3 studied datasets. Numbers indicated p-values and numbers in bold indicated the loss of significant differences at low taxonomic resolution.

Dataset	Subset	Factors				Groups	Taxonomic resolution				
							Species	Genus	Family	Order	Class
Dataset 1	1	Substrate x Location x Time	PERMANOVA factors interaction (p-value)				0.001	0.001	0.001	0.001	0.001
			Pairwise combinations (p-value)	Enseada de Laxe	March 2018	ASMS 1, ASMS 2	0.009	0.009	0.008	0.008	0.015
					June 2018	ASMS 1, ASMS 2	0.008	0.008	0.008	**0.08**	**0.201**
				Enseada de S. Cristovo	March 2018	ASMS 1, ASMS 2	0.008	0.006	0.01	0.011	**0.145**
					June 2018	ASMS 1, ASMS 2	0.008	0.012	0.008	0.005	0.013
	2	Substrate x Time	PERMANOVA factors interaction (p-value)				0.001	0.001	0.001	0.001	0.004
			Pairwise combinations (p-value)	Enseada de Laxe	March 2018	ASMS 1, ASMS 2	0.008	0.01	0.011	0.007	0.011
						ASMS 1, *G. baccata*	0.005	0.008	0.008	**0.086**	**0.126**
						ASMS 2, *G. baccata*	0.009	0.007	0.01	0.006	0.01
					June 2018	ASMS 1, ASMS 2	0.009	0.01	0.008	**0.067**	**0.193**
						ASMS 1, *G. baccata*	0.008	0.011	0.012	0.015	**0.098**
						ASMS 2, *G. baccata*	0.13	0.007	0.014	0.037	**0.239**
	3	Substrate x Time	PERMANOVA factors interaction (p-value)				0.001	0.001	0.001	0.001	0.001
			Pairwise combinations (p-value)	Enseada de S. Cristovo	March 2018	ASMS 1, ASMS 2	0.009	0.007	0.005	0.011	**0.147**
						ASMS 1, *H. siliquosa*	0.007	0.007	0.009	0.012	0.006
						ASMS 2, *H. siliquosa*	0.009	0.007	0.01	0.009	0.013
					June 2018	ASMS 1, ASMS 2	0.007	0.007	0.007	0.012	0.013
						ASMS 1, *H. siliquosa*	0.006	0.008	0.01	0.007	0.013
						ASMS 2, *H. siliquosa*	0.008	0.007	0.007	0.009	0.009
Dataset 2	1	Substrate x Location	PERMANOVA factors interaction (p-value)				0.001	0.001	0.001	0.001	0.001
			Pairwise combinations (p-value)	Enseada de Laxe	June 2018	ASMS 1, ACMS	0.011	0.009	0.009	0.008	0.012
				Enseada de S. Cristovo	June 2018	ASMS 1, ACMS	0.015	0.005	0.01	0.19	0.017
Dataset 3	1	Location x Time	PERMANOVA factors interaction (p-value)				0.001	0.001	0.001	0.001	0.001
			Pairwise combinations (p-value)		September 2018	Enseada de Laxe, Enseada de S. Cristovo	0.011	0.009	0.011	0.011	0.009
					December 2018	Enseada de Laxe, Enseada de S. Cristovo	0.007	0.007	0.012	0.009	0.016
					March 2019	Enseada de Laxe, Enseada de S. Cristovo	0.004	0.009	0.007	0.009	0.007
					June 2018	Enseada de Laxe, Enseada de S. Cristovo	0.008	0.007	0.011	0.011	0.006

spatial patterns (Dethier and Schoch, 2006; Pitacco et al., 2019; Sánchez-Moyano et al., 2006), but more detailed data may be necessary to explain detailed and succinct differences in time and space.

As emphasized by Karakassis and Hatziyanni (2000), TS should be considered in the specific objectives of a given study, not establishing general rules for the selection of the taxonomic level without previous documentation of the effects of decreasing taxonomic resolution in each case of study. Besides, the rationale underlying the cost/benefit index utilization is grounded in recognizing variations in the information loss rate and reducing the number of taxa at each taxonomic level. In this context, a sudden shift in either information loss or taxa count may pinpoint the optimal level for macrofaunal analysis. It is essential to highlight that for monitoring programs the cost/benefit index is primarily used for selecting the "second best" taxonomic level, as monitoring approaches are inherently designated with the species level as the "best taxonomic level" by maxim, according to the extensive literature in marine benthic research (Karakassis and Hatziyanni, 2000). Guerra-García and García-Gómez (2005) reported that species-level identification is imperative for accurately detecting ecological differences in scenarios influenced by chemical pollutants, showing that TS is not always the best approach. Consequently, in some cases, species data should not be disregarded in comparative assemblage studies, and a nuanced balance must be struck based on the specific objectives of each study. An optimal balance in determining the taxonomic level of aggregation should be based on the particular objectives of each situation. Furthermore, maintaining a comprehensive understanding of the sampling sites over the long term is crucial for identifying potential sources of variability (such as annual variations in recruitment and upwelling periods) that may be unrelated to the primary issue justifying the study.

One of the limitations of the TS approach becomes evident when specific species play pivotal ecological roles in the community or possess intrinsic value due to their rarity, non-indigenous status, or endemism, potentially leading to the obscuration of their ecological significance (Terlizzi et al., 2003). TS may not be the ideal approach to adopt in specific comparative analyses. For instance, considering dataset 3, if the primary objective was to assess whether hydrodynamic conditions drive

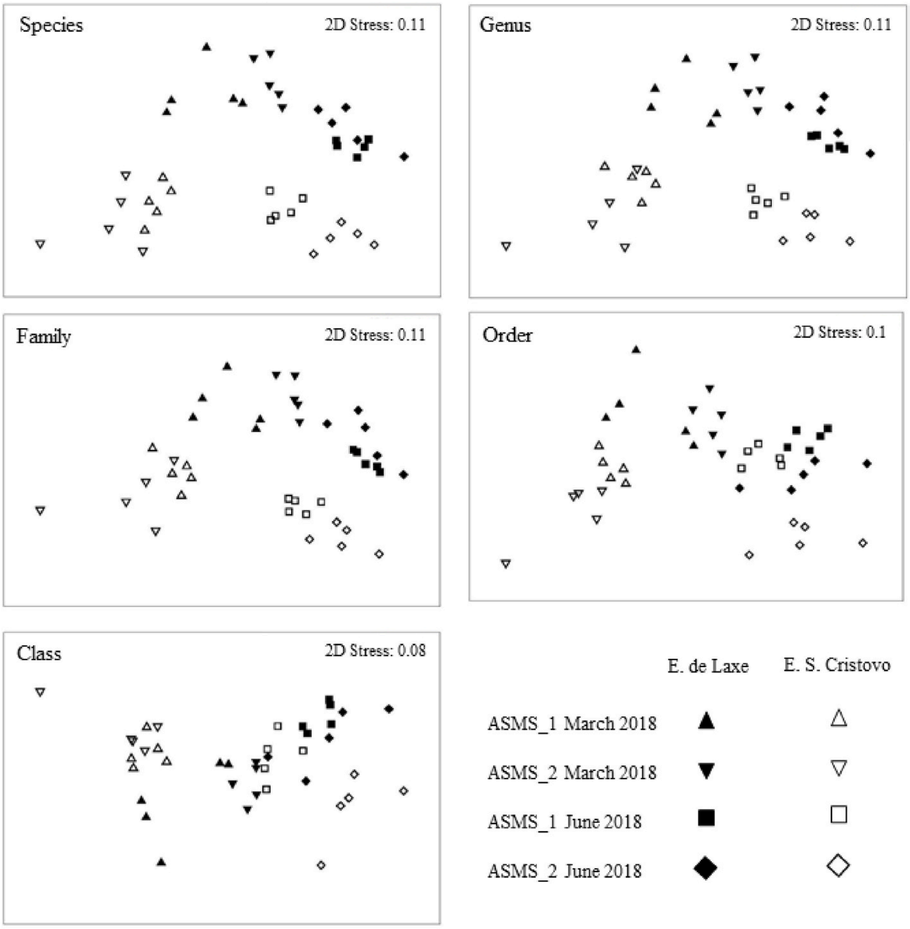

Fig. 5. Non-metric multidimensional scaling (nMDS) plot of epifaunal assemblages of ASMS1 and ASMS 2 at Enseada de Laxe and Enseada de San Cristovo for 3 months of colonization (T1) and 6 months of colonization (T2) at different taxonomic resolutions using Dataset 1.

macrofaunal assemblages, TS might overlook crucial information. According to Conradi et al. (1997), *Stenothoe tergestina* (Nebeski, 1881) is indicative of environments with low hydrodynamics, and *Stenothoe monoculoides* (Montagu, 1813) thrive in higher hydrodynamic conditions. Consequently, if identifications were limited to the genus level, potential differences in hydrodynamics could be obscured.

Additionally, TS can potentially mask variations in species turnover at a local scale or along a latitudinal gradient. In dataset 3, for example, *Ericthonius punctatus* (Spence Bate, 1857) was exclusively found in Bajo Tofiño, whereas the genus *Ericthonius* was present at both locations. The effectiveness of the TS approach may also be compromised when detecting non-indigenous invasive species. In the extended monitoring of dataset 3, the application of TS for the genus *Caprella* might overlook the introduction of NIS. For example, the NIS species *Caprella scaura* Templeton, 1836 with ecologically similar traits to other amphipods in the genus *Caprella* like *Caprella equilibra* Say, 1818; Ros et al. (2015) could be neglected. Studies lacking species-level identification may inadvertently overlook the presence of *C. scaura,* which, according to Ros et al. (2015), has its latitudinal north limit in the 39° parallel of the Atlantic coast of the Iberian Peninsula. Such lack of information may compromise mitigation strategies for non-indigenous species or simply ignore their presence.

The incorporation of TS in methodologies utilizing AS for macrofauna assemblage monitoring can enhance the cost-effectiveness of specific monitoring studies. This enhancement is primarily attributed to the substantial reduction in the time required for sample processing and identification, including additional replicates or extending of studies to broader areas within the same effort. The time needed to sort and identify the lowest taxonomic level is estimated at least twice as long as identifying major taxonomic groups (Chapman, 1998). This efficiency gain in data collection time can significantly boost the spatial resolution of monitoring studies under identical time constraints or serve as a viable strategy for biodiversity assessments that prioritize rapid and continuous data acquisition over high taxonomic resolution (de Oliveira et al., 2020; Sánchez-Moyano et al., 2006). Another advantage of the TS approach in AS is detecting subtle impacts in assemblage monitoring because the aggregation of species into lower taxonomic levels diminishes the inherent variability in species abundances, potentially enhancing the detection of less conspicuous impacts or condition variations (Sánchez-Moyano et al., 2006). On the one hand, according to Warwick (1988), natural environmental variation has a higher effect on macrofaunal assemblages at the species level, whereas anthropogenic impacts do so at higher taxonomic levels. On the other, James et al. (1995) proposed that in natural environments, the spatial distributions of macrofaunal communities remained consistent regardless of whether they were analyzed at the family or species level.

The findings of this study could have significant practical implications for coastal ecosystem management. Understanding the optimal level of taxonomic resolution is pivotal for designing efficient and cost-effective monitoring programs based on ASMS/ACMS. Authorities responsible for coastal management could benefit from adopting a TS identification approach, striking a balance between precision and resource expenditure. This approach would enable the acquisition of biodiversity data while reducing the time and initial financial investments associated with species-level identifications. TS can offer valuable insights into addressing identification challenges, particularly

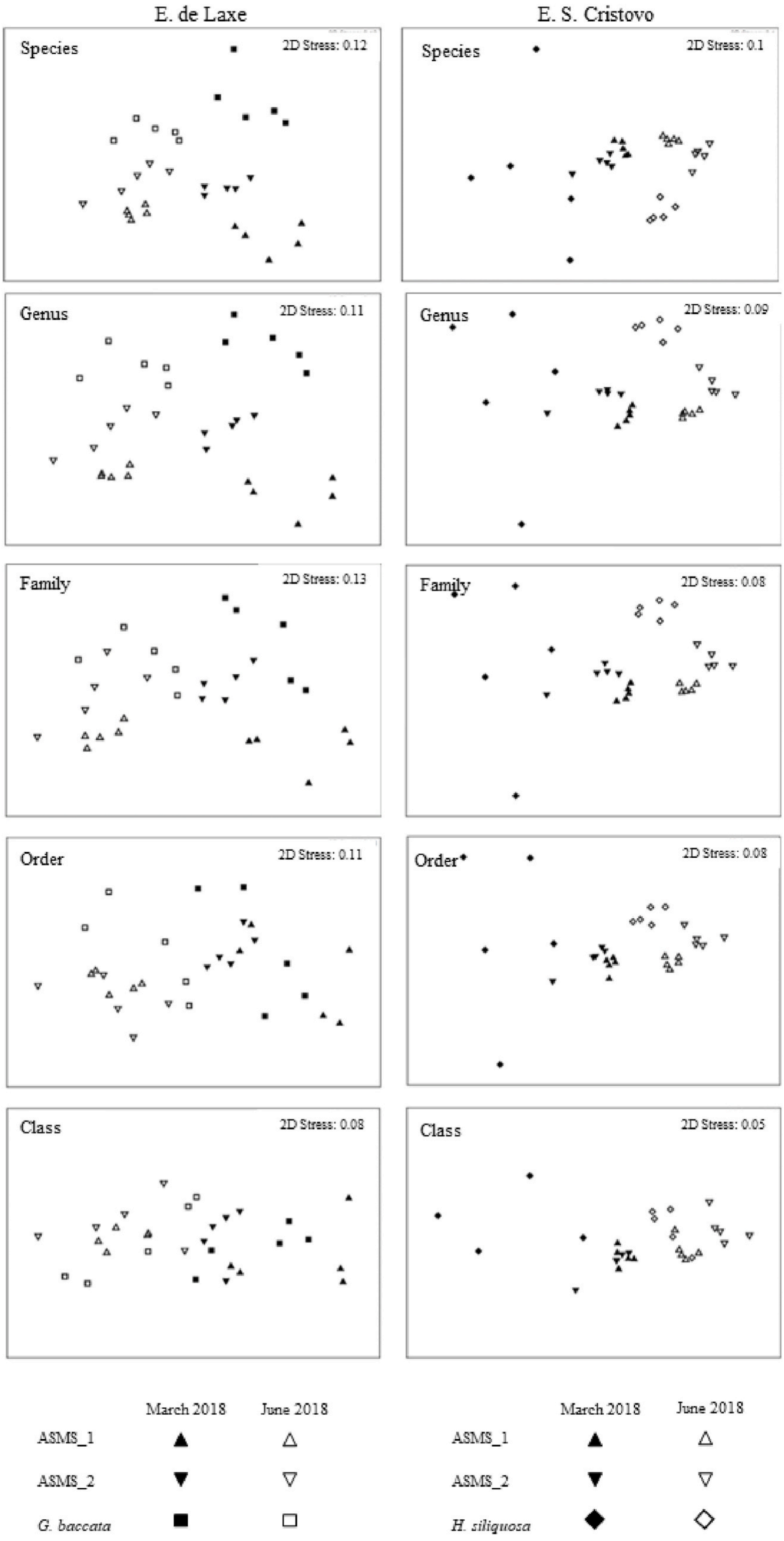

Fig. 6. Non-metric multidimensional scaling (nMDS) plot of epifaunal assemblages of ASMS1 and ASMS 2 compared with natural assemblages of *G. baccata* at Enseada de Laxe and *H. siliquosa* at Enseada de San Cristovo after 3 months of colonization (March 2018) and 6 months of colonization (June 2018) at different taxonomic resolutions using Dataset 1.

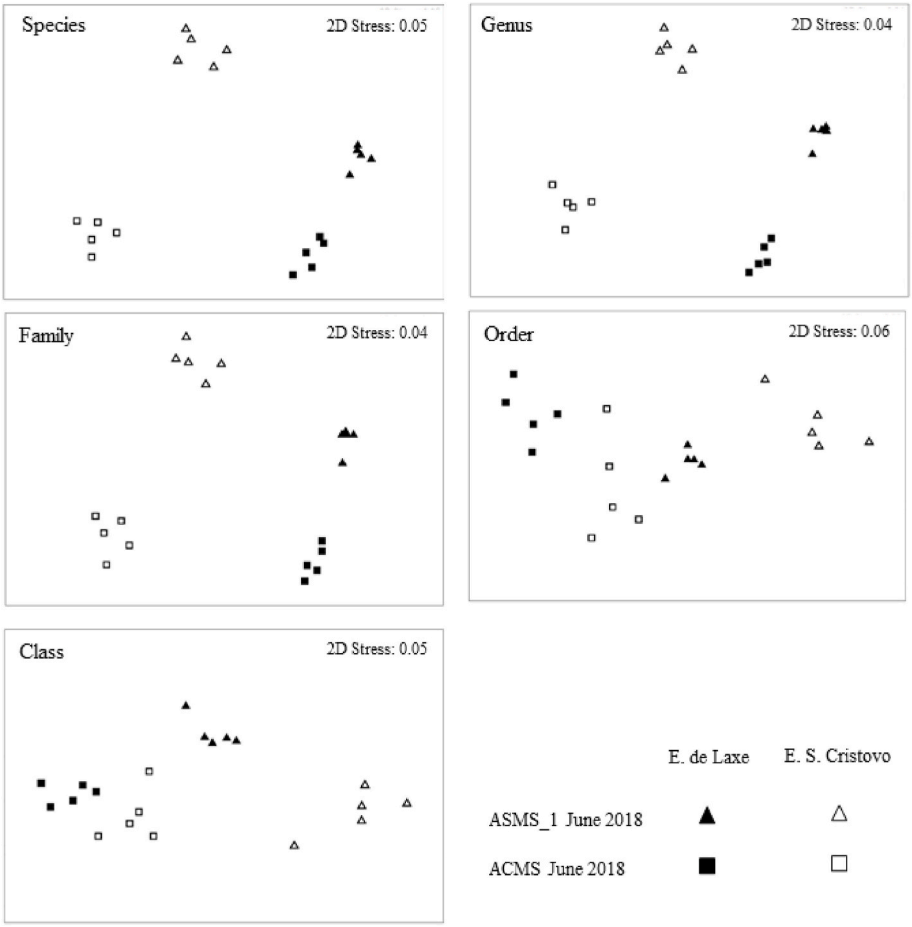

Fig. 7. Non-metric multidimensional scaling (nMDS) plot of epifaunal assemblages of ASMS1 and ACMS at Enseada de Laxe and Enseada de San Cristovo after 3 months of colonization (June 2018) at different taxonomic resolutions using Dataset 2.

in cases where achieving precise species identification is more complicated than narrowing down to the genus or family level. Species identification is inherently more susceptible to errors, and applying TS could enhance the overall accuracy of this process, primarily when identification is not performed by or under the expertise of taxonomic specialists for each group. This is particularly challenging in monitoring studies involving numerous taxonomic groups, making it difficult to achieve excellence across all macrobenthic groups. In specific scenarios, prioritizing a well-identified genus or family over attempting uncertain species identification may prove more prudent, preventing the introduction of potential errors within the scientific community (Ellis, 1985), and from a biological and statistical point of view the limitation of identification to higher levels may be preferable to incorrect species identification (Green, 1979).

Future investigations might explore hybrid approaches that combine TS with targeted molecular analyses to overcome these limitations. Combining the efficiency of TS with the detailed species-level information provided by molecular analyses could offer a more holistic perspective on biodiversity. This approach leverages the cost-effective benefits of TS at the family level while incorporating precise and detailed genetic information from molecular analyses, enhancing our ability to detect and understand subtle ecological patterns. Researchers are encouraged to explore these synergies to improve the comprehensiveness of biodiversity assessments, combining classical taxonomy with integrated taxonomy. Future research endeavors may also delve into the potential variations in the effectiveness of taxonomic sufficiency at different spatial and temporal scales, addressing existing gaps in the current literature.

5. Conclusions

This study aims to unravel the efficiency of TS used in benthic monitoring studies applicable across diverse geographical and time scales, utilizing artificial substrates. Our exploration confirms that the family level emerged as a pragmatic compromise, balancing precision and taxonomic effort favorably. The cost/benefit ratio analysis also supported the efficacy of TS, emphasizing the stability of correlation values between species-genus and species-family levels. Our results also showed that the reduction in taxonomic resolution to the family level does not entail a significant Loss of Information since, considering abundance data, relative abundance remains constant despite the aggregation of taxa to higher levels. However, it is essential to recognize that the foundation of monitoring studies lies at the species level. This means that initial reference data should be collected at the species level to establish a baseline. Once this baseline is established, the TS method can be applied effectively, reducing identification time and monitoring costs while maintaining robust ecological assessments. Additionally, the effectiveness of the TS method should be tested across different spatial and temporal scales to ensure its reliability before widespread application in monitoring programs based on AS. This consideration ensures that applying the TS approach aligns with the broader goals of comprehensive biodiversity assessments and effective coastal ecosystem management.

Financial support

This work was supported by the “Contrato-Programa” UIDB/04050/

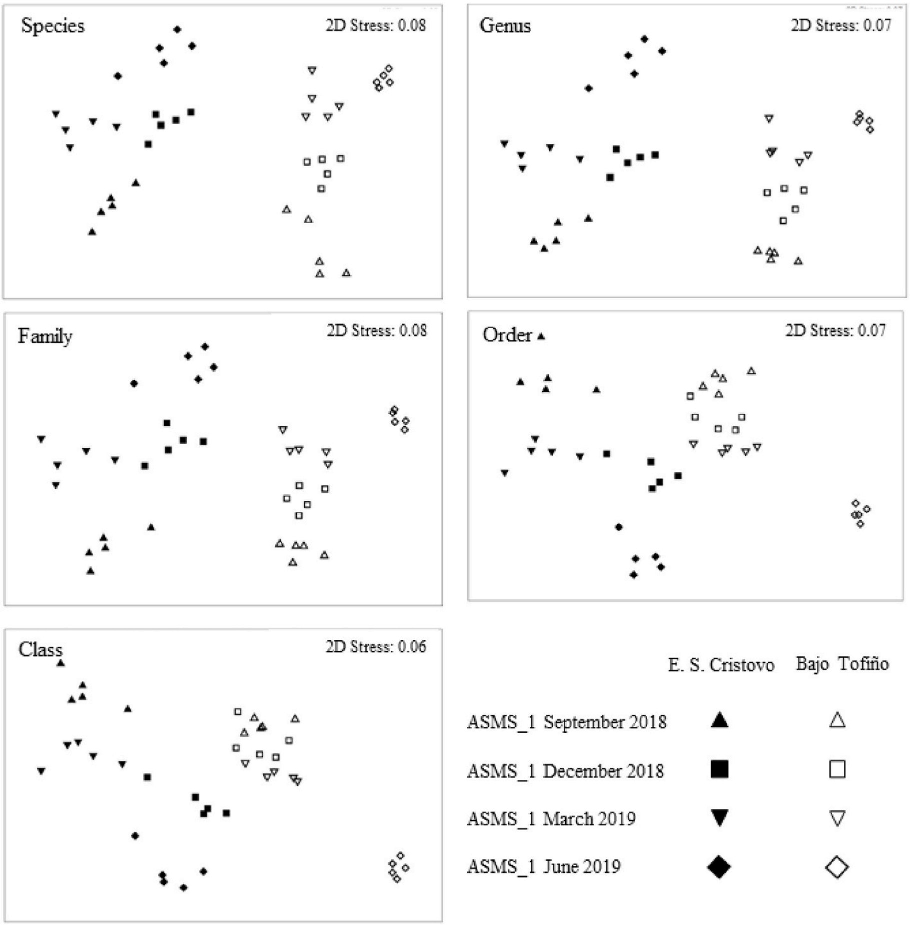

Fig. 8. Non-metric multidimensional scaling (nMDS) plot of epifaunal assemblages of ASMS 1 at Enseada de San Cristovo and Bajo Tofiño after 3 months of colonization (September 2018), 6 months (December 2018), 9 months (March 2019) and 12 months (June 2019) at different taxonomic resolutions using Dataset 3.

2020 (https://doi.org/10.54499/UIDB/04050/2020) and under the project UIDB/04033/2020 (https://doi.org/10.54499/UIDB/04033/2020), both funded by national funds through the FCT I.P. This work was also supported by ARNET (https://doi.org/10.54499/LA/P/0069/2020).

CRediT authorship contribution statement

Diego Carreira-Flores: Writing – original draft, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Marcos Rubal:** Writing – review & editing, Validation, Formal analysis, Conceptualization. **Edna Cabecinha:** Writing – review & editing, Supervision, Conceptualization. **Guillermo Díaz-Agras:** Writing – review & editing, Supervision, Conceptualization. **Pedro T. Gomes:** Writing – review & editing, Validation, Supervision, Methodology, Investigation, Conceptualization.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data availability

Data will be made available on request.

Acknowledgments

We would like to acknowledge the three anonymous reviewers, as well as the editor, for all the helpful comments and suggestions, which greatly improved this paper.

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